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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:47:09 : Search time 44.1552 Seconds
(without alignments)
129.360 Million cell updates/sec

Title: US-09-662-293-7

Perfect score: 64

Sequence: 1 DKONYLALVRELK 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 897420

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: A_Geneseq_21:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	100.0	13	3	AAV52516 House dus
2	64	100.0	13	5	AAU96320 Der HMM-m
3	35	54.7	16	2	AAW45120 Human car
4	31	48.4	21	5	AD180376 Human leu
5	30	46.9	13	3	AAV98022 HLA class
6	30	46.9	13	7	ADM33519 HLA bindi
7	30	46.9	13	7	ADM34752 HLA bindi
8	30	46.9	13	2	AAK60745 Lolium pe
9	30	46.9	16	7	ADM35806 HLA bindi
10	30	46.9	16	7	ADM34573 HLA bindi
11	29	45.3	20	4	AAW97099 Peptide F
12	29	45.3	10	4	AAW42730 Mycoplasma
13	29	45.3	16	2	AAW45121 Human car
14	28	43.8	10	4	AAW95826 Human com
15	28	43.8	12	6	ABP68019 Bacillus
16	28	43.8	13	6	ABP68026 Bacillus
17	28	43.8	15	8	ADJ38607 HSV-4 BFL
18	28	43.8	15	8	ADJ38608 HSV-4 BFL
19	28	43.8	16	3	AAAR41980 Human T C
20	28	43.8	16	3	AAV51484 Human TRF
21	28	43.8	16	3	AAAB28946 Peptide C
22	28	43.8	16	3	AAV90112 Cat TRFP
23	28	43.8	16	3	AAV87687 Feline hu
24	28	43.8	17	7	ADD94191 Mouse HUT

25	28	43.8	17	8	ADT94021	Adt94021 rFel d 1 (
26	28	43.8	17	9	ADM77438	Adm77438 Human pla
27	28	43.8	19	2	AAAR41978	AAar41978 Human T c
28	28	43.8	19	2	AAAR36545	AAar36545 Peptide A
29	28	43.8	19	3	AAV51482	AAv51482 Human TRF
30	28	43.8	19	3	AAAB28944	AAb28944 Peptide A
31	28	43.8	19	3	AAV90110	AAv90110 Cat TRFP
32	28	43.8	19	3	AAV87685	AAv87685 Feline hu
33	28	43.8	20	2	AAAR41982	AAar41982 Human T c
34	28	43.8	20	2	AAAR36547	AAar36547 Peptide C
35	28	43.8	20	2	AAAD265094	AAa265094 Haemophil
36	27	42.2	10	9	ADX39028	ADx39028 Amyloidosis
37	27	42.2	11	3	AAV51511	AAv51511 Human TRF
38	27	42.2	11	3	AAAB28970	AAb28970 Peptide e
39	27	42.2	11	3	AAV90128	AAv90128 TRFP deri
40	27	42.2	11	3	AAV87714	AAv87714 Feline hu
41	27	42.2	11	8	ADV25368	ADv25368 Human ATI
42	27	42.2	13	2	AAAR94334	AAar94334 Anti-ethro
43	27	42.2	15	2	AAAR60741	AAar60741 Lolium pe
44	27	42.2	15	2	AAAR60742	AAar60742 Lolium pe
45	27	42.2	15	7	ADM35287	Adm35287 HLA bindi
46	27	42.2	15	7	ADM34054	Adm34054 HLA bindi
47	27	42.2	16	2	AAW40941	AAw40941 Cryptic p
48	27	42.2	16	2	AAV25530	AAv25530 Human MHC
49	27	42.2	16	7	ADC34823	ADc34823 Cat aller
50	27	42.2	16	8	ADM12206	Adm12206 MHC class
51	27	42.2	16	8	ADO38424	ADo38424 Cat aller
52	27	42.2	16	8	ADQ26736	ADq26736 Topo V Hh
53	27	42.2	20	2	AAV11500	AAv11500 Human 5'
54	27	42.2	21	2	AAW35818	AAw35818 Human Prb
55	27	42.2	21	5	AD180351	AD180351 Human leu
56	27	42.2	21	5	AD180351	AD180351 Human leu
57	27	42.2	21	5	AD180343	AD180343 Human leu
58	27	42.2	21	5	AD180347	AD180347 Human leu
59	27	42.2	21	5	AD180348	AD180348 Human leu
60	27	42.2	21	5	AD180345	AD180345 Human leu
61	27	42.2	21	5	AD180326	AD180326 Human leu
62	27	42.2	21	5	AD180355	AD180355 Human leu
63	27	42.2	21	5	AD180371	AD180371 Human leu
64	27	42.2	21	5	AD180354	AD180354 Human leu
65	26	40.6	10	4	AAAG87550	AAag87550 Saccharom
66	26	40.6	10	4	AAAG87551	AAag87551 Saccharom
67	26	40.6	11	8	ADV25385	ADv25385 Human som
68	26	40.6	11	8	ADV25369	ADv25369 Human bra
69	26	40.6	11	8	AEAR45034	AEa45034 Apolipop
70	26	40.6	12	7	ADG85031	ADg85031 Phage dis
71	26	40.6	13	3	AAV99111	AAv99111 HLA class
72	26	40.6	13	6	ABP68022	ABp68022 Bacillus
73	26	40.6	14	9	ADV57875	ADv57875 G protein
74	26	40.6	14	9	ADV58630	ADv58630 G protein
75	26	40.6	14	9	ADV59434	ADv59434 G protein
76	26	40.6	15	4	AAW98979	AAw98979 Vaccine r
77	26	40.6	15	4	AAAB45751	AAab45751 Human Zal
78	26	40.6	15	4	AAAB89578	AAab89578 HIV gp120
79	26	40.6	15	4	AAAB89577	AAab89577 HIV gp120
80	26	40.6	15	4	AAAB89579	AAab89579 HIV gp120
81	26	40.6	15	8	ADG42415	ADg42415 Human Zal
82	26	40.6	16	6	ABP82426	ABp82426 G protein
83	26	40.6	16	6	ABP83583	ABp83583 G protein
84	26	40.6	17	2	AAAR3663	AAar3663 HIV princ
85	26	40.6	17	8	ADM19017	ADm19017 HLA-DR bo
86	26	40.6	17	8	ADM19032	ADm19032 HLA-DR bo
87	26	40.6	18	4	AAAB89626	AAab89626 HIV gp120
88	26	40.6	18	4	AAAB89624	AAab89624 HIV gp120
89	26	40.6	18	4	AAAB89625	AAab89625 HIV gp120
90	26	40.6	20	5	AAU85583	AAu85583 Lung tumo
91	26	40.6	20	5	AAU70993	AAu70993 M. tuberc
92	26	40.6	20	6	ABU65555	ABu65555 Human lun
93	26	40.6	20	6	ABU66458	ABu66458 Lung can
94	26	40.6	20	7	ADH47370	ADh47370 Human lun
95	26	40.6	20	8	ADJ21289	ADj21289 Human lun
96	26	40.6	20	9	AEBO7909	AEb07909 Peptide b
97	26	40.6	21	4	AAAB89492	AAab89492 HIV gp120

98	26	40.6	21	4	AAB89193	AAB89193	HIV	gp120
99	26	40.6	21	4	AAB89491	AAB89491	HIV	gp120
100	26	40.6	21	4	AAB89192	AAB89192	HIV	gp120

ALIGNMENTS

RESULT 1

AAV52516
ID AAV52516 standard; peptide; 13 AA.

AC AAV52516;

XX 22-FEB-2000 (first entry)

DE House dust mite allergen protein (map) A/B fragment map(6).

XX Mite allergen protein; map; high molecular weight; HMW-map; allergy;

KW house dust mite; IGE; immunoglobulin E; allergen; mapA; mapB;

KM hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;

XX canine; veterinary; antibody; vaccine; immunisation.

XX Dermacophagoides farinae.

XX MO9954349-A2.

XX 28-OCT-1999.

XX 16-APR-1999; 99WO-US008524.

XX 17-APR-1998; 98US-00062013.

XX 13-MAY-1998; 98US-0085295P.

XX 02-SEP-1998; 98US-0089309P.

XX (HESK-) HESKA CORP.

XX Mccall CA, Hunter SW, Weber ER;

XX WPI; 2000-052700/04.

XX Novel high molecular weight Dermatophagoides nucleic acid polypeptides

XX used to modify an animals' hypersensitivity to mite allergens.

XX Claim 3; Page 69; 154pp; English.

XX Sequences AAV52510-V52522 represent proteolytic fragments of

CC Dermacophagoides farinae high molecular weight mite allergen protein (HM

CC -map) composition. The HMW-map composition was isolated from a D. farinae

CC homogenate by gel filtration, with each fraction being analysed for the

CC presence of proteins that bound to IGE present in mite-allergic dog

CC antisera. The HMW-map composition comprises mapA (a 109 kD protein) and

CC mapB (98 kD). Mite allergenic proteins and peptides, and nucleic acids

CC encoding them, may be used in therapeutic compositions to modify an

CC animal's hypersensitivity reaction to mite allergens. Animals that may be

CC treated include mammals and birds, especially felines, canines, equines,

CC humans, other pets, and work or domestic animals. The proteins or

CC fragments may also be used to diagnose allergies via a skin test. The

CC proteins and peptides can also be used to raise antibodies, which have a

CC variety of potential uses. For example, they can be used as vaccines to

CC passively immunise animals against dust mite hypersensitivity, as

CC positive controls in test kits and as tools to recover desired dust mite

CC allergens from a mixture of proteins

XX Sequence 13 AA;

XX Query Match 100.0%; Score 64; DB 3; Length 13;

XX Best Local Similarity 100.0%; Pred. No. 0.00013;

XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DKONYLALVRELK 13

DB 1 DKONYLALVRELK 13

RESULT 2
AAU96320
ID AAU96320 standard; peptide; 13 AA.

AC AAU96320;

XX 15-JUL-2002 (first entry)

DE Der HMW-map polypeptide #7.

XX Der HMW-map; American house dust mite; antiallergic; mite; IGE;

KW mite allergenic protein; immunoglobulin E; hypersensitivity;

KM immunocomplex formation.

XX Dermacophagoides farinae.

XX MO200222807-A2.

XX 21-MAR-2002.

XX 14-SEP-2001; 2001WO-US028730.

XX 14-SEP-2000; 2000US-00662293.

XX (HESK-) HESKA CORP.

XX Mccall CA, Hunter SW, Weber ER;

XX WPI; 2002-351888/38.

XX New mite allergenic protein isolated from Dermatophagoides, designated

XX Der HMW-map protein, useful as a vaccine for treating mite allergy.

XX Claim 12; Page 70; 161pp; English.

XX The invention relates to an isolated mite allergenic protein of

CC Dermacophagoides, designated Der HMW-map protein, and its related nucleic

CC acid. The Der HMW-map protein is useful for eliciting an immune response

CC against Der HMW-map protein. The protein or a reagent comprising a non-

CC proteinaceous epitope is useful for identifying an animal (e.g., dog,

CC cat) susceptible to or having an allergic response to a mite. A

CC therapeutic composition is useful for desensitising a host animal to an

CC allergic response to a mite. The DNA and protein can be used in the

CC detection of anti-Der HMW-map antibodies in animal fluids, and inhibition

CC of immunoglobulin (Ig) E or Der HMW-map protein activity associated with a

CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting

CC binding of proteins to IGE, to prevent immunocomplex formation, thus

CC reducing hypersensitivity responses to mite allergens, and as vaccines

CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342

CC represent Der HMW-map polypeptides of the invention

XX Sequence 13 AA;

XX Query Match 100.0%; Score 64; DB 5; Length 13;

XX Best Local Similarity 100.0%; Pred. No. 0.00013;

XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DKONYLALVRELK 13

DB 1 DKONYLALVRELK 13

RESULT 3

AAW45120

ID AAW45120 standard; peptide; 16 AA.

XX AAW45120;

XX 28-APR-1998 (first entry)

XX Human cartilage glycoprotein 39 derived peptide #21.

KW	Articular cartilage; immunosuppressive therapy; antigen; autoantigen;
KM	immunological tolerance; T-cell; human cartilage glycoprotein 39;
KM	HC gp-39; rheumatoid arthritis; epitope.
XX	
OS	Synthetic.
OS	Homo sapiens.
PN	MO9740068-A1.
PD	30-OCT-1997.
PE	22-APR-1997; 97WO-BP002051.
PR	24-APR-1996; 96EP-00201106.
PA	(ALKU) AKZO NOBEL NV.
Pt	Boots AMH, Verheljden GFM;
DR	WPJ, 1997-535775/49.
PT	Peptide suitable for use in antigen specific immunosuppressive therapy -
PT	resembles or mimics epitope present on HC-gp-39, so inducing systemic
PT	immunological tolerance to rheumatoid arthritis autoantigen.
XX	
PS	Disclosure; Page 16; 82pp; English.
XX	
CC	The present sequence represents a peptide which resembles or mimics an
CC	epitope present on human cartilage glycoprotein 39 (HC gp-39), an
CC	autoantigen in rheumatoid arthritis. The invention relates to peptides
CC	consisting of 16-55 amino acid residues comprising at least one of the
CC	following 19 sequences: LVCYYSMS; FLCTHLYS; IIVSPANS; LKTLISVG; FKSVSWPF; FQGLDIAWL; LYGRSRDK; YDIATISOH; LDFTSIMTY; FISIMTYDF; CFROEIDSP; VAVGYMLRL; MRLGAPAS; LAVEICDF; LRGVTVRT; YLKRDQLAG; LACAMVVAL; VWALDDDF; or LDLDRQS. They can be used medically in antigen
CC	specific immunosuppressive therapy, particularly the treatment of T-cell
CC	mediated destruction of articular cartilage in autoimmune diseases (e.g.
CC	rheumatoid arthritis). They can also be used to detect activated
CC	autoreactive T cells in an individual. The peptides have a specific
CC	effect on the autoreactive T cells, thus leaving the other components of
CC	the immune system intact, unlike the non-specific suppressive effect of
CC	immunosuppressive drugs, and do not cause toxic side effects. The
CC	peptides are predominantly recognised by autoreactive T cells from
CC	rheumatoid arthritis patients, but rarely by those from healthy donors
XX	
SO	Sequence 16 AA:
OY	Query Match 54.7%; Score 35; DB 2; Length 16;
Dn	Best Local Similarity 41.7%; Pred. No. 29;
	Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0,
	1 DKONTLAIVREL 12 :: ::
	5 DKOHTFLIKEM 16
ADIB0376 standard; peptide; 21 AA.	
ADI80376	
ADI80376;	
22-APR-2004 (first entry)	
Human leukocyte antigen A sub-type peptide region 110-130 group 15.	
Major Histocompatibility Complex; MHC; CD8; CD4; Immunosuppressive;	
antiidiabetic; antirheumatic; antiarthritic; neuroprotective;	
antiinflammatory; gene therapy; T cell response; autoimmune disorder;	
graft-versus-host disease; graft rejection; Rheumatoid arthritis;	
celiac disease; dermatitis herpetiformis; diabetes; multiple sclerosis;	
Crohn's disease; psoriasis; human leukocyte antigen.	

XX	Homo sapiens.
OS	Synthetic.
XX	
PN	WO200277030-A2.
XX	
PD	03-OCT-2002.
XX	
PJ	27-MAR-2002; 2002WO-GB001499.
XX	
PR	27-MAR-2001; 2001GB-00007628.
XX	
PA	(AVID-) AVIDEX LTD.
XX	
P1	Jakobsen BK, Cameron BJ;
DR	WPI, 2002-723521/78.
XX	
PT	New modified Major Histocompatibility Complex (MHC) molecule or nucleic acid encoding the MHC molecule, useful in medicine, particularly useful for treating autoimmune disorders, e.g. graft-versus-host disease or graft rejection.
PS	Disclosure: Fig 11; 107bp; English.
XX	
CC	The invention relates to a novel modified Major Histocompatibility Complex (MHC) molecule or a nucleic acid encoding the modified MHC molecule. The binding of the MHC molecule of a selected type to CD8 or CD4 is inhibited, but it can present the same peptide or peptides as unmodified molecules of the MHC type, which is for use in medicine. The invention further comprises: inhibiting the activity of T cells against a cell presenting molecules of a selected MHC type, by causing the cell to present modified molecules of the MHC type; a cell, which presents molecules of a selected MHC type and the modified molecules of the selected MHC subtype whose binding to CD8 or CD4 is inhibited, but which can present the same peptide or peptides as unmodified molecules of the MHC type; a nucleic acid molecule encoding the modified MHC molecules or its complementary sequence; a vector comprising the nucleic acid molecule ; and a host cell including the vector. The modified MHC molecule has the following activities: immunosuppressive, antidiabetic, antirheumatic, antiarthritic, neuroprotective, and antiinflammatory. The nucleic acid encoding the modified MHC molecule can be used in gene therapy to treat disorders. The modified MHC molecule, as well as the nucleic acid encoding the molecule, are useful in the manufacture of a medicament for inhibiting T cell response. The modified MHC molecule is particularly useful for treating an autoimmune disorder (which may be due to endogenous or exogenous etiology), graft-versus-host disease or graft rejection. These disorders also include rheumatoid arthritis, celiac disease, dermatitis herpetiformis, diabetes, multiple sclerosis, Crohn's disease, or psoriasis. This sequence represents a human leukocyte antigen polypeptide relating to the modified MHC molecule of the invention.
Sequence 21 AA:	
OY	1 DKONYLALVREL 12 : : Db 10 DGNVIALNEDL 21
Query Match	48.4%; Score 31; DB 5; Length 21;
Best Local Similarity	50.0%; Pred. No. 2.1e+02;
Matches	6; Conservative 3; Mismatches 3; Indels 0; Gaps 0,
RESULT 5	
AAAY9022	
ID	AAAY9022 standard; peptide: 13 AA.
XX	AAAY9022;
AC	
DT	07-AUG-2000 (first entry)
XX	
DE	HLA class II binding antigen epitope peptide #211.
XX	

KM Human leucocyte antigen: HLA class II; antigen epitope; pharmaceutical;
KM immune response; chronic viral disease; cancer; autoimmune disease;
KM rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS;
KM allograft rejection; allergy; Lyme disease; hepatitis; prostate cancer;
KM glomerulonephritis; food hypersensitivity; malaria.
XX
OS Unidentified.
XX
PN WO9961916-A1.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US012066.
XX
PR 29-MAY-1998; 98US-0087192P.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Southwood S, Sidney J;
XX
DR WPI; 2000-097143/08.
XX
PT New compositions containing immunogenic peptide epitopes for various HLA
XX
PS class II DR molecules useful for inducing helper T cell response.
XX
PS Claim 1; Page 43; 60pp; English.
XX
XX The present invention relates to a new pharmaceutical composition
XX comprising a unit dose form of a peptide, or analogue, comprising an
XX epitope selected from those represented by peptides MAY9812-Y99339 which
XX are derived from various antigens for various human leucocyte antigen
XX class DR molecules, representative of the world wide population. The
XX peptide/analogue binds to an HLA class II molecule at an IC-50 of less
XX than or equal to 1,000 nM. The pharmaceutical focuses the immune response
XX helper T cell response. The pharmaceutical focuses the immune response
XX towards selected determinants and could therefore be used in cases of
XX chronic viral diseases and cancer. Examples of diseases that can be
XX treated using the peptide containing pharmaceutical include autoimmune
XX diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia
XX gravis), allograft rejection, allergies, Lyme disease, hepatitis, post-
XX streptococcal endocarditis or glomerulonephritis and food
XX hypersensitivities. The peptide epitopes can be used to enhance immune
XX responses against other immunogens administered with the peptides.
XX Diseases which can be treated using immunogenic mixtures include prostate
XX cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical
XX carcinoma, lymphoma, and carcinoma acuminatum. The peptides may also be
XX used to make monoclonal antibodies useful as potential diagnostic or
XX therapeutic agents. The peptides may also be useful as diagnostic or
XX reagents, for example, to determine the susceptibility of an individual
XX to a treatment regimen. Also, the peptides may be used to predict which
XX individuals will be at substantial risk of developing chronic infection.
XX The selection of appropriate T and B cell epitopes should allow the
XX development of epitope based vaccines particularly towards conserved
XX epitopes of pathogens which are characterized by high sequence
XX variability such as HIV, HCV and Malaria
XX
SQ Sequence 13 AA;
XX
XX Query Match 46.9%; Score 30; DB 3; Length 13;
XX Best Local Similarity 85.7%; Pred. No. 1.9e+02;
XX Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 2 KONYIAL 8
XX |||||
Db 5 KONYLKL 11

RESULT 6
ADM33519
ID ADM33519 standard; peptide; 13 AA.
XX
XX ADM33519;
XX

DT 10-MAR-2005 (first entry)
XX
XX HLA binding epitope #4269.
XX
XX Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;
XX MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
XX viral disease; cancer.
XX
OS Unidentified.
XX
XX WO2003040165-A2.
XX
XX 15-MAY-2003.
XX
XX 18-OCT-2001; 2001WO-US051650.
XX
XX 19-OCT-2000; 2000US-0242350P.
XX
XX 20-APR-2001; 2001US-0285624P.
XX
XX (EPIM-) EPIMMUNE INC.
XX
XX Sette A, Sidney J, Southwood S;
XX
XX WPI; 2003-441519/41.
XX
XX New composition comprising at least one peptide having allele-specific
XX binding motifs for HLA, useful for preventing, treating or diagnosing
XX viral diseases and cancer.
XX
XX Claim 1; Page 52-379; 382pp; English.
XX
XX The invention relates to a composition comprising at least one peptide
XX having an isolated, prepared epitope selected from any of the sequences
XX from 30 lists given in the specification. Also disclosed is a method for
XX inducing a cytotoxic T cell response against a pre-selected antigen in a
XX patient expressing a specific MHC class I allele by contacting cytotoxic
XX T cells from the patient with the composition cited above. The
XX composition comprises an epitope that is joined by an amino acid linker.
XX The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
XX bound to an HLA molecule on the antigen-presenting cell, where when an A2
XX -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
XX binds to a complex of the HLA molecule and the epitope. Specifically
XX claimed are peptides having allele-specific binding motifs for HLA. The
XX compositions and methods are useful for preventing, treating or
XX diagnostic agents for viral diseases and cancer. The peptide epitopes are useful as
XX and for evaluating efficacy of a vaccine. Sequences given in ADM2951-
XX ADM37745 represent epitopes of the invention as given in Tables 2-31.
XX
SQ Sequence 13 AA;
XX
XX Query Match 46.9%; Score 30; DB 7; Length 13;
XX Best Local Similarity 85.7%; Pred. No. 1.9e+02;
XX Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 2 KONYIAL 8
XX |||||
Db 5 KONYLKL 11

RESULT 7
ADM34752
ID ADM34752 standard; peptide; 13 AA.
XX
XX ADM34752;
XX
XX 10-MAR-2005 (first entry)
XX
XX HLA binding epitope #5502.
XX
XX Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;
XX MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
XX viral disease; cancer.
XX

XX OS Unidentified.
 XX PN WO2003040165-A2.
 XX PD 15-MAY-2003.
 XX PF 18-OCT-2001; 2001WO-US051650.
 XX PR 19-OCT-2000; 2000US-0242350P.
 XX PR 20-APR-2001; 2001US-0285624P.
 XX PA (EPIM-) EPIMMUNE INC.
 XX PI Sette A, Sidney J, Southwood S;
 XX DR WPI; 2003-441519/41.
 XX PT New composition comprising at least one peptide having allele-specific
 PT binding motifs for HLA, useful for preventing, treating or diagnosing
 PT viral diseases and cancer.
 XX PS Claim 1; Page 52-379; 382pp; English.
 XX SQ The invention relates to a composition comprising at least one peptide
 CC having an isolated, prepared epitope selected from any of the sequences
 CC from 30 lists given in the specification. Also disclosed is a method for
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a
 CC patient expressing a specific MHC class I allele by contacting cytotoxic
 CC T cells from the patient with the composition cited above. The
 CC composition comprises an epitope that is joined by an amino acid linker.
 CC The epitope is admitted or joined to a CTL or HTL epitope. The epitope is
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
 CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
 CC binds to a complex of the HLA molecule and the epitope. Specifically
 CC claimed are peptides having allele-specific binding motifs for HLA. The
 CC compositions and methods are useful for preventing, treating or
 CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
 CC diagnostic agents for evaluating immune responses, for making antibodies
 CC and for evaluating efficacy of a vaccine. Sequences given in ADW329251-
 CC ADW37745 represent epitopes of the invention as given in Tables 2-31.
 XX SQ Sequence 13 AA;
 Query March 46.9%; Score 30; DB 7; Length 13;
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 2 KONTYLA 8
 Db 5 KONTYKL 11
 RESULT 8
 AAR60745
 ID AAR60745 standard; peptide: 15 AA.
 XX AC AAR60745;
 XX DT 25-MAR-2003 (revised)
 DT 01-JUN-1995 (first entry)
 XX DE Lolium perenne protein allergen internal sequence LPI-16-10.
 XX KM Lolium perenne protein allergen; Lol PI; ryegrass pollen allergen;
 KM Dac GI; Poa PI; Phl PI.
 XX OS Lolium perenne.
 XX PN WO9421675-A2.
 XX PD 29-SEP-1994.
 XX

PF 09-MAR-1994; 94WO-US002537.
 XX PR 12-MAR-1993; 93US-00031001.
 XX PA (IMMU-) IMMUNOLOGIC PHARM CORP.
 XX PI Griffith IJ, Kuo M, Lugman M, Powers S;
 XX DR WPI; 1994-316937/39.
 XX PT Isolated peptide(s) of Lol or P I, major protein allergen of species
 PT Lolium perenne. - useful for diagnosis and treatment of sensitivity to
 PT rye-grass pollen allergen.
 XX PS Claim 2; Fig 4; 125pp; English.
 XX CC AAQ73596 is the PCR generated full length clone c26j, which encodes Lol
 CC PI (AAR60703) a major protein allergen of Lolium perenne (ryegrass).
 CC Internal peptides isolated from Lol PI, which contain at least one T cell
 CC epitope are described in AAR60710-R60757. These peptides can be used in
 CC the treatment and diagnosis of sensitivity to ryegrass pollen protein, or
 CC pollen proteins that are immunologically related to Lol PI e.g. Dac GI,
 CC Phl PI and Poa PI. (updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 15 AA;
 Query March 46.9%; Score 30; DB 2; Length 15;
 Best Local Similarity 55.6%; Pred. No. 2.2e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 OY 1 DKONTYLA 9
 Db 1 DEPNYLA 9
 RESULT 9
 ADW35806
 ID ADW35806 standard; peptide: 16 AA.
 XX AC ADW35806;
 XX DT 10-MAR-2005 (first entry)
 XX DE HLA binding epitope #6556.
 XX KM Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;
 KM MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
 KM viral disease; cancer.
 XX OS Unidentified.
 XX PN WO2003040165-A2.
 XX PD 15-MAY-2003.
 XX PF 18-OCT-2001; 2001WO-US051650.
 XX PR 19-OCT-2000; 2000US-0242350P.
 PR 20-APR-2001; 2001US-0285624P.
 XX PA (EPIM-) EPIMMUNE INC.
 XX PI Sette A, Sidney J, Southwood S;
 XX DR WPI; 2003-441519/41.
 XX PT New composition comprising at least one peptide having allele-specific
 PT binding motifs for HLA, useful for preventing, treating or diagnosing
 PT viral diseases and cancer.
 XX PS Claim 1; Page 52-379; 382pp; English.
 XX SQ The invention relates to a composition comprising at least one peptide

RESULT 12
AAM42730
ID AAM42730 standard; peptide; 10 AA.
XX
AC AAM42730;
XX
DT 22-OCT-2001 (first entry)
DE Mycoplasma genitalium intermolecular complementary peptide, SEQ ID 39.
XX
KM Mycoplasma genitalium; complementary peptide; ligand;
XX protein-protein interaction; drug design; intermolecular; intramolecular.
OS Mycoplasma genitalium.
XX
PN WO200142278-A2.
XX
PD 14-JUN-2001.
XX
PF 13-DEC-2000; 2000WO-GB004778.
XX
PR 13-DEC-1999; 99GB-00029466.
XX
PA (PROT-) PROTEOM LTD.
XX
PI Roberts GW, Heal JR;
XX
DR WPI; 2001-514238/56.
XX
PT Complementary peptide ligands as reagents and drugs for drug discovery
XX programs and as lead ligands to facilitate drug design and development,
XX are generated from microbial genome sequences.
PS Example 2; Page 55; 161pp; English.
XX
CC The present sequence is one of a large number of complementary peptide
CC ligands generated from Mycoplasma genitalium genome sequences. These
CC specific complementary peptides interact with their relevant target
CC proteins encoded by the microbial genome. They are capable of
CC antagonizing or agonising specific interaction of a protein with another
CC protein or receptor and are thus useful as reagents and drugs, and as
CC lead ligands to facilitate drug design and development. They are useful
CC as tools for functional genomic studies, reagents for the configuration
CC of high-throughput screens, as a starting point for medicinal chemistry
CC manipulation, for peptide mimetics and as therapeutic agents. The
CC analysis and acquisition of peptide sequences facilitates understanding
CC of protein-protein interactions. The method allows for analysis of an
CC entire database at a time, thus overcoming sampling problems. The set of
CC complementary peptides includes both intermolecular (between proteins)
CC and intermolecular (within a protein) sequences
XX
SQ Sequence 10 AA;
XX
Query Match 45.3%; Score 29; DB 4; Length 10;
Best Local Similarity 55.6%; Pred. NO. 2.1e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
OY 5 YLALVRELK 13
DB 1 FLSLVKEVK 9
XX
RESULT 13
AAM45121
ID AAM45121 standard; peptide; 16 AA.
XX
AC AAM45121;
XX
DT 28-APR-1998 (first entry)
XX
DE Human cartilage glycoprotein 39 derived peptide #22.

XX
KM Articular cartilage; immunosuppressive therapy; antigen; autoantigen;
KM Immunological tolerance; T-cell; human cartilage glycoprotein 39;
KM HC gp-39; rheumatoid arthritis; epitope.
XX
OS Synthetic.
OS Homo sapiens.
XX
EN WO9740068-A1.
XX
PD 30-OCT-1997.
XX
PF 22-APR-1997; 97WO-EP002051.
XX
PR 24-APR-1996; 96EP-00201106.
XX
PA (ALKU) AKZO NOBEL NV.
XX
PI Boots AMH, Verheijden GFW;
XX
DR WPI; 1997-535775/49.
XX
PT Peptide suitable for use in antigen specific immunosuppressive therapy -
XX resembles or mimics epitope present on HC gp-39, so inducing systemic
XX immunological tolerance to rheumatoid arthritis autoantigen.
PS Disclosure; Page 16; 82pp; English.
XX
CC The present sequence represents a peptide which resembles or mimics an
CC epitope present on human cartilage glycoprotein 39 (HC gp-39), an
CC autoantigen in rheumatoid arthritis. The invention relates to peptides
CC consisting of 16-55 amino acid residues comprising at least one of the
CC following 19 sequences: LVCYTWS; FLCTHITS; IITSFNIS; LKTLSSVG;
CC FKSVPFL; EDGDLAWL; LYPGRADQ; YDIAKISQ; LDFISMTY; FLSMTYDF;
CC FRGOEDASP; YAVGYMLL; MLRIGAPAS; LAYEICDF; LRGAIVHT; YLKDROLAG;
CC LAGAWMAL; VWALDLPDF; or LDLDPOGS. They can be used medically in antigen
CC specific immunosuppressive therapy, particularly the treatment of T-cell
CC mediated destruction of articular cartilage in autoimmune diseases (e.g.
CC rheumatoid arthritis). They can also be used to detect activated
CC autoreactive T cells in an individual. The peptides have a specific
CC effect on the autoreactive T cells, thus leaving the other components of
CC the immune system intact, unlike the non-specific suppressive effect of
CC immunosuppressive drugs, and do not cause toxic side effects. The
CC peptides are predominantly recognised by autoreactive T cells from
CC rheumatoid arthritis patients, but rarely by those from healthy donors
XX
SQ Sequence 16 AA;
XX
Query Match 45.3%; Score 29; DB 2; Length 16;
Best Local Similarity 36.4%; Pred. NO. 3.6e+02;
Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
OY 3 QNYALVRELK 13
DB 1 QHFTLLIKEMK 11
XX
RESULT 14
AAG95826
ID AAG95826 standard; peptide; 10 AA.
XX
AC AAG95826;
XX
DT 18-SEP-2001 (first entry)
XX
DE Human complementary peptide, SEQ ID NO: 2020.
XX
KM Human; complementary peptide; ligand; drug discovery; drug design.
XX
OS Homo sapiens.
XX
PN WO200142277-A2.
XX

PD 14-JUN-2001.
XX 13-DEC-2000; 2000WO-GB004776.
XX 13-DEC-1999; 99GB-00029464.
XX (PROT-) PROTEOM LTD.
XX Robert G, Heal JR;
XX WPI; 2001-408419/43.
XX
XX A set of peptide ligands consisting of specific complementary peptides to
XX proteins encoded by genes of the human genome, useful in an assay for
XX screening and identifying of one or more novel peptides which are drug
XX candidates or pro-drugs.
XX
XX Example 4; Page 332; 646pp; English.
XX
XX The invention relates to a set of complementary peptide ligands generated
XX from the human genome. The complementary peptides interact with their
XX relevant target proteins encoded in the human genome. They can be used as
XX reagents in drug discovery and as lead ligands to facilitate drug design
XX and development. The present sequence is a complementary peptide provided
XX in the specification
XX
XX Sequence 10 AA:
SQ

Query Match 43.8%; Score 28; DB 4; Length 10;
Best Local Similarity 62.5%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DKONYLAL 8
| : : | | | |
DB 2 DEERYLAL 9

RESULT 15
ABP68019
ID ABP68019 standard; peptide; 12 AA.
XX
XX ABP68019;
XX
XX 08-JAN-2003 (first entry)
XX
XX Bacillus thuringiensis toxin Cry related peptide #12.
XX
XX Bacillus thuringiensis; insecticide; toxin; Cry; pepsin cleavage site;
XX pepsin; PCS.
XX
XX Bacillus thuringiensis.
XX Synthetic.
XX
XX FR2822157-A1.
XX
XX 20-SEP-2002.
XX
XX 19-MAR-2001; 2001FR-00003691.
XX
XX 19-MAR-2001; 2001FR-00003691.
XX
XX (AVET) AVENTIS CROPS SCIENCE SA.
XX
XX Freysinet G, Rang C, Frutos R;
XX WPI; 2003-002439/01.
XX
XX New modified Cry protein, useful as insecticide, comprises at least one
XX additional pepsin cleavage site to reduce persistence in mammalian gut.
XX
XX Example 2; Page 21; 134pp; French.
XX
XX The present invention describes a modified Cry protein (I) that is

CC sensitive to pepsin and comprises at least one additional pepsin cleavage
CC site (PCS). Also described: (a) increasing pepsin sensitivity of Cry
CC proteins by incorporating at least one extra PCS; (b) polynucleotides
CC (II) that encode (I); (c) chimeric genes (CG) that contain a promoter,
CC (II) and terminator; (d) expression or transformation vector (III) that
CC contains CG; (e) host organism (IV) transformed with (III), also, where
CC the organism is a plant, its parts and seeds; (f) production of (I) by
CC growing (IV); and (g) mono- or polyclonal antibodies (Ab) directed
CC against (I). (I) has insecticide activity. (I) can be used as
CC insecticides, particularly where expressed in transgenic plants. (I) are
CC sensitive to enzymes in the digestive tract of mammals, so do not persist
CC in the tract (lack of persistence is required by regulatory authorities
CC for use, in foods, of seeds containing Cry proteins). Extra PCS do not
CC increase degradation in the digestive tract of insects, so have no effect
CC on insecticidal activity. ABV93450 to ABV93909 and ABP67997 to ABP68308
CC represent sequences used in the exemplification of the present invention
XX
XX Sequence 12 AA:
SQ

Query Match 43.8%; Score 28; DB 6; Length 12;
Best Local Similarity 60.0%; Pred. No. 4e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 QNYLALVREL 12
| : : | : | |
DB 1 QNYLALREL 10

RESULT 16
ABP68026
ID ABP68026 standard; peptide; 13 AA.
XX
XX ABP68026;
XX
XX 08-JAN-2003 (first entry)
XX
XX Bacillus thuringiensis toxin Cry related peptide #19.
XX
XX Bacillus thuringiensis; insecticide; toxin; Cry; pepsin cleavage site;
XX pepsin; PCS.
XX
XX Bacillus thuringiensis.
XX Synthetic.
XX
XX FR2822157-A1.
XX
XX 20-SEP-2002.
XX
XX 19-MAR-2001; 2001FR-00003691.
XX
XX 19-MAR-2001; 2001FR-00003691.
XX
XX 19-MAR-2001; 2001FR-00003691.
XX
XX (AVET) AVENTIS CROPS SCIENCE SA.
XX
XX Freysinet G, Rang C, Frutos R;
XX WPI; 2003-002439/01.
XX
XX New modified Cry protein, useful as insecticide, comprises at least one
XX additional pepsin cleavage site to reduce persistence in mammalian gut.
XX
XX Example 2; Page 21; 134pp; French.
XX
XX The present invention describes a modified Cry protein (I) that is
XX sensitive to pepsin and comprises at least one additional pepsin cleavage
XX site (PCS). Also described: (a) increasing pepsin sensitivity of Cry
XX proteins by incorporating at least one extra PCS; (b) polynucleotides
XX (II) that encode (I); (c) chimeric genes (CG) that contain a promoter,
XX (II) and terminator; (d) expression or transformation vector (III) that
XX contains CG; (e) host organism (IV) transformed with (III), also, where
XX the organism is a plant, its parts and seeds; (f) production of (I) by
XX growing (IV); and (g) mono- or polyclonal antibodies (Ab) directed
XX against (I). (I) has insecticide activity. (I) can be used as

insecticides, particularly where expressed in transgenic plants. (1) are sensitive to enzymes in the digestive tract of mammals, so do not persist in the tract (lack of persistence is required by regulatory authorities for use, in foods, of seeds containing Cry proteins). Extra PCS do not increase degradation in the digestive tract of insects, so have no effect on insecticidal activity. ABV93450 to ABV93909 and ABP67997 to ABP68308 represent sequences used in the exemplification of the present invention

Sequence 13 AA;

Query Match 43.8%; Score 28; DB 6; Length 13;
Best Local Similarity 60.0%; Pred. No. 4.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 3 NYTALVREL 12
|||:|
Db 1 QNWLALEEL 10

RESULT 17

ADJ38607
ID ADJ38607 standard; peptide, 15 AA.

AC ADJ38607;

DT 06-MAY-2004 (first entry)

DE HSV-4 BFLF2 protein late domain motif mutant peptide #6.

KM Virucide; HSV infection; antiviral; late domain motif; mutein; mutant.

OS Human herpesvirus 4.

OS Synthetic.

FT Key Location/Qualifiers

FT Misc-difference 8 /note= "Wild-type residue replaced with Ala"

XX WO2004009027-A2.

XX 29-JAN-2004.

XX 21-JUL-2003; 2003WO-US022828.

XX 19-JUL-2002; 2002US-0397265P.

XX 19-JUL-2002; 2002US-0397477P.

XX 19-JUL-2002; 2002US-0397479P.

XX 03-MAR-2003; 2003US-0451903P.

XX (MYRI-) MYRIAD GENETICS INC.

XX Morham S, Zavitz K, Hobden A;

XX WPI; 2004-123282/12.

XX Example 14; Page 68; 74pp; English.

The present invention relates to cells displaying herpes simplex virus (HSV) altered budding phenotype which are useful for the manufacture of a medicament for treating HSV infection. The medicament further comprises an adjuvant capable of stimulating cellular immune response e.g. IL-2, IL-4, IL-12, IL-18 or gamma-interferon. The cells are human cells and contain a nucleic acid encoding a mutant HSV protein or a nucleic acid encoding the polypeptide sufficient for virus-like particle assembly but devoid of late-domain motifs. The nucleic acid is within an HSV genome. The genome is devoid of late domain motifs capable of effecting viral budding. The composition also comprises a compound capable of interfering with the protein-protein interaction between a host cell protein capable of binding a late domain motif and a HSV protein containing a late domain motif. The composition further comprises another HSV protein or its motif. The composition further comprises another HSV protein or its

immunogenic fragment, and/or a nucleic acid encoding the other HSV protein or the immunogenic fragment. The present sequence is a mutant HSV peptide, derived from the wild-type peptide ADJ38601, used to illustrate the invention.

Sequence 15 AA;

Query Match 43.8%; Score 28; DB 8; Length 15;
Best Local Similarity 60.0%; Pred. No. 5.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 4 NYTALVRELK 13
|||:|
Db 5 NYTALILENK 14

RESULT 18

ADJ38608
ID ADJ38608 standard; peptide, 15 AA.

AC ADJ38608;

DT 06-MAY-2004 (first entry)

DE HSV-4 BFLF2 protein late domain motif mutant peptide #7.

KM Virucide; HSV infection; antiviral; late domain motif; mutein; mutant.

OS Human herpesvirus 4.

OS Synthetic.

FT Key Location/Qualifiers

FT Misc-difference 7.8 /note= "Wild-type residues replaced with Ala Ala"

XX WO2004009027-A2.

XX 29-JAN-2004.

XX 21-JUL-2003; 2003WO-US022828.

XX 19-JUL-2002; 2002US-0397265P.

XX 19-JUL-2002; 2002US-0397477P.

XX 19-JUL-2002; 2002US-0397479P.

XX 03-MAR-2003; 2003US-0451903P.

XX (MYRI-) MYRIAD GENETICS INC.

XX Morham S, Zavitz K, Hobden A;

XX WPI; 2004-123282/12.

XX Example 14; Page 68; 74pp; English.

The present invention relates to cells displaying herpes simplex virus (HSV) altered budding phenotype which are useful for the manufacture of a medicament for treating HSV infection. The medicament further comprises an adjuvant capable of stimulating cellular immune response e.g. IL-2, IL-4, IL-12, IL-18 or gamma-interferon. The cells are human cells and contain a nucleic acid encoding a mutant HSV protein or a nucleic acid encoding the polypeptide sufficient for virus-like particle assembly but devoid of late-domain motifs. The nucleic acid is within an HSV genome. The genome is devoid of late domain motifs capable of effecting viral budding. The composition also comprises a compound capable of interfering with the protein-protein interaction between a host cell protein capable of binding a late domain motif and a HSV protein containing a late domain motif. The composition further comprises another HSV protein or its immunogenic fragment, and/or a nucleic acid encoding the other HSV protein or the immunogenic fragment. The present sequence is a mutant HSV peptide, derived from the wild-type peptide ADJ38601, used to illustrate

CC the invention.

XX Sequence 15 AA;

Query Match 43.8%; Score 28; DB 8; Length 15;
 Best Local Similarity 60.0%; Pred. No. 5.1e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 NYLALVRELK 13
 |||:|:
 Db 5 NYAALILENK 14

RESULT 19

AA41980

AA41980 standard; peptide; 16 AA.

XX AAR41980;

XX 25-MAR-2003 (revised)

DT 21-APR-1994 (first entry)

XX Human T cell reactive feline protein fragment C.

XX Human; T cell; reactive; feline; protein; immune response; antigen;
 tolerance; mammal; Dermatophagoides; Felis; Ambrosia; Lolium; Canis;
 Cryptomeria; Alternaria; Alder; Betula; Quercus; Olea; Artemesia;
 Plantago; Parietaria; Biatella; Apis; Feriplaneta; autoantigen; ss.

XX Homo sapiens.

XX WO9319178-A2.

XX 30-SEP-1993.

XX 25-MAR-1993; 93WO-US002462.

XX 25-MAR-1992; 92US-00857311.

XX 15-MAY-1992; 92US-00884718.

XX 15-JAN-1993; 93US-00006116.

XX (IMMU-) IMMUNOLOGIC PHARM CORP.

XX Gelfer ML, Garman RD, Greenstein JL, Kuo M, Briner TJ;

XX Morville M;

XX WPI; 1993-32074/40.

XX New peptide(s) for inducing tolerance - comprise one or more epitope(s)
 of an allergen administered subcutaneously, for treating sensitivity to
 cats, bees, etc.

XX Claim 1; Fig 3; 107pp; English.

XX The sequences given in AAR41975-82 are peptides derived from a human T
 cell reactive feline protein. These peptides are used in a therapeutic
 composition which is useful in treating diseases which involve an immune
 response to a protein antigen. This composition may be used to induce
 tolerance in a mammal to Dermatophagoides, Felis, Ambrosia, Lolium,
 Cryptomeria, Alternaria, Alder, Betula, Quercus, Olea, Artemesia,
 Plantago, Parietaria, Canis, Biatella, Apis, Feriplaneta and to
 autoantigens in humans. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 16 AA;

Query Match 43.8%; Score 28; DB 2; Length 16;
 Best Local Similarity 41.7%; Pred. No. 5.5e+02;
 Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DKONYALVREL 12
 ||:|:|:|:
 Db 3 DKENALSLDKI 14

RESULT 20

AA51484

AA51484 standard; protein; 16 AA.

XX AAY51484;

XX 22-MAY-2000 (first entry)

XX Human TRFP derived peptide C.

XX T-cell reactive feline protein; TRFP; T cell epitope; T cell receptor;
 down regulation; immune response; allergen; immunoglobulin E;
 sensitivity; cat protein allergen; human.

XX Homo sapiens.

XX US6019972-A.

XX 01-FEB-2000.

XX 02-SEP-1994; 94US-00300928.

XX 03-NOV-1989; 89US-00431565.

XX 28-FEB-1991; 91US-00662276.

XX 13-DEC-1991; 91US-00807529.

XX 25-MAR-1992; 92US-00857311.

XX 15-MAY-1992; 92US-00884718.

XX 15-JAN-1993; 93US-00006116.

XX (IMMU-) IMMUNOLOGIC PHARM CORP.

XX Garman RD, Greenstein JL, Kuo M, Briner TJ, Morville M;

XX Gelfer ML;

XX WPI; 2000-146862/13.

XX Peptides of human T cell reactive feline protein for treating sensitivity

XX to cat protein allergens comprise at least one T cell epitope recognized
 by a T cell receptor specific for the human T cell reactive feline
 protein.

XX Claim 8; Col 89-90; 105pp; English.

XX This invention describes a novel peptide (I) of human T cell reactive
 feline protein (hTRFP) having at least one T cell epitope recognized by a
 T cell receptor specific for the human T cell reactive feline protein.
 CC the peptide consisting of at least 7-30 amino acids, and having an amino
 acid sequence derived from an amino acid sequence comprising 94, 96, 97,
 CC 109, or 111 residues, given in the specification. The peptides down
 CC regulate the immune response to the allergen. The peptides have reduced
 CC immunoglobulin E binding and reduce T cell responsiveness. The peptide
 CC (I) is useful in compositions for treating sensitivity to a cat protein
 CC allergen in a subject. This sequence represents the human TRFP derived
 CC peptide used in the method of the invention

XX Sequence 16 AA;

Query Match 43.8%; Score 28; DB 3; Length 16;
 Best Local Similarity 41.7%; Pred. No. 5.5e+02;
 Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DKONYALVREL 12
 ||:|:|:|:
 Db 3 DKENALSLDKI 14

RESULT 21
 AAB28946

AAB28946 standard; peptide; 16 AA.

XX AAB28946;

DT 29-JAN-2001 (first entry)
 XX Peptide C derived from T cell reactive feline protein.
 XX Cat; allergy; human T cell reactive feline protein; hTRFP; immunotherapy.
 XX Felis sp.
 XX US6120769-A.
 XX 19-SEP-2000.
 XX 28-APR-1995; 95US-00431184.
 XX 03-NOV-1989; 89US-00431565.
 XX 28-FEB-1991; 91US-00662276.
 XX 13-DEC-1991; 91US-00807529.
 XX 25-MAR-1992; 92US-00857311.
 XX 15-MAY-1992; 92US-00884718.
 XX 15-JAN-1993; 93US-00006116.
 XX 02-SEP-1994; 94US-00300928.
 XX (IMMU-) IMMUNOLOGIC PHARM CORP.
 XX Gelfer ML, Garman RD, Greenstein JL, Bond JF;
 XX WPI: 2000-601477/57.
 XX Detecting, preventing and treating sensitivity to cat protein allergen
 PT comprising combining a biological sample with a human T cell reactive
 PT feline protein and determining the extent of binding that occurs.
 XX Claim 2; Fig 17; 106pp; English.
 XX The present invention relates to the detection of sensitivity to a cat
 CC protein allergen by combining a blood sample from a subject with a
 CC peptide of human T cell reactive feline protein (hTRFP). This method and
 CC the hTRFP peptides are useful for diagnosing, preventing and treating cat
 CC allergies by reducing or abolishing an individual's allergic response to
 CC a cat allergen. DNA encoding the TRFP may be used as probes to locate
 CC equivalent sequences present in other species. These may further be used
 CC to study the mechanism of immunotherapy of cat allergy, and to design
 CC modified derivatives, analogues or functional equivalents useful in
 CC immunotherapy. The present sequence was used in the invention
 CC XX
 SQ Sequence 16 AA;
 Query Match 43.8%; Score 28; DB 3; Length 16;
 Best Local Similarity 41.7%; Pred. NO. 5.5e+02;
 Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DKONYALVREL 12
 ||:|:|:|:|:
 Db 3 DKENALSLDKI 14
 RESULT 22
 ID AAY90112 standard; peptide; 16 AA.
 XX AAY90112;
 XX 12-SEP-2003 (revised)
 DT 13-JUL-2000 (first entry)
 XX Cat TRFP derived peptide, peptide C.
 XX Cat; TRFP; human T-cell reactive feline protein; cat protein allergen;
 KW house dust; Fel d I; cat allergy; Felis domesticus sensitivity; therapy;
 KW diagnosis; goat; sheep; horse; rabbit; dog.
 XX Felis catus.
 XX

PN US6025162-A.
 XX 15-FEB-2000.
 XX 28-APR-1995; 95US-00430944.
 XX 03-NOV-1989; 89US-00431565.
 XX 28-FEB-1991; 91US-00662276.
 XX 13-DEC-1991; 91US-00807529.
 XX 25-MAR-1992; 92US-00857311.
 XX 15-MAY-1992; 92US-00884718.
 XX 15-JAN-1993; 93US-00006116.
 XX 02-SEP-1994; 94US-00300928.
 XX (IMMU-) IMMUNOLOGIC PHARM CORP.
 XX Morgenstern JP, Griffitht JI, Rogers BL;
 XX WPI: 2000-181812/16.
 XX New human T cell reactive feline protein, useful for desensitizing cat
 PT allergic individuals to cat allergens.
 XX Claim 9; Fig 17; 108pp; English.
 XX This sequence is a peptide derived from the human T cell reactive feline
 CC protein (TRFP) of the invention. The protein is a cat protein allergen,
 CC and was isolated from a vacuum bag extract obtained by affinity
 CC purification of house dust collected from several homes with cats. TRFP
 CC is composed of two covalently linked peptide chains, and is also referred
 CC to as Fel d I. TRFP and its peptides are useful for reducing or
 CC preventing the adverse effects that exposure to cat allergens normally
 CC has on cat allergic individuals (i.e. to desensitize individuals to cat
 CC allergens or block the effect of the allergens). TRFP is also used in
 CC methods of diagnosing sensitivity to Felis domesticus in an individual.
 CC DNA sequences encoding TRFP can be used as probes to locate equivalent
 CC sequences present in other species, e.g. goat, sheep, horse, rabbit and
 CC dog, that may be useful in diagnostic and/or therapeutic applications.
 CC (Updated on 12-SEP-2003 to standardise OS field)
 CC XX
 SQ Sequence 16 AA;
 Query Match 43.8%; Score 28; DB 3; Length 16;
 Best Local Similarity 41.7%; Pred. NO. 5.5e+02;
 Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DKONYALVREL 12
 ||:|:|:|:|:
 Db 3 DKENALSLDKI 14
 RESULT 23
 ID AAY87687 standard; protein; 16 AA.
 XX AAY87687;
 XX 22-AUG-2000 (first entry)
 DT Feline human TRFP peptide C.
 XX T-cell reactive feline protein; TRFP; Fel d I; cat allergen;
 KW antiallergic; T cell stimulator; diagnostic; immunotherapy.
 XX Felis sp.
 XX US6048962-A.
 XX 11-APR-2000.
 XX 27-APR-1995; 95US-00430014.
 XX 03-NOV-1989; 89US-00431565.
 XX

PR 28-FEB-1991; 91US-00662276.
 PR 13-DEC-1991; 91US-00807529.
 PR 25-MAR-1992; 92US-00857311.
 PR 15-MAY-1992; 92US-00884718.
 PR 15-JAN-1993; 93US-00006116.
 PR 02-SEP-1994; 94US-00300928.
 XX
 PA (IMMU-) IMMUNOLOGIC PHARM CORP.
 XX
 PI Kuo M, Rogers BL, Gefter ML, Morgenstern JP, Brauer AW;
 PI Greenstein JL, Griffith ID, Garman RD;
 XX
 DR WPI; 2000-316905/27.
 XX
 PT New human T cell reactive feline protein useful for reducing or
 PT abolishing individual's allergic response to cat allergen comprising two
 PT different covalently linked peptide chains.
 XX
 PS Example 5; Col 89-90; 106pp; English.
 XX
 CC This invention describes a novel naturally occurring cat protein allergen
 CC (I), human T cell reactive feline protein (TRFP), comprising two
 CC different covalently linked peptide chains with a molecular weight of 20
 CC kD, 40 kD or 130 kD under non-reducing conditions and 5 kD or 10-18 kD
 CC under reducing conditions. The products of the invention have
 CC antiallergic activity and act as human T cell stimulators. TRFP is useful
 CC for reducing or preventing the adverse effects of cat allergens on cat
 CC allergic individuals and in ex vivo diagnostic tests to determine which
 CC peptides cause sensitivity so as to selectively use them to desensitize a
 CC cat sensitive individual. Purified TRFP is also useful for studying the
 CC mechanism of immunotherapy of cat allergy and to design modified
 CC derivatives, analogs or functional equivalents that are more useful in
 CC immunotherapy against cat allergy. DNA sequences encoding TRFP are useful
 CC as probes to locate equivalent sequences present in other species (goats,
 CC sheep, dogs, rabbits or horses) that may be useful in diagnostics and/or
 CC therapeutics. Fully defined and characterized TRFP provides complete and
 CC a very simple desensitization therapy. This sequence represents a human T
 CC cell reactive feline protein (also known as Fel d I) derived peptide C
 CC which is described in the method of the invention
 CC
 SQ Sequence 16 AA:
 Query Match 43.8%; Score 28; DB 3; Length 16;
 Best Local Similarity 41.7%; Pred. No. 5.5e+02;
 Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DKONYLALVREL 12
 DB 3 DKENALSLDKI 14
 RESULT 24
 ID ADD94191 standard; peptide: 17 AA.
 AC ADD94191;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Mouse HUIV26 antibody mutant light chain CDR amino acid sequence SeqID76.
 XX
 KW grafted antibody; complementarity determining region; CDR, light CDR;
 KW heavy CDR; cryptic collagen epitope; solid tumour;
 KW new blood vessel growth; angiogenesis; tumour growth; cyrostatic;
 KW collagen agonist; collagen antagonist; cancer metastasis;
 KW anti-cryptic collagen; HUIV26; variable region light chain; mouse;
 KW murine; mutant; mutein.
 XX
 OS Synthetic.
 OS Mus musculus.
 XX
 PN WO2003046204-A2.
 XX

PD 05-JUN-2003.
 XX
 PR 26-NOV-2002; 2002MO-US038147.
 XX
 PR 26-NOV-2001; 2001US-00995529.
 PR 06-DEC-2001; 2001US-00011250.
 XX
 PA (CELL-) CELL MATRIX INC.
 XX
 PI Waking JD, Huse WD, Tang Y, Broek D, Brooks PC;
 PI WPI; 2003-513649/48.
 XX
 DR WPI; 2003-513649/48.
 XX
 PT New cryptic collagen antibody with one or more complementarity
 PT determining regions, useful for diagnosing and treating disorders
 PT associated with angiogenesis, tumor growth and/or cancer metastasis.
 XX
 PS Claim 2; SEQ ID NO 76; 232pp; English.
 XX
 CC This invention relates to a novel grafted antibody or its functional
 CC fragment comprising one or more complementarity determining regions
 CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino
 CC acid (aa) substitution where the antibody has specific binding activity
 CC for a cryptic collagen epitope. The growth of all solid tumours requires
 CC new blood vessel growth, angiogenesis, inhibition of which is an approach
 CC to limiting tumor growth. The invention may allow development of
 CC therapeutics with a cyrostatic activity as a collagen agonist or
 CC antagonist. The invention is useful for diagnosing and treating disorders
 CC associated with angiogenesis, tumor growth and/or cancer metastasis. The
 CC present sequence is the amino acid sequence of a mutant mouse anti-
 CC cryptic collagen site antibody HUIV26 variable region light chain CDR
 CC which may be used during the creation of an antibody of the invention.
 XX
 SQ Sequence 17 AA:
 Query Match 43.8%; Score 28; DB 7; Length 17;
 Best Local Similarity 71.4%; Pred. No. 5.9e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DKONYLA 7
 DB 11 NKKNYLA 17
 RESULT 25
 ID ADT94021 standard; peptide: 17 AA.
 AC ADT94021;
 XX
 DT 27-JAN-2005 (first entry)
 XX
 DE rFel d 1(2+1) fusion product, tryptic fragment T16+T17.
 XX
 KW Recombinant Fel d 1; rFel d 1; Felis domesticus allergen 1;
 KW Fel d 1 chain 1; Fel d 1 chain 2; fusion product; cat allergy;
 KW antiallergic; domestic cat; mutant; mutein; tryptic fragment.
 XX
 OS Felis catus.
 OS Synthetic.
 XX
 PN WO2004094639-A2.
 XX
 PD 04-NOV-2004.
 XX
 PF 22-APR-2004; 2004WO-IB001583.
 PF 24-APR-2003; 2003GB-00009345.
 PR
 XX
 PA (CLIN-) CLINOVATION.
 XX
 PI Groenlund H, Van Hage- Hamsten M;
 XX

DR WPI: 2004-775941/76.

XX New recombinant Fel d 1 fusion product comprising a Fel d 1 chain 1, a
PT Fel d 1 chain 2 and a linker, useful for treating or preventing cat
PT allergy.

PS Example 3; Page 13; 36pp; English.

XX
CC The invention relates to a recombinant Felis domesticus allergen 1 (rFel
CC d 1) fusion product comprising a Fel d 1 chain 1, a Fel d 1 chain 2 and a
CC linker, e.g. a carbon-nitrogen bond or a short peptide linker, which
CC links the N-terminal amino acid of one chain to the C-terminal amino acid
CC of the other chain. Also disclosed are (i) a homodimer consisting of two
CC non-covalently associated fusion products, (ii) a DNA sequence encoding
CC the fusion product, (iii) an expression vector having the DNA sequence
CC inserted into it in an operable form, (iv) a host cell transformed with
CC the expression vector, (v) a pharmaceutical composition comprising an
CC immunotherapeutic amount of the fusion product and/or the homodimer and
CC a pharmaceutical carrier, excipient or diluent, (vi) a kit, for
CC diagnosing cat allergy, comprising the fusion product and/or the
CC homodimer and instructions for using the kit, (vii) a method for
CC diagnosing cat allergy, (viii) a process for preparing a fusion product,
CC and (ix) a process for preparing a recombinant Fel d 1 polypeptide. The
CC recombinant Fel d 1 fusion product comprises a fully defined sequence of
CC 172 amino acids (SEQ ID NO: 4). The fusion product and/or the homodimer
CC are useful for preparing a medicament for the treatment or prevention of
CC cat allergy. The composition, kits, and method are useful for diagnosing,
CC treating or preventing cat allergy. This sequence represents a clyptic
CC fragment of the rFel d 1(2+1) fusion product.

XX
SQ Sequence 17 AA:

Query Match 43.8%; Score 28; DB 8; Length 17;
Best Local Similarity 41.7%; Pred. No. 5.9e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 DKONYLALVREL 12
Db 6 DKENALSLDKI 17

Search completed: January 26, 2006, 07:57:55
Job time : 48.1552 secs

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OM protein - protein search, using bw model

Run on: January 26, 2006, 07:50:06 : Search time 12.2155 Seconds
(without alignments)
87.985 Million cell updates/sec

Title: US-09-662-293-7
Perfect score: 64
Sequence: 1 DKONYLALVRELK 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 229350

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5_COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/6_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/RB_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	64	100.0	13	2	US-09-292-225-7
2	35	54.7	16	2	US-09-171-705-21
3	35	54.7	16	2	US-09-657-757-21
4	30	46.9	20	2	US-09-446-504-7
5	30	46.9	20	2	US-09-712-266-7
6	29	45.3	16	2	US-09-171-705-22
7	29	45.3	16	2	US-09-657-757-22
8	28	43.8	16	2	US-08-300-928C-22
9	28	43.8	16	2	US-08-430-944D-22
10	28	43.8	16	2	US-08-430-944D-22
11	28	43.8	16	2	US-08-431-184-22
12	28	43.8	16	4	PCT-US93-02462-12
13	28	43.8	19	1	US-07-807-529A-10
14	28	43.8	19	2	US-08-300-928C-20
15	28	43.8	19	2	US-08-430-944D-20
16	28	43.8	19	2	US-08-430-944D-20
17	28	43.8	19	2	US-08-431-184-20
18	28	43.8	19	4	PCT-US93-02462-10
19	28	43.8	20	4	PCT-US93-02462-14
20	27	42.2	11	2	US-07-807-529A-27
21	27	42.2	11	2	US-08-300-928C-76
22	27	42.2	11	2	US-08-430-944D-76
23	27	42.2	11	2	US-08-430-944D-76
24	27	42.2	11	2	US-08-431-184-76
25	27	42.2	11	2	US-09-142-885C-9
26	27	42.2	21	1	US-08-832-877-3
27	26	40.6	10	2	US-08-441-507-52

28	26	40.6	10	2	US-09-106-568E-46	Sequence 46, Appl
29	26	40.6	11	2	US-08-974-549A-63	Sequence 63, Appl
30	26	40.6	11	2	US-08-912-951-63	Sequence 63, Appl
31	26	40.6	11	2	US-09-402-181B-63	Sequence 63, Appl
32	26	40.6	11	2	US-09-721-456-63	Sequence 63, Appl
33	26	40.6	18	2	US-09-386-962C-9	Sequence 9, Appl
34	26	40.6	20	2	US-09-736-457-1851	Sequence 1851, Ap
35	26	40.6	20	2	US-10-017-754-1851	Sequence 1851, Ap
36	25	39.1	7	2	US-08-620-840C-13	Sequence 13, Appl
37	25	39.1	15	1	US-08-311-611A-4	Sequence 4, Appl
38	25	39.1	15	1	US-08-372-783-4	Sequence 4, Appl
39	25	39.1	15	1	US-08-372-105-4	Sequence 4, Appl
40	25	39.1	15	1	US-08-306-473A-4	Sequence 4, Appl
41	25	39.1	15	1	US-08-473-344-4	Sequence 4, Appl
42	25	39.1	15	1	US-08-621-603-1	Sequence 1, Appl
43	25	39.1	15	1	US-08-485-445A-4	Sequence 4, Appl
44	25	39.1	15	2	US-09-119-263-91	Sequence 4, Appl
45	25	39.1	15	2	US-08-657-162-4	Sequence 4, Appl
46	25	39.1	15	2	US-09-224-480-4	Sequence 4, Appl
47	25	39.1	15	2	US-09-093-539-4	Sequence 4, Appl
48	25	39.1	15	2	US-09-217-352-1	Sequence 1, Appl
49	25	39.1	15	2	US-09-790-230-4	Sequence 4, Appl
50	25	39.1	15	2	US-09-689-097-6	Sequence 6, Appl
51	25	39.1	15	2	PCT-US94-02465-4	Sequence 4, Appl
52	25	39.1	15	4	PCT-US95-00498-4	Sequence 4, Appl
53	25	39.1	15	4	PCT-US95-00656-4	Sequence 4, Appl
54	25	39.1	15	4	US-09-459-749D-3	Sequence 3, Appl
55	25	39.1	16	2	US-09-627-896B-16	Sequence 16, Appl
56	25	39.1	17	2	US-09-339-596A-16	Sequence 16, Appl
57	25	39.1	18	2	US-09-101-146-42	Sequence 42, Appl
58	25	39.1	21	2	US-08-787-137-103	Sequence 103, Appl
59	25	39.1	9	1	US-08-388-267C-14	Sequence 14, Appl
60	24	37.5	13	1	US-08-390-156A-104	Sequence 94, Appl
61	24	37.5	14	1	US-08-439-817-94	Sequence 94, Appl
62	24	37.5	14	1	US-08-545-860D-61	Sequence 61, Appl
63	24	37.5	14	2	US-09-428-082B-159	Sequence 159, Appl
64	24	37.5	14	4	PCT-US94-04496-61	Sequence 61, Appl
65	24	37.5	15	1	US-10-198-053-508	Sequence 25, Appl
66	24	37.5	15	2	US-08-218-025A-26	Sequence 26, Appl
67	24	37.5	16	1	US-08-241-054-108	Sequence 108, Appl
68	24	37.5	16	1	US-08-390-156A-91	Sequence 91, Appl
69	24	37.5	16	1	US-08-485-508-108	Sequence 108, Appl
70	24	37.5	16	1	US-08-439-817-88	Sequence 88, Appl
71	24	37.5	16	1	US-08-353-400-30	Sequence 30, Appl
72	24	37.5	17	1	US-08-467-520A-10	Sequence 10, Appl
73	24	37.5	17	1	US-08-388-267C-17	Sequence 17, Appl
74	24	37.5	17	1	US-08-470-110A-10	Sequence 10, Appl
75	24	37.5	17	1	US-08-667-769A-10	Sequence 10, Appl
76	24	37.5	17	1	US-08-940-371-10	Sequence 10, Appl
77	24	37.5	17	2	US-08-637-647-10	Sequence 10, Appl
78	24	37.5	17	2	US-09-277-220-17	Sequence 17, Appl
79	24	37.5	17	2	US-09-563-222C-26	Sequence 26, Appl
80	24	37.5	17	2	US-10-746-400-10	Sequence 10, Appl
81	24	37.5	17	2	US-10-146-305-9	Sequence 9, Appl
82	24	37.5	17	2	US-10-170-448B-1	Sequence 1, Appl
83	24	37.5	17	2	US-09-630-722C-15	Sequence 15, Appl
84	24	37.5	17	4	PCT-US93-08435-22	Sequence 22, Appl
85	24	37.5	17	4	PCT-US93-08435-35	Sequence 35, Appl
86	24	37.5	17	4	PCT-US95-17082A-10	Sequence 10, Appl
87	24	37.5	18	2	US-08-940-095-200	Sequence 200, Appl
88	24	37.5	18	2	US-08-940-096-200	Sequence 200, Appl
89	24	37.5	18	2	US-08-940-096-200	Sequence 200, Appl
90	24	37.5	18	2	US-09-465-719-200	Sequence 200, Appl
91	24	37.5	18	2	US-09-453-838-200	Sequence 200, Appl
92	24	37.5	18	2	US-09-461-325-423	Sequence 423, Appl
93	24	37.5	18	2	US-08-940-136-200	Sequence 200, Appl
94	24	37.5	18	2	US-09-453-833-200	Sequence 200, Appl
95	24	37.5	18	2	US-10-012-542-423	Sequence 423, Appl

ALIGNMENTS

RESULT 1

US-09-292-225-7
; Sequence 7, Application US/09292225
; Patent No. 645566
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-7

Query Match 100.0%; Score 64; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 6,4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DKONYLALVREL 13
|||:|||||
Db 1 DKONYLALVRELK 13

RESULT 2

US-09-171-705-21
; Sequence 21, Application US/09171705
; Patent No. 6184204
; GENERAL INFORMATION:
; APPLICANT: BOOTS, ANNA M.H.
; APPLICANT: VERHEIJDEN, GILBERTUS F.M.
; TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC
; TITLE OF INVENTION: IMMUNOSUPPRESSIVE THERAPY
; FILE REFERENCE: O/96198 US
; CURRENT APPLICATION NUMBER: US/09/171,705
; CURRENT FILING DATE: 1999-02-09
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM
; OTHER INFORMATION: SEQUENCE OF HUMAN CARTILAGE (HC) -39 PROTEIN
US-09-171-705-21

Query Match 54.7%; Score 35; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 10;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 DKONYLALVREL 12
|||:|||||
Db 5 DKOHTTLIKEM 16

RESULT 3

US-09-657-757-21
; Sequence 21, Application US/09657757
; Patent No. 6881824
; GENERAL INFORMATION:
; APPLICANT: BOOTS, ANNA M.H.
; APPLICANT: VERHEIJDEN, GILBERTUS F.M.
; TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC
; TITLE OF INVENTION: IMMUNOSUPPRESSIVE THERAPY
; FILE REFERENCE: O/96198 US
; CURRENT APPLICATION NUMBER: US/09/657,757
; CURRENT FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US/09/171,705
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM
; OTHER INFORMATION: SEQUENCE OF HUMAN CARTILAGE (HC) -39 PROTEIN
US-09-657-757-21

Query Match 54.7%; Score 35; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 10;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 DKONYLALVREL 12
|||:|||||
Db 5 DKOHTTLIKEM 16

RESULT 4

US-09-446-504-7
; Sequence 7, Application US/09446504
; Patent No. 6218150
; GENERAL INFORMATION:
; APPLICANT: UEMORI, Takashi
; APPLICANT: SATO, Yoshimi
; APPLICANT: FUJITA, Tomoko
; APPLICANT: MIYAKE, Kazuo
; APPLICANT: MIYAKI, Hiroyuki
; APPLICANT: ASADA, Kiyozo
; APPLICANT: KATO, Ikunoshin
; TITLE OF INVENTION: DNA POLYMERASE-RELATED FACTORS
; FILE REFERENCE: 1422-408PCT
; CURRENT APPLICATION NUMBER: US/09/446,504
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/JP98/02845
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: JP 9-187496
; PRIOR FILING DATE: 1997-06-26
; PRIOR APPLICATION NUMBER: JP 9-320692
; PRIOR FILING DATE: 1997-11-27
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Pyrococcus furiosus
US-09-446-504-7

Query Match 46.9%; Score 30; DB 2; Length 20;
Best Local Similarity 54.5%; Pred. No. 97;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 DKONYLALVRE 11
|||:|||||
Db 2 DKEGFLNKVRE 12

RESULT 5

US-09-712-266-7
Sequence 7, Application US/09712266
Patent No. 633158
GENERAL INFORMATION:
APPLICANT: UEMORI, Takashi
APPLICANT: SATO, Yoshimi
APPLICANT: FUJITA, Tomoko
APPLICANT: MIYAKE, Kazuo
APPLICANT: MUKAI, Hiroyuki
APPLICANT: ASADA, Kiyozo
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: DNA POLYMERASE-RELATED FACTORS
FILE REFERENCE: 1422-408PCT
CURRENT APPLICATION NUMBER: US/09/712,266
CURRENT FILING DATE: 2000-11-15
PRIOR APPLICATION NUMBER: US 09/446,504
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: PCT/JP98/02845
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: JP 9-187496
PRIOR FILING DATE: 1997-06-26
PRIOR APPLICATION NUMBER: JP 9-320692
PRIOR FILING DATE: 1997-11-27
NUMBER OF SEQ ID NOS: 92
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 20
TYPE: PRT
ORGANISM: Pyrococcus furiosus
US-09-712-266-7

Query Match 46.9%; Score 30; DB 2; Length 20;
Best Local Similarity 54.5%; Pred. No. 97;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DKONYLALVRE 11
DB 2 DKSGFLNKVRE 12

RESULT 6

US-09-171-705-22
Sequence 22, Application US/09171705
Patent No. 6184204
GENERAL INFORMATION:
APPLICANT: BOOTS, ANNA M.H.
APPLICANT: VERHEIJDEN, GILBERTUS F.M.
TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC
FILE REFERENCE: O/96198 US
CURRENT APPLICATION NUMBER: US/09/171,705
CURRENT FILING DATE: 1999-02-09
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM
OTHER INFORMATION: SEQUENCE OF HUMAN CARTILAGE (HC) -39 PROTEIN
US-09-171-705-22

Query Match 45.3%; Score 29; DB 2; Length 16;
Best Local Similarity 36.4%; Pred. No. 1.2e+02;
Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 3 QNYLALVRELK 13
DB 1 QHFTTLIKEWK 11

RESULT 7

US-09-657-757-22
Sequence 22, Application US/09657757
Patent No. 6881824
GENERAL INFORMATION:
APPLICANT: BOOTS, ANNA M.H.
APPLICANT: VERHEIJDEN, GILBERTUS F.M.
TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC
FILE REFERENCE: O/96198 US
CURRENT APPLICATION NUMBER: US/09/657,757
CURRENT FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: US/09/171,705
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM
OTHER INFORMATION: SEQUENCE OF HUMAN CARTILAGE (HC) -39 PROTEIN
US-09-657-757-22

Query Match 45.3%; Score 29; DB 2; Length 16;
Best Local Similarity 36.4%; Pred. No. 1.2e+02;
Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 3 QNYLALVRELK 13
DB 1 QHFTTLIKEWK 11

RESULT 8

US-08-300-928C-22
Sequence 22, Application US/08300928C
Patent No. 6019972
GENERAL INFORMATION:
APPLICANT: GEFFER, Malcolm L. et al.
TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: Massachusetts
COUNTRY: USA
ZIP: 02145
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/300,928C
FILING DATE: September 2, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,529
FILING DATE: December 13, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: AMY E. MANDRAGOURAS
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 002.6US (IMI-044)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-300-928C-22

Query Match 43.8%; Score 28; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 1.7e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DKONYALVREL 12
Db 3 DKENALSLDKI 14

RESULT 9
US-08-430-944D-22
Sequence 22, Application US/08430944D
Patent No. 6025162
GENERAL INFORMATION:
APPLICANT: Bruce L. Rogers et al.
TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,944D
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/430,014
FILING DATE: 27-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,928
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-044DV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-430-944D-22

Query Match 43.8%; Score 28; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 1.7e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DKONYALVREL 12
Db 3 DKENALSLDKI 14

RESULT 10

US-08-430-014-22
Sequence 22, Application US/08430014
Patent No. 6048962
GENERAL INFORMATION:
APPLICANT: GERTER, Malcolm L. et al.
TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: Massachusetts
COUNTRY: USA
ZIP: 02145
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,014
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/300,928
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 002.6US (IMI-044)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-430-014-22

Query Match 43.8%; Score 28; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 1.7e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DKONYALVREL 12
Db 3 DKENALSLDKI 14

RESULT 11
US-08-431-184-22
Sequence 22, Application US/08431184
Patent No. 6120769
GENERAL INFORMATION:
APPLICANT: Bruce L. Rogers et al.
TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,184
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/430,014
FILING DATE: 27-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,928
FILING DATE: 02-SEPT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-044DV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-431-184-22

Query Match 43.8%; Score 28; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 1.7e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DKONYALVREL 12
||:|:|:|:
Db 3 DKENALSLDKI 14

RESULT 12
PCT-US93-02462-12
Sequence 12, Application PC/TUS9302462
GENERAL INFORMATION:
APPLICANT: Gelter, Malcolm L.
APPLICANT: Garman, Richard D.
APPLICANT: Greenstein, Julia L.
APPLICANT: Kuo, Mei-chang
APPLICANT: Briner, Thomas J.
APPLICANT: Morville, Malcolm
TITLE OF INVENTION: PEPTIDES USEFUL FOR TOLERIZATION
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02462
FILING DATE: 19930325
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/006,116
FILING DATE: 15-JAN-1993
APPLICATION NUMBER: US 07/884,718
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: 07/857,311
FILING DATE: 25-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: IPC-031PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
PCT-US93-02462-12

Query Match 43.8%; Score 28; DB 4; Length 16;
Best Local Similarity 41.7%; Pred. No. 1.7e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DKONYALVREL 12
||:|:|:|:
Db 3 DKENALSLDKI 14

RESULT 13
US-07-807-529A-10
Sequence 10, Application US/07807529A
Patent No. 5547669
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce L.
APPLICANT: Morgenstern, Jay
APPLICANT: Bond, Julian F.
APPLICANT: Garman, Richard D.
APPLICANT: Greenstein, Julia L.
APPLICANT: Kuo, Mei-chang
APPLICANT: Morville, Malcolm
TITLE OF INVENTION: RECOMBITOPE PEPTIDES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION
STREET: One Kendall Square, Building 600
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/807,529A
FILING DATE: 19911213
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,276
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: US 07/431,565
FILING DATE: 03-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Channing, Stacey L.
REGISTRATION NUMBER: 31,095
REFERENCE/DOCKET NUMBER: IPC-027/IMI-015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 494-0060
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-07-807-529A-10

Query Match 43.8%; Score 28; DB 1; Length 19;
Best Local Similarity 41.7%; Pred. No. 2.1e+02;

NAME: AMY E. MANDRAGOURAS
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 002.6US (IMI-044)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-430-014-20

Query Match 43.8%; Score 28; DB 2; Length 19;
Best Local Similarity 41.7%; Pred. No. 2.1e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 DKONYLALVREL 12
Db 3 DKENALSLDKI 14

RESULT 17

US-08-431-184-20
Sequence 20, Application US/08431184
Patent No. 6120769
GENERAL INFORMATION:
APPLICANT: Bruce L. Rogers et al.
TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,184
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/430,014
FILING DATE: 27-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,928
FILING DATE: 02-SEPT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-044DV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-431-184-20

Query Match 43.8%; Score 28; DB 2; Length 19;
Best Local Similarity 41.7%; Pred. No. 2.1e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 DKONYLALVREL 12
Db 3 DKENALSLDKI 14

RESULT 18

PCT-US93-02462-10
Sequence 10, Application PC/TUS9302462
GENERAL INFORMATION:
APPLICANT: Gelfer, Malcolm L.
APPLICANT: Garman, Richard D.
APPLICANT: Greenstein, Julia L.
APPLICANT: Kuo, Mei-chang
APPLICANT: Briner, Thomas J.
APPLICANT: Morville, Malcolm
TITLE OF INVENTION: PEPTIDES USEFUL FOR TOLERIZATION
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02462
FILING DATE: 19930325
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/006,116
FILING DATE: 15-JAN-1993
APPLICATION NUMBER: US 07/884,718
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: 07/857,311
FILING DATE: 25-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IPC-031PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
PCT-US93-02462-10

Query Match 43.8%; Score 28; DB 4; Length 19;
Best Local Similarity 41.7%; Pred. No. 2.1e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 DKONYLALVREL 12
Db 3 DKENALSLDKI 14

RESULT 19

PCT-US93-02462-14
Sequence 14, Application PC/TUS9302462
GENERAL INFORMATION:
APPLICANT: Gelfer, Malcolm L.
APPLICANT: Garman, Richard D.
APPLICANT: Greenstein, Julia L.
APPLICANT: Kuo, Mei-chang

APPLICANT: Briner, Thomas J.
APPLICANT: Morville, Malcolm
TITLE OF INVENTION: PEPTIDES USEFUL FOR TOLERIZATION
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02462
FILING DATE: 19930325
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/006,116
FILING DATE: 15-JAN-1993
APPLICATION NUMBER: US 07/884,718
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: 07/857,311
FILING DATE: 25-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IPC-031PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
PCT-US93-02462-14

Query Match 43.8%; Score 28; DB 4; Length 20;
Best Local Similarity 41.7%; Pred. 2.2e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DKONYALVREL 12
Db 4 DKENALSLDKI 15

RESULT 20
US-07-807-529A-27
Sequence 27, Application US/07807529A
Patent No. 5547669
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce L.
APPLICANT: Morgenstern, Jay
APPLICANT: Bond, Julian F.
APPLICANT: Garman, Richard D.
APPLICANT: Greenstein, Julia L.
APPLICANT: Kuo, Mei-chang
APPLICANT: Morville, Malcolm
TITLE OF INVENTION: RECOMBITOPE PEPTIDES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: One Kendall Square, Building 600
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/807,529A
FILING DATE: 19911213
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,276
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: US 07/431,565
FILING DATE: 03-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Channing, Stacey L.
REGISTRATION NUMBER: 31,095
REFERENCE/DOCKET NUMBER: IPC-027/im1-015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 494-0060
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-807-529A-27

Query Match 42.2%; Score 27; DB 1; Length 11;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DKONYALV 9
Db 3 DKENALSL 11

RESULT 21
US-08-300-928C-76
Sequence 76, Application US/08300928C
Patent No. 6019972
GENERAL INFORMATION:
APPLICANT: GEFTER, Malcolm L. et al.
TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: Massachusetts
COUNTRY: USA
ZIP: 02145
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/300,928C
FILING DATE: September 2, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,529
FILING DATE: December 13, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: AMY E. MANDRAGOURAS
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 002.6US(IMI-044)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 76:

SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-300-928C-76

Query Match 42.2%; Score 27; DB 2; Length 11;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DKONYLALV 9
||:|:|:
Db 3 DKENALSL 11

RESULT 22
US-08-430-944D-76
; Sequence 76, Application US/08430944D
; Patent No. 6025162
; GENERAL INFORMATION:
; APPLICANT: Bruce L. Rogers et al.
; TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430.944D
; FILING DATE: 28-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/430.014
; FILING DATE: 27-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/300.928
; FILING DATE: 02-SEPT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-044DV2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-430-944D-76

Query Match 42.2%; Score 27; DB 2; Length 11;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DKONYLALV 9
||:|:|:
Db 3 DKENALSL 11

RESULT 23
US-08-430-014-76
; Sequence 76, Application US/08430014

Patent No. 6048962
; GENERAL INFORMATION:
; APPLICANT: GEFTER, Malcolm L. et al.
; TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02145
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430.014
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/300,928
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: 002.6US(IMI-044)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-430-014-76

Query Match 42.2%; Score 27; DB 2; Length 11;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DKONYLALV 9
||:|:|:
Db 3 DKENALSL 11

RESULT 24
US-08-431-184-76
; Sequence 76, Application US/08431184
; Patent No. 6120769
; GENERAL INFORMATION:
; APPLICANT: Bruce L. Rogers et al.
; TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431.184

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; FILING DATE: 28-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/430,014
; FILING DATE: 27-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/300,928
; FILING DATE: 02-SEPT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-044DV3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-431-184-76

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Query Match 42.2%; Score 27; DB 2; Length 11;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 DKONYLALV 9
Db 3 DKENALSL 11

```

```

RESULT 25
US-09-142-885C-9
; Sequence 9, Application US/09142885C
; Patent No. 6737406
; GENERAL INFORMATION:
; APPLICANT: Kay, Anthony
; APPLICANT: Larche, Mark
; TITLE OF INVENTION: Cryptic Peptides and Method for Their Identification
; FILE REFERENCE: 4028/75652
; CURRENT APPLICATION NUMBER: US/09/142,885C
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: PCT/GB97/00783
; PRIOR FILING DATE: 1997-03-20
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Felis domesticus
US-09-142-885C-9

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Query Match 42.2%; Score 27; DB 2; Length 16;
Best Local Similarity 55.6%; Pred. No. 2.6e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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QY 1 DKONYLALV 9
Db 6 DKENALSL 14

```

Search completed: January 26, 2006, 08:06:59
 Job time : 13.3822 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 26, 2006, 08:04:12 ; Search time 42.25 Seconds
(without alignments)
128.563 Million cell updates/sec

Title: US-09-662-293-7

Perfect score: 64
Sequence: 1 DKONYLALVRELK 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 369445

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

Published Applications AA Main:*

- 1: /cgnt2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgnt2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgnt2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgnt2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgnt2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgnt2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	100.0	13	4	US-10-218-743-7
2	30	46.9	20	3	US-09-971-309-7
3	29	45.3	10	3	US-09-573-822C-39
4	28	43.8	10	3	US-09-572-404B-2020
5	28	43.8	17	3	US-09-995-529-76
6	28	43.8	17	3	US-09-995-529-76
7	28	43.8	19	2	US-08-464-363-10
8	28	43.8	19	4	US-10-463-113-10
9	27	42.2	11	2	US-08-464-363-37
10	27	42.2	11	4	US-10-463-113-27
11	27	42.2	16	4	US-10-245-871-163
12	27	42.2	16	4	US-10-253-286-163
13	27	42.2	16	4	US-10-702-400-104
14	27	42.2	16	5	US-10-809-689-8
15	27	42.2	16	5	US-10-805-650-104
16	26	40.6	10	3	US-09-994-595-46
17	26	40.6	11	4	US-10-044-632-63
18	26	40.6	11	4	US-10-044-632-63
19	26	40.6	11	4	US-10-325-810-63
20	26	40.6	11	5	US-10-877-124-63
21	26	40.6	11	5	US-10-877-022-63
22	26	40.6	11	5	US-10-877-146-63
23	26	40.6	14	2	US-08-908-864-23
24	26	40.6	14	3	US-09-908-323-23
25	26	40.6	15	4	US-10-084-813-684
26	26	40.6	15	4	US-10-084-813-685
27	26	40.6	15	4	US-10-084-813-686

28	26	40.6	15	4	US-10-239-313A-82	Sequence 82, App1
29	26	40.6	15	4	US-10-461-093-6	Sequence 6, App1
30	26	40.6	16	4	US-10-225-567A-1099	Sequence 1099, App
31	26	40.6	16	4	US-10-225-567A-2256	Sequence 2256, App
32	26	40.6	17	4	US-10-676-909-52	Sequence 52, App1
33	26	40.6	17	4	US-10-676-909-52	Sequence 67, App1
34	26	40.6	18	4	US-10-084-813-731	Sequence 731, App
35	26	40.6	18	4	US-10-084-813-732	Sequence 732, App
36	26	40.6	18	4	US-10-084-813-733	Sequence 733, App
37	26	40.6	18	4	US-10-615-383-9	Sequence 9, App1
38	26	40.6	18	4	US-10-690-184-9	Sequence 9, App1
39	26	40.6	18	4	US-10-689-082-9	Sequence 9, App1
40	26	40.6	20	3	US-09-736-457-1851	Sequence 1851, App
41	26	40.6	20	3	US-09-902-941-1851	Sequence 1851, App
42	26	40.6	20	3	US-09-849-626-1851	Sequence 1851, App
43	26	40.6	20	3	US-10-017-754-1851	Sequence 1851, App
44	26	40.6	20	4	US-10-113-872-1851	Sequence 1851, App
45	26	40.6	20	4	US-10-283-017-1851	Sequence 1851, App
46	26	40.6	20	5	US-10-451-304-14	Sequence 14, App1
47	26	40.6	20	6	US-11-021-928A-301	Sequence 301, App
48	26	40.6	21	4	US-10-084-813-299	Sequence 299, App
49	26	40.6	21	4	US-10-084-813-300	Sequence 300, App
50	26	40.6	21	4	US-10-084-813-597	Sequence 597, App
51	26	40.6	21	4	US-10-084-813-598	Sequence 598, App
52	26	40.6	21	4	US-10-084-813-599	Sequence 599, App
53	25	39.1	7	3	US-09-910-346C-13	Sequence 13, App1
54	25	39.1	7	4	US-10-163-106B-7	Sequence 7, App1
55	25	39.1	7	5	US-10-757-077-7	Sequence 7, App1
56	25	39.1	11	5	US-10-783-311-176	Sequence 176, App
57	25	39.1	13	4	US-10-428-408A-12	Sequence 12, App1
58	25	39.1	13	4	US-10-428-694-12	Sequence 12, App1
59	25	39.1	13	4	US-10-699-874-12	Sequence 12, App1
60	25	39.1	15	3	US-09-765-527-1	Sequence 1, App1
61	25	39.1	15	4	US-10-446-828-4	Sequence 4, App1
62	25	39.1	15	4	US-10-319-786-4	Sequence 4, App1
63	25	39.1	16	3	US-09-459-749D-3	Sequence 3, App1
64	25	39.1	16	4	US-10-270-871-3	Sequence 3, App1
65	25	39.1	17	3	US-09-249-011A-16	Sequence 16, App1
66	25	39.1	17	4	US-10-225-567A-2179	Sequence 2179, App
67	25	39.1	17	5	US-10-986-089A-16	Sequence 16, App1
68	25	39.1	18	5	US-10-953-901-838	Sequence 838, App
69	25	39.1	20	5	US-10-690-276-583	Sequence 583, App
70	25	39.1	21	3	US-09-782-977-1	Sequence 1, App1
71	25	39.1	21	3	US-09-974-879-555	Sequence 555, App
72	25	39.1	21	3	US-09-305-736-561	Sequence 561, App
73	25	39.1	21	3	US-09-818-683-561	Sequence 561, App
74	25	39.1	21	3	US-09-818-683-561	Sequence 561, App
75	25	39.1	21	3	US-10-621-401-555	Sequence 555, App
76	24	37.5	9	4	US-10-158-596A-33	Sequence 33, App1
77	24	37.5	9	4	US-10-157-775B-33	Sequence 33, App1
78	24	37.5	9	4	US-10-254-446A-33	Sequence 33, App1
79	24	37.5	9	4	US-10-155-883B-33	Sequence 33, App1
80	24	37.5	9	4	US-10-057-475B-10908	Sequence 10908, App
81	24	37.5	9	4	US-10-057-475B-10959	Sequence 10959, App
82	24	37.5	9	4	US-10-154-884B-10908	Sequence 10908, App
83	24	37.5	9	4	US-10-154-884B-10959	Sequence 10959, App
84	24	37.5	9	4	US-10-668-800-33	Sequence 33, App1
85	24	37.5	9	5	US-10-158-596A-33	Sequence 33, App1
86	24	37.5	10	4	US-10-117-337-546	Sequence 546, App
87	24	37.5	10	4	US-10-657-622-554	Sequence 554, App
88	24	37.5	10	5	US-10-734-049A-169	Sequence 169, App
89	24	37.5	10	6	US-11-067-664-546	Sequence 546, App
90	24	37.5	11	6	US-11-067-159-546	Sequence 546, App
91	24	37.5	11	5	US-10-783-311-152	Sequence 152, App
92	24	37.5	12	5	US-10-858-706-19	Sequence 19, App1
93	24	37.5	13	4	US-10-302-447-111	Sequence 111, App
94	24	37.5	13	4	US-10-702-400-85	Sequence 85, App1
95	24	37.5	13	5	US-10-805-650-85	Sequence 85, App1
96	24	37.5	13	5	US-10-948-707-978	Sequence 978, App
97	24	37.5	14	3	US-09-840-277-77	Sequence 77, App1
98	24	37.5	14	4	US-10-609-217-159	Sequence 159, App
99	24	37.5	14	4	US-10-632-388-159	Sequence 159, App
100	24	37.5	14	4	US-10-651-723-159	Sequence 159, App

ALIGNMENTS

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RESULT 1
US-10-218-743-7
; Sequence 7, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-7

Query Match          100.0%; Score 64; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DKONYLALVREIK 13
Db      1 DKONYLALVREIK 13

RESULT 2
US-09-971-309-7
; Sequence 7, Application US/09971309
; Patent No. US20020106675A1
; GENERAL INFORMATION:
; APPLICANT: UEMORI, Takashi
; APPLICANT: SATO, Yoshimi
; APPLICANT: FUJITA, Tomoko
; APPLICANT: MIYAKE, Kazue
; APPLICANT: MUKAI, Hiroyuki
; APPLICANT: ASADA, Kiyozo
; APPLICANT: KATO, Ikumoshin
; TITLE OF INVENTION: DNA POLYMERASE-RELATED FACTORS
; FILE REFERENCE: 1422-0494P
; CURRENT APPLICATION NUMBER: US/09/971,309
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 09/446,504
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/J998/02845
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: JP 9-187496
; PRIOR FILING DATE: 1997-06-26
; PRIOR APPLICATION NUMBER: JP 9-320692
; PRIOR FILING DATE: 1997-11-27
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 20
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; TYPE: PRT
; ORGANISM: Pyrococcus furiosus
US-09-971-309-7
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Query Match          46.9%; Score 30; DB 3; Length 20;
Best Local Similarity 54.5%; Pred. No. 3.2e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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QY      1 DKONYLALVRE 11
Db      2 DKSGFLNKVRE 12
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RESULT 3
US-09-573-822C-39
; Sequence 39, Application US/09573822C
; Publication No. US20030199011A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome seq
; FILE REFERENCE: Microbe patent
; CURRENT APPLICATION NUMBER: US/09/573,822C
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 804
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 39
; LENGTH: 10
; TYPE: PRT
; ORGANISM: mycoplasma genitalium
; FEATURE:
; OTHER INFORMATION: Sequence located in MG017 at 15-24 and may interact with Sequence
US-09-573-822C-39
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Query Match          45.3%; Score 29; DB 3; Length 10;
Best Local Similarity 55.6%; Pred. No. 2.3e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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```
QY      5 YLALVREIK 13
Db      1 FLSLVKEVK 9
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RESULT 4
US-09-572-404B-2020
; Sequence 2020, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 2020
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Sequence located in SFRS8 OR SWAP at 110-119 and may interact with
US-09-572-404B-2020
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Query Match          43.8%; Score 28; DB 3; Length 10;
Best Local Similarity 62.5%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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```
QY      1 DKONYLAL 8
Db      2 DERRYLAL 9
```



```

RESULT 5
US-09-995-529-76
; Sequence 76, Application US/09995529
; Publication No. US2003009655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-76
Query Match      43.8%; Score 28; DB 3; Length 17;
Best Local Similarity 71.4%; Pred. No. 6.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 DKONYLA 7
       :|:|:|:|
Db      11 NKNKYLA 17

RESULT 6
US-09-995-529-76
; Sequence 76, Application US/09995529
; Publication No. US20040091482A9
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-76
Query Match      43.8%; Score 28; DB 3; Length 17;
Best Local Similarity 71.4%; Pred. No. 6.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 DKONYLA 7
       :|:|:|:|
Db      11 NKNKYLA 17

```

```

APPLICANT: Greenstein, Julia L.
APPLICANT: Kuo, Mei-chang
APPLICANT: Morville, Malcolm
TITLE OF INVENTION: RECOMBITOPE PEPTIDES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSER: Lahive & Cockfield
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,363
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/807,529
FILING DATE: 13-DEC-1991
APPLICATION NUMBER: US 07/662,276
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: US 07/431,565
FILING DATE: 03-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-015CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-464-363-10
Query Match      43.8%; Score 28; DB 2; Length 19;
Best Local Similarity 41.7%; Pred. No. 6.9e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      1 DKONYLALVREL 12
       ||:|:|:|:|
Db      3 DKENALSLDIXI 14

RESULT 8
US-10-463-113-10
; Sequence 10, Application US/10463113
; Publication No. US20040057959A1
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce L.
; APPLICANT: Morgenshtern, Jay
; APPLICANT: Bond, Julian F.
; APPLICANT: Garman, Richard D.
; APPLICANT: Greenstein, Julia L.
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Morville, Malcolm
TITLE OF INVENTION: RECOMBITOPE PEPTIDES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSER: Lahive & Cockfield, LLP
STREET: 28 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:

```

```

1 MEDIUM TYPE: Floppy disk
2 COMPUTER: IBM PC compatible
3 OPERATING SYSTEM: PC-DOS/MS-DOS
4 SOFTWARE: ASCII TEXT
5
6 CURRENT APPLICATION DATA:
7 APPLICATION NUMBER: US/10/463,113
8 FILING DATE: 16-Jun-2003
9
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: US 07/807,529
12 FILING DATE: 13-DEC-1991
13 APPLICATION NUMBER: US 07/662,276
14 FILING DATE: 28-FEB-1991
15 APPLICATION NUMBER: US 07/431,565
16 FILING DATE: 03-NOV-1989
17
18 ATTORNEY/AGENT INFORMATION:
19 NAME: Amy E. Mandragouras
20 REGISTRATION NUMBER: 36,207
21 REFERENCE/DOCKET NUMBER: IMI-015C
22
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE: (617) 227-7400
25 TELEFAX: (617) 742-4214
26
27 INFORMATION FOR SEQ ID NO: 10:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 19 amino acids
30 TYPE: amino acid
31 TOPOLOGY: linear
32 MOLECULE TYPE: peptide
33 FRAGMENT TYPE: internal
34
35 SEQUENCE DESCRIPTION: SEQ ID NO: 10:
36
37 US-10-463-113-10

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Query Match	43.8%;	Score 28;	DB 4;	Length 19
Best Local Similarity	41.7%;	Pred. No. 6.9e+02;		
Matches	5;	Conservative	2;	Indels

QY	1 DKONYLALVREL	12
	: :::	
Db	3 DKENALSLDKI	14

RESULT 9
US-08-464-363-27
Sequence 27, Application US/08464363
Publication No. US20030035815A1
GENERAL INFORMATION:
APPLICANT: Rogere, Bruce L.
APPLICANT: Morgestern, Jay
APPLICANT: Bond, Julian F.
APPLICANT: Garman, Richard D.
APPLICANT: Greenstein, Julia L.
APPLICANT: Kuo, Mei-chang
APPLICANT: Morville, Malcolm
TITLE OF INVENTION: RECOMBOTOPE PEPTIDES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Lahaye & Cockfield
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,363
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/807,529
FILING DATE: 13-DEC-1991
APPLICATION NUMBER: US 07/662,276

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? FILING DATE: 28-FEB-1991
? APPLICATION NUMBER: US 07/431,565
? FILING DATE: 03-NOV-1989
? ATTORNEY/AGENT INFORMATION:
? NAME: Amy E. Mandragouras
? REGISTRATION NUMBER: 36,207
? REFERENCE/DOCKET NUMBER: IMI-015CN
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (617) 227-7400
? INFORMATION FOR SEQ ID NO: 27:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 11 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
US-08-464-363-27

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Query Match	42.2%	Score 27	DB 2	Length 11
Best Local Similarity	55.6%	Pred. No. 5.7e+02		
Matches	5	Conservative	3	Mismatches 1
				Indels 0
				Gaps 0

QY	1 DKQNYLALV 9
	: : :
Db	3 DKENALSL 11

RESULT 10
US-10-463-113-27
; Sequence 27, Application US/10463113
; Publication No. US20040057959A1
ORIGINAL DOCUMENT

APPLICANT: Rogers, Bruce L.
Morgenstern, Jay
Bond, Julian F.
Gordon, Richard

Greenstein, Julia L
Kuo, Mei-chang
Morvile, Malcolm
MURPHY, Raymond

TITLE OF INVENTION: RECOMBINANT PEPTIDES
 NUMBER OF SEQUENCES: 76
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lahive & Cockfield, LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII TEXT
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/463,113
 FILING DATE: 16-Jun-2003
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/807,529
 FILING DATE: 13-DEC-1991
 APPLICATION NUMBER: US 07/662,276
 FILING DATE: 28-FEB-1991
 APPLICATION NUMBER: US 07/431,565
 FILING DATE: 03-NOV-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Amy E. Mandragouras
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: IM1-015CN
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 742-4214
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-463-113-27

Query Match 42.2%; Score 27; DB 4; Length 11;
Best Local Similarity 55.6%; Pred. No. 5.7e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DKONYALV 9
Db 3 DKENALSL 11

RESULT 11
US-10-245-871-163

Sequence 163, Application US/10245871
Publication No. US20030235594A1
GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
APPLICANT: XU, MINZHEN
TITLE OF INVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: RH-2013
CURRENT APPLICATION NUMBER: US/10/245,871
CURRENT FILING DATE: 2003-01-09
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 09/396,813
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 905
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 163
LENGTH: 16
TYPE: PRT
ORGANISM: Felis domesticus
US-10-245-871-163

Query Match 42.2%; Score 27; DB 4; Length 16;
Best Local Similarity 55.6%; Pred. No. 8.6e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DKONYALV 9
Db 6 DKENALSL 14

RESULT 12
US-10-253-286-163

Sequence 163, Application US/10253286
Publication No. US2004005881A1
GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
APPLICANT: XU, MINZHEN
TITLE OF INVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: RH-2015
CURRENT APPLICATION NUMBER: US/10/253,286
CURRENT FILING DATE: 2003-01-13
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 09/396,813
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 905
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 163
LENGTH: 16
TYPE: PRT
ORGANISM: Felis domesticus
US-10-253-286-163

Query Match 42.2%; Score 27; DB 4; Length 16;
Best Local Similarity 55.6%; Pred. No. 8.6e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DKONYALV 9
Db 6 DKENALSL 14

RESULT 13
US-10-702-400-104

Sequence 104, Application US/10702400
Publication No. US20040197800A1
GENERAL INFORMATION:
APPLICANT: Borns, Michael
TITLE OF INVENTION: DNA Polymerase Blends and Uses Thereof
FILE REFERENCE: 25436/2364
CURRENT APPLICATION NUMBER: US/10/702,400
CURRENT FILING DATE: 2003-11-05
NUMBER OF SEQ ID NOS: 113
SOFTWARE: PatentIn version 3.1
SEQ ID NO 104
LENGTH: 16
TYPE: PRT
ORGANISM: Methanopyrus kandleri
US-10-702-400-104

Query Match 42.2%; Score 27; DB 4; Length 16;
Best Local Similarity 62.5%; Pred. No. 8.6e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 6 LALVLEIK 13
Db 6 LSLVLEIK 13

RESULT 14
US-10-809-689-8

Sequence 8, Application US/10809689
Publication No. US20040265342A1
GENERAL INFORMATION:
APPLICANT: Eric Potter Clarkson
TITLE OF INVENTION: Methods and compositions for desensitisation
FILE REFERENCE: 5538/1010
CURRENT APPLICATION NUMBER: US/10/809,689
CURRENT FILING DATE: 2004-03-25
PRIOR APPLICATION NUMBER: PCT/GB99/00080
PRIOR FILING DATE: 1999-01-11
PRIOR APPLICATION NUMBER: GB/9800445.0
PRIOR FILING DATE: 1998-01-09
PRIOR APPLICATION NUMBER: GB/9820474.6
PRIOR FILING DATE: 1998-09-21
NUMBER OF SEQ ID NOS: 124
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
LENGTH: 16
TYPE: PRT
ORGANISM: Felis catus
US-10-809-689-8

Query Match 42.2%; Score 27; DB 5; Length 16;
Best Local Similarity 55.6%; Pred. No. 8.6e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DKONYALV 9
Db 6 DKENALSL 14

RESULT 15
US-10-805-650-104

Sequence 104, Application US/10805650
Publication No. US20050048530A1
GENERAL INFORMATION:
APPLICANT: Borns, Michael
TITLE OF INVENTION: DNA Polymerase Fusions and Uses Thereof
FILE REFERENCE: 25436/2382

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; CURRENT APPLICATION NUMBER: US/10/805,650
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/457,426
; PRIOR FILING DATE: 2003-03-25
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Methanopyrus kandleri
US-10-805-650-104

Query Match          42.2%; Score 27; DB 5; Length 16;
Best Local Similarity 62.5%; Pred. No. 8.6e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      6 LALVRELK 13
       |||:|:|
Db      6 LSLVLEIK 13

RESULT 16
US-09-994-595-46
; Sequence 46, Application US/09994595
; Publication No. US20030039981A1
; GENERAL INFORMATION:
; APPLICANT: Bhattacharjee, J.
; APPLICANT: Suvarna, Kalavati
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DETECTING FUNGAL PATHOGENS IN
; FILE REFERENCE: 96,247-A
; CURRENT APPLICATION NUMBER: US/09/994,595
; CURRENT FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 08/650,809
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 46
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide segment of ACVS_EMENT shown in Figure 4.
US-09-994-595-46

Query Match          40.6%; Score 26; DB 3; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.7e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5 YLALVRELK 13
       |||:|:|
Db      2 YLALRRHK 10

RESULT 17
US-10-044-692-63
; Sequence 63, Application US/10044692
; Publication No. US20030096344A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor

```

```

; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,692
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-00260005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /note="motif E peptide from
; Drosophila melanogaster TART non-LTR
; retrotransposible element reverse
; transcriptase"
; SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-10-044-692-63

Query Match          40.6%; Score 26; DB 4; Length 11;
Best Local Similarity 50.0%; Pred. No. 8.6e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      2 KQNTALV 9
       |||:|:|
Db      3 KQSYLGVI 10

RESULT 18
US-10-044-539-63
; Sequence 63, Application US/10044539
; Publication No. US20030100093A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS

```

```

NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,539
FILING DATE: 11-Jan-2002
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..11
OTHER INFORMATION: /note="motif E peptide from
Drosophila melanogaster TART non-LTR
retrotransposable element reverse
transcriptase"
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-10-044-539-63
Query Match 40.6%; Score 26; DB 4; Length 11;
Best Local Similarity 50.0%; Pred. No. 8.6e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 2 KONYALV 9
Db 3 KOSYLGVI 10

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```

Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,810
FILING DATE: 20-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181
FILING DATE: 29-Sep-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausenhuis, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..11
OTHER INFORMATION: /note="motif E peptide from
Drosophila melanogaster TART non-LTR
retrotransposable element reverse
transcriptase"
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-10-325-810-63
Query Match 40.6%; Score 26; DB 4; Length 11;
Best Local Similarity 50.0%; Pred. No. 8.6e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 2 KONYALV 9
Db 3 KOSYLGVI 10

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RESULT 20
US-10-877-124-63
Sequence 63, Application US/10877124
Publication No. US20040242529A1
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/877,124
FILING DATE: 24-Jun-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-Nov-1999
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-Oct-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..11
OTHER INFORMATION: /note= "motif E peptide from
Drosophila melanogaster TART non-LTR

retrotransposable element reverse
transcriptase"
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-10-877-124-63
Query Match 40.6%; Score 26; DB 5; Length 11;
Best Local Similarity 50.0%; Pred. No. 8.6e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 2 KONTALV 9
DB 3 KQSYLGI 10
RESULT 21
US-10-877-022-63
Sequence 63, Application US/10877022
Publication No. US20040247613A1
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/877,022
FILING DATE: 24-Jun-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-Nov-1999
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-Oct-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..11
OTHER INFORMATION: /note="motif E peptide from
Drosophila melanogaster TART non-LTR
retrotransposable element reverse
transcriptase"
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-10-877-022-63
Query Match 40.6%; Score 26; DB 5; Length 11;
Best Local Similarity 50.0%; Pred. No. 8.6e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 2 KONTYALV 9
Db 3 KOSTYGVY 10
RESULT 22
US-10-877-146-63
Sequence 63, Application US/10877146
Publication No. US20050013825A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/877,146
FILING DATE: 24-Jun-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-Nov-1999
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..11
OTHER INFORMATION: /note="motif E peptide from
Drosophila melanogaster TART non-LTR
retrotransposable element reverse
transcriptase"
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-10-877-146-63
Query Match 40.6%; Score 26; DB 5; Length 11;
Best Local Similarity 50.0%; Pred. No. 8.6e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 2 KONTYALV 9
Db 3 KOSTYGVY 10
RESULT 23
US-08-908-884-23
Sequence 23, Application US/08908884
Publication No. US2002013872A1
GENERAL INFORMATION:
APPLICANT: Dong et al.
TITLE OF INVENTION: ACQUIRED RESISTANCE GENES AND USES THEREOF
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,884
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/023,851
FILING DATE: August 9, 1996
APPLICATION NUMBER: 60/035,166
FILING DATE: January 10, 1997
APPLICATION NUMBER: 60/046,769
FILING DATE: May 16, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L

REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/339004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-908-884-23

Query Match 40.6%; Score 26; DB 2; Length 14;
Best Local Similarity 41.7%; Pred. No. 1.1e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 KONYLALVRELK 13
Db 2 KORYMEIOETLK 13

RESULT 24
US-09-908-323-23
Sequence 23, Application US/09908323
Patent No. US20020073447A1
GENERAL INFORMATION:
APPLICANT: Dong et al.
TITLE OF INVENTION: ACQUIRED RESISTANCE GENES AND USES THEREOF
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,323
FILING DATE: 17-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/908,884
FILING DATE: <Unknown>
APPLICATION NUMBER: 60/035,166
FILING DATE: January 10, 1997
APPLICATION NUMBER: 60/046,769
FILING DATE: May 16, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L.
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/339004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-908-323-23

Query Match 40.6%; Score 26; DB 3; Length 14;
Best Local Similarity 41.7%; Pred. No. 1.1e+03;

Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 KONYLALVRELK 13
Db 2 KORYMEIOETLK 13

RESULT 25
US-10-084-813-684
Sequence 684, Application US/10084813
Publication No. US2003006615A1
GENERAL INFORMATION:
APPLICANT: SAXINGER, CARL
TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
FILE REFERENCE: 215875
CURRENT APPLICATION NUMBER: US/10/084,813
PRIOR FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: PCT/US00/23505
PRIOR FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US 60/151,270
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 1242
SOFTWARE: PatentIn version 3.1
SEQ ID NO 684
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-684

Query Match 40.6%; Score 26; DB 4; Length 15;
Best Local Similarity 30.8%; Pred. No. 1.2e+03;
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DKONYLALVRELK 13
Db 3 DQGNFPLIKNLK 15

Search completed: January 26, 2006, 08:38:34
Job time : 44.25 secs

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OM protein - protein search, using sw model

Run on: January 26, 2006, 08:05:12 : Search time 2.46552 Seconds
(without alignments)
57.099 Million cell updates/sec

Title: US-09-662-293-7
Perfect score: 64
Sequence: 1 DKQNYLALVRELK 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 37628

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries,

Database : Published Applications AA New:
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2: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
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8: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42.2	16	7	US-11-033-039-163	Sequence 163, App
2	40.6	19	7	US-11-166-412-150	Sequence 150, App
3	39.1	7	6	US-10-753-537-13	Sequence 13, Appl
4	39.1	7	7	US-11-039-268-13	Sequence 13, Appl
5	37.5	17	6	US-10-981-356A-18	Sequence 18, Appl
6	37.5	17	6	US-10-981-356A-24	Sequence 24, Appl
7	37.5	17	7	US-11-096-046-18	Sequence 18, Appl
8	37.5	17	7	US-11-096-046-24	Sequence 24, Appl
9	37.5	17	7	US-11-105-708-23	Sequence 23, Appl
10	37.5	17	7	US-11-136-559-27	Sequence 27, Appl
11	35.9	12	7	US-11-021-305-31	Sequence 31, Appl
12	35.9	20	7	US-11-041-893-201	Sequence 201, Appl
13	34.4	7	6	US-10-484-781-6	Sequence 6, Appl
14	34.4	9	7	US-11-045-024-3529	Sequence 3529, App
15	34.4	9	7	US-11-045-024-3575	Sequence 3575, App
16	34.4	9	7	US-11-045-024-3576	Sequence 3576, App
17	34.4	9	7	US-11-045-024-10581	Sequence 10581, A
18	34.4	9	7	US-11-045-024-10582	Sequence 10582, A
19	34.4	9	7	US-11-045-024-10720	Sequence 10720, A
20	34.4	9	7	US-11-045-024-12381	Sequence 12381, A
21	34.4	9	7	US-11-045-024-12385	Sequence 12385, A
22	34.4	9	7	US-11-045-024-12445	Sequence 12445, A
23	34.4	9	7	US-11-045-024-12456	Sequence 12456, A
24	34.4	9	7	US-11-045-024-13960	Sequence 13960, A
25	34.4	10	7	US-11-045-024-3581	Sequence 3581, App
	34.4	10	7	US-11-045-024-3582	Sequence 3582, App

26	34.4	10	7	US-11-045-024-10647	Sequence 10647, A
27	34.4	10	7	US-11-045-024-10716	Sequence 10716, A
28	34.4	10	7	US-11-045-024-12440	Sequence 12440, A
29	34.4	10	7	US-11-045-024-12452	Sequence 12452, A
30	34.4	11	7	US-11-045-024-3558	Sequence 3558, App
31	34.4	11	7	US-11-045-024-10541	Sequence 10541, A
32	34.4	11	7	US-11-045-024-12349	Sequence 12349, A
33	34.4	11	7	US-11-104-117-7	Sequence 7, Appl
34	34.4	12	6	US-10-501-111A-100	Sequence 100, App
35	34.4	12	6	US-10-501-111A-137	Sequence 137, App
36	34.4	12	6	US-11-021-305-29	Sequence 29, Appl
37	34.4	14	6	US-10-494-781-27	Sequence 27, Appl
38	34.4	15	6	US-10-494-781-28	Sequence 28, Appl
39	34.4	15	6	US-10-984-376-18	Sequence 18, Appl
40	34.4	15	7	US-11-045-024-13314	Sequence 13314, A
41	34.4	15	7	US-11-045-024-13324	Sequence 13324, A
42	34.4	15	7	US-11-045-024-13327	Sequence 13327, A
43	34.4	15	7	US-11-045-024-13345	Sequence 13345, A
44	34.4	15	7	US-11-045-024-13351	Sequence 13351, A
45	34.4	15	7	US-11-045-024-13359	Sequence 13359, A
46	34.4	15	7	US-11-045-024-13515	Sequence 13515, A
47	34.4	15	7	US-11-045-024-13516	Sequence 13516, A
48	34.4	15	7	US-11-045-024-14259	Sequence 14259, A
49	34.4	15	7	US-11-045-024-14521	Sequence 14521, A
50	34.4	19	6	US-10-503-575-296	Sequence 296, App
51	34.4	20	7	US-11-127-877-574	Sequence 574, App
52	34.4	20	7	US-11-166-412-90	Sequence 90, Appl
53	34.4	21	7	US-11-041-893-205	Sequence 205, App
54	33.6	18	7	US-11-010-748A-673	Sequence 673, App
55	32.8	6	6	US-10-485-788A-253	Sequence 253, App
56	32.8	7	6	US-10-485-788A-254	Sequence 254, App
57	32.8	8	6	US-10-485-788A-255	Sequence 255, App
58	32.8	8	7	US-11-045-024-4239	Sequence 4239, App
59	32.8	8	7	US-11-045-024-4240	Sequence 4240, App
60	32.8	8	7	US-11-045-024-9440	Sequence 9440, App
61	32.8	8	7	US-11-045-024-9481	Sequence 9481, App
62	32.8	8	7	US-11-045-024-11503	Sequence 11503, A
63	32.8	8	7	US-11-045-024-11525	Sequence 11525, A
64	32.8	9	7	US-11-045-024-4265	Sequence 4265, App
65	32.8	9	7	US-11-045-024-4266	Sequence 4266, App
66	32.8	9	7	US-11-045-024-9443	Sequence 9443, App
67	32.8	9	7	US-11-045-024-11505	Sequence 11505, A
68	32.8	9	7	US-11-045-024-14063	Sequence 14063, A
69	32.8	9	7	US-11-045-024-14063	Sequence 14063, A
70	32.8	10	7	US-11-045-024-9446	Sequence 9446, App
71	32.8	10	7	US-11-045-024-9482	Sequence 9482, App
72	32.8	10	7	US-11-045-024-11508	Sequence 11508, A
73	32.8	10	7	US-11-045-024-11536	Sequence 11536, A
74	32.8	11	7	US-11-045-024-4301	Sequence 4301, App
75	32.8	11	7	US-11-045-024-7450	Sequence 7450, App
76	32.8	11	7	US-11-045-024-7469	Sequence 7469, App
77	32.8	11	7	US-11-045-024-12664	Sequence 12664, A
78	32.8	12	6	US-10-973-977-4	Sequence 4, Appl
79	32.8	12	6	US-10-501-111A-49	Sequence 49, Appl
80	32.8	12	6	US-10-501-111A-64	Sequence 64, Appl
81	32.8	12	6	US-10-501-111A-133	Sequence 133, App
82	32.8	12	6	US-10-501-111A-143	Sequence 143, App
83	32.8	12	6	US-10-501-111A-144	Sequence 144, App
84	32.8	12	7	US-11-021-305-36	Sequence 36, Appl
85	32.8	13	6	US-10-511-559-1147	Sequence 1147, App
86	32.8	13	7	US-11-045-024-14262	Sequence 14262, A
87	32.8	13	7	US-11-045-024-14511	Sequence 14511, A
88	32.8	13	7	US-11-045-024-14513	Sequence 14513, A
89	32.8	14	6	US-10-889-197-27	Sequence 27, Appl
90	32.8	15	7	US-11-054-515-2234	Sequence 2234, App
91	32.8	15	7	US-11-045-024-13097	Sequence 13097, A
92	32.8	15	7	US-11-045-024-13404	Sequence 13404, A
93	32.8	15	7	US-11-045-024-13407	Sequence 13407, A
94	32.8	17	6	US-10-834-397-201	Sequence 201, App
95	32.8	17	6	US-10-834-197-229	Sequence 229, App
96	32.8	17	6	US-10-973-977-74	Sequence 74, Appl
97	32.8	18	6	US-10-467-657-3550	Sequence 3550, App
98	32.8	18	7	US-11-033-039-1237	Sequence 1237, App

99 21 32.8 18 7 US-11-220-439-4 Sequence 4, Appli
100 21 32.8 18 7 US-11-220-439-22 Sequence 22, Appli

ALIGNMENTS

RESULT 1
US-11-033-039-163

/ Sequence 163, Application US/11033039
/ Publication No. US20060002947A1
/ GENERAL INFORMATION:
/ APPLICANT: HUMPHREYS, ROBERT
/ APPLICANT: XU, MINZHEN
/ TITLE OF INVENTION: LT-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
/ FILE REFERENCE: REF-20170S01
/ CURRENT APPLICATION NUMBER: US/11/033,039
/ CURRENT FILING DATE: 2005-01-11
/ PRIOR APPLICATION NUMBER: 10/245,871
/ PRIOR FILING DATE: 2002-09-17
/ PRIOR APPLICATION NUMBER: 10/197,000
/ PRIOR FILING DATE: 2002-07-17
/ PRIOR APPLICATION NUMBER: 09/396,813
/ PRIOR FILING DATE: 1999-09-14
/ NUMBER OF SEQ ID NOS: 1452
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 163
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Felis catus
US-11-033-039-163

Query Match 42.2%; Score 27; DB 7; Length 16;
Best Local Similarity 55.6%; Pred. No. 19;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 DKONYLALV 9
|||:|:|:
Db 6 DKENALSL 14

RESULT 2
US-11-166-412-150

/ Sequence 150, Application US/11166412
/ Publication No. US20060014231A1
/ GENERAL INFORMATION:
/ APPLICANT: Van Rompaey, Luc
/ APPLICANT: Tonne, Peter H. M.
/ TITLE OF INVENTION: Methods and Compositions To Promote Bone Homeostasis
/ FILE REFERENCE: P27,927-D USA
/ CURRENT APPLICATION NUMBER: US/11/166,412
/ CURRENT FILING DATE: 2005-06-24
/ PRIOR APPLICATION NUMBER: 60/582,704
/ PRIOR FILING DATE: 2004-06-24
/ PRIOR APPLICATION NUMBER: 60/630,449
/ PRIOR FILING DATE: 2004-11-23
/ PRIOR APPLICATION NUMBER: 60/673,206
/ PRIOR FILING DATE: 2005-04-20
/ NUMBER OF SEQ ID NOS: 231
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 150
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Protein domain fragment
US-11-166-412-150

Query Match 40.6%; Score 26; DB 7; Length 19;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 5 YLALVRELLK 13

Db 3 YLAVVYPLK 11
|||:|:|

RESULT 3
US-10-753-537-13

/ Sequence 13, Application US/10753537
/ Publication No. US20050260230A1
/ GENERAL INFORMATION:
/ APPLICANT: STEWARD, LANCE E
/ APPLICANT: FERNANDEZ-SALAS, ESTER
/ APPLICANT: HERRINGTON, TODD M
/ APPLICANT: AOKI, KEI R
/ TITLE OF INVENTION: Leucine-based motif and clostridial neurotoxins
/ FILE REFERENCE: D-2885CIP
/ CURRENT APPLICATION NUMBER: US/10/753,537
/ CURRENT FILING DATE: 2004-01-08
/ PRIOR APPLICATION NUMBER: US/09/910,346C
/ PRIOR FILING DATE: 2000-07-21
/ PRIOR APPLICATION NUMBER: US 09/620,840
/ PRIOR FILING DATE: 2000-07-21
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 13
/ LENGTH: 7
/ TYPE: PRT
/ ORGANISM: frog
US-10-753-537-13

Query Match 39.1%; Score 25; DB 6; Length 7;
Best Local Similarity 83.3%; Pred. No. 5.8e+04;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DKONYL 6
|||:|:|
Db 2 DKONLL 7

RESULT 4
US-11-039-268-13

/ Sequence 13, Application US/11039268
/ Publication No. US20050276820A1
/ GENERAL INFORMATION:
/ APPLICANT: Steward, Lance
/ APPLICANT: HERRINGTON, Todd
/ APPLICANT: Aoki, Kei
/ TITLE OF INVENTION: LEUCINE-BASED MOTIF AND CLOSTRIDIAL NEUROTOXINS
/ FILE REFERENCE: ALLE0014-106 (17355DIV1)
/ CURRENT APPLICATION NUMBER: US/11/039,268
/ CURRENT FILING DATE: 2005-01-19
/ PRIOR APPLICATION NUMBER: 09/620,840
/ PRIOR FILING DATE: 2000-07-21
/ PRIOR APPLICATION NUMBER: DIV of 09/620,840
/ PRIOR FILING DATE: 2000-07-21
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 13
/ LENGTH: 7
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Fragment having properties substantially similar to that of
US-11-039-268-13

Query Match 39.1%; Score 25; DB 7; Length 7;
Best Local Similarity 83.3%; Pred. No. 5.8e+04;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DKONYL 6
|||:|:|
Db 2 DKONLL 7

```
RESULT 5
US-10-981-356A-18
; Sequence 18, Application US/10981356A
; Publication No. US20060015952A1
; GENERAL INFORMATION:
; APPLICANT: FILVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P2068R1
; CURRENT APPLICATION NUMBER: US/10/981,356A
; PRIOR FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 18
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-18

Query Match      37.5%; Score 24; DB 6; Length 17;
Best Local Similarity 57.1%; Pred. No. 73;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 DKONYLA 7
       : : : : :
Db      11 NOKNYLA 17

RESULT 6
US-10-981-356A-24
; Sequence 24, Application US/10981356A
; Publication No. US20060015952A1
; GENERAL INFORMATION:
; APPLICANT: FILVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P2068R1
; CURRENT APPLICATION NUMBER: US/10/981,356A
; PRIOR FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 24
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-981-356A-24

Query Match      37.5%; Score 24; DB 6; Length 17;
Best Local Similarity 57.1%; Pred. No. 73;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 DKONYLA 7
       : : : : :
Db      11 NOKNYLA 17

RESULT 7
US-11-096-046-18
; Sequence 18, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
```

```
APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954R1US
; CURRENT APPLICATION NUMBER: US/11/096,046
; PRIOR FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 18
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-096-046-18

Query Match      37.5%; Score 24; DB 7; Length 17;
Best Local Similarity 57.1%; Pred. No. 73;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 DKONYLA 7
       : : : : :
Db      11 NOKNYLA 17

RESULT 8
US-11-096-046-24
; Sequence 24, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954R1US
; CURRENT APPLICATION NUMBER: US/11/096,046
; PRIOR FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 24
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-096-046-24

Query Match      37.5%; Score 24; DB 7; Length 17;
Best Local Similarity 57.1%; Pred. No. 73;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 DKONYLA 7
       : : : : :
Db      11 NOKNYLA 17

RESULT 9
US-11-105-708-23
; Sequence 23, Application US/11105708
; Publication No. US20050281821A1
; GENERAL INFORMATION:
; APPLICANT: Pernasetti, Flavia
; APPLICANT: Freimark, Bruce
; APPLICANT: Van Bopp, Dennis
; APPLICANT: Brooks, Peter C
; TITLE OF INVENTION: Method and Composition for Angiogenesis Inhibition
; FILE REFERENCE: 30797-704.501
; CURRENT APPLICATION NUMBER: US/11/105,708
; PRIOR FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: 09/478,977
; PRIOR FILING DATE: 2000-01-06
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PRIOR APPLICATION NUMBER: 60/152,496
PRIOR FILING DATE: 1999-09-02
PRIOR APPLICATION NUMBER: 60/143,534
PRIOR FILING DATE: 1999-09-02
PRIOR APPLICATION NUMBER: 60/114,878
PRIOR FILING DATE: 1999-01-06
PRIOR APPLICATION NUMBER: 60/114,877
PRIOR FILING DATE: 1999-01-06
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.2
SEQ ID NO 23
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-11-105-708-23

Query Match 37.5% Score 24; DB 7; Length 17;
Best Local Similarity 57.1% Pred. No. 73;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 DKONYLA 7
Db 11 NQKNYLA 17

RESULT 10
US-11-136-559-27
Sequence 27, Application US/11136559
Publication No. US20050287164A1
GENERAL INFORMATION:
APPLICANT: PATTI, Joseph M
APPLICANT: HUTCHINS, Jeff T
APPLICANT: DOMANSKI, Paul
APPLICANT: PATEL, Pratiksha
APPLICANT: HALL, Andrea
TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLPA PROTEIN . . .
FILE REFERENCE: P07069US04/BAS
CURRENT APPLICATION NUMBER: US/11/136,559
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US/10/056,052
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: 60/308,116
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/298,413
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/274,611
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: 60/264,072
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27
LENGTH: 17
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-11-136-559-27

Query Match 37.5% Score 24; DB 7; Length 17;
Best Local Similarity 57.1% Pred. No. 73;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 DKONYLA 7
Db 11 NQKNYLA 17

RESULT 11
US-11-021-305-31
Sequence 31, Application US/11021305
Publication No. US20050282733A1
GENERAL INFORMATION:

APPLICANT: Prins, Johannes B
APPLICANT: Hutley, Louise J
TITLE OF INVENTION: Differentiation-modulating agents and uses therefor
FILE REFERENCE: DAV1169.001CPI
CURRENT APPLICATION NUMBER: US/11/021,305
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: USSN 60/392,130
PRIOR FILING DATE: 2002-06-27
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PatentIn version 3.3
SEQ ID NO 31
LENGTH: 12
TYPE: PRT
ORGANISM: mammalian
US-11-021-305-31

Query Match 35.9% Score 23; DB 7; Length 12;
Best Local Similarity 62.5% Pred. No. 75;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 NYLALVRE 11
Db 2 SYLALYTE 9

RESULT 12
US-11-041-893-201
Sequence 201, Application US/11041893
Publication No. US2006002941A1
GENERAL INFORMATION:
APPLICANT: Mahairas, Gregory G.
TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
FILE REFERENCE: 100123.401
CURRENT APPLICATION NUMBER: US/11/041,893
CURRENT FILING DATE: 2005-01-24
PRIOR APPLICATION NUMBER: US 60/616,855
PRIOR FILING DATE: 2004-10-06
PRIOR APPLICATION NUMBER: US 60/538,713
PRIOR FILING DATE: 2004-01-23
NUMBER OF SEQ ID NOS: 295
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 201
LENGTH: 20
TYPE: PRT
ORGANISM: Plasmodium falciparum
US-11-041-893-201

Query Match 35.9% Score 23; DB 7; Length 20;
Best Local Similarity 36.4% Pred. No. 1,4e+02;
Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 3 QNYLALVREIK 13
Db 4 ESYQELVKLR 14

RESULT 13
US-10-494-781-6
Sequence 6, Application US/10494781
Publication No. US20050244895A1
GENERAL INFORMATION:
APPLICANT: King's College London
TITLE OF INVENTION: Diagnosis of Demyelinating or Spongiform Disease
FILE REFERENCE: IT/KE/N13246
CURRENT APPLICATION NUMBER: US/10/494,781
CURRENT FILING DATE: 2004-05-06
PRIOR APPLICATION NUMBER: GB 0127000.8
PRIOR FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: GB 0202562.5
PRIOR FILING DATE: 2002-02-04
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1

SEQ ID NO 6
LENGTH: 7
TYPE: PRT
ORGANISM: Bovine
US-10-494-781-6

Query Match 34.4%; Score 22; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKON 4
DB 4 DKON 7

RESULT 14
US-11-045-024-3529
Sequence 3529, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:

APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Celis, Esteban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045.024
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3529

LENGTH: 9
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3529

Query Match 34.4%; Score 22; DB 7; Length 9;
Best Local Similarity 55.6%; Pred. No. 5.8e+04;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 YLALVRELK 13
DB 1 YLALITALIK 9

RESULT 15
US-11-045-024-3575
Sequence 3575, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:

APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Celis, Esteban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045.024
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3575

LENGTH: 9
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3575

Query Match 34.4%; Score 22; DB 7; Length 9;
Best Local Similarity 62.5%; Pred. No. 5.8e+04;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 LALVRELK 13
DB 2 LELLELRLK 9

RESULT 16
US-11-045-024-3576
Sequence 3576, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:

APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Celis, Esteban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045.024
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205


```
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
FILE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
PRIOR FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10720
LENGTH: 9
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-10720
```

```
Query Match 34.4% Score 22; DB 7; Length 9;
Best Local Similarity 62.5%; Pred. No. 5.8e+04;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 6 LALVREIK 13
DB 2 LELLEBK 9

RESULT 20
US-11-045-024-12381
Sequence 12381, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Cells, Esteban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
FILE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
PRIOR FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
```

```
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12381
LENGTH: 9
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12381
```

```
Query Match 34.4% Score 22; DB 7; Length 9;
Best Local Similarity 55.6%; Pred. No. 5.8e+04;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 5 LALVREIK 13
DB 1 YLALITALIK 9

RESULT 21
US-11-045-024-12445
Sequence 12445, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Cells, Esteban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
FILE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
PRIOR FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12445
LENGTH: 9
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12445
```

```
Query Match 34.4% Score 22; DB 7; Length 9;
Best Local Similarity 62.5%; Pred. No. 5.8e+04;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 6 LALVREIK 13
DB 2 LELLEBK 9
```

```
RESULT 22
US-11-045-024-12496
; Sequence 12496, Application US/11045024
; Publication NO. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Estebean
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12496
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12496

Query Match      34.4%; Score 22; DB 7; Length 9;
Best Local Similarity 62.5%; Pred. No. 5.8e+04;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
RESULT 23
US-11-045-024-13980
; Sequence 13980, Application US/11045024
; Publication NO. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Estebean
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13980

Query Match      34.4%; Score 22; DB 7; Length 9;
Best Local Similarity 55.6%; Pred. No. 5.8e+04;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
RESULT 24
US-11-045-024-3581
; Sequence 3581, Application US/11045024
; Publication NO. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Estebean
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3581
```


LENGTH: 10
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3581

Query Match 34.4%; Score 22; DB 7; Length 10;
Best Local Similarity 62.5%; Pred. No. 94;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 6 LALVRELK 13
| : |||
Db 3 LELLEELK 10

RESULT 25
US-11-045-024-3582
Sequence 3582, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Celis, Eserben
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045.024
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3582
LENGTH: 10
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3582

Query Match 34.4%; Score 22; DB 7; Length 10;
Best Local Similarity 62.5%; Pred. No. 94;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 6 LALVRELK 13
| : |||
Db 3 LELLEELK 10

Search completed: January 26, 2006, 08:39:06
Job time : 2.46552 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:48:50 ; Search time 6.5 Seconds

(without alignments)
192,434 Million cell updates/sec

Title: US-09-662-293-7

Perfect score: 64

Sequence: 1 DKONYLALVRELK 13

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 4071

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: PIR.80:*
2: p1r1:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	39.1	15	2 A41338	isocitrate lyase (
2	25	39.1	20	2 S19615	globin - polychaet
3	24	37.5	18	2 A20923	light meromyosin -
4	24	37.5	20	2 S35970	ribosomal protein
5	24	37.5	21	2 S35978	ribosomal protein
6	23	35.9	20	2 A44921	hydroxypyruvate re
7	22	34.4	14	2 PA0015	seed storage prote
8	21	32.8	18	2 S49026	ribosomal protein
9	21	32.8	20	2 S71017	hypothetical prote
10	21	32.8	20	2 S4465	pyrithocorcin - Py
11	20	31.2	11	2 PU0034	dextranucrase (EC
12	20	31.2	17	2 I55226	myosin heavy chain
13	20	31.2	17	2 E29501	fibritinopeptide A -
14	20	31.2	17	2 A35550	adrenocortical cel
15	20	31.2	20	2 B53875	creatinase kinase (E
16	20	31.2	20	2 A61150	2-oxoglutarate dec
17	20	31.2	21	2 PD0015	actin-binding prot
18	19	29.7	7	2 S71867	glutathione transf
19	19	29.7	11	2 I52980	glucose-6-phosphat
20	19	29.7	14	2 S29486	GTP-binding protei
21	19	29.7	15	2 PQ0193	scylar glycoprotei
22	19	29.7	15	2 PQ0784	T-cell receptor al
23	19	29.7	16	2 S10809	T-cell receptor al
24	19	29.7	16	2 PH1778	protein kinase C i
25	19	29.7	16	2 PH1781	T cell receptor al
26	19	29.7	17	2 PC2196	zymogen granule me
27	19	29.7	17	2 PH0769	T-cell receptor be
28	19	29.7	18	2 B44995	alkanal monooxygen
29	19	29.7	18	2 PH1792	T cell receptor al

30	19	29.7	19	2 JP0054	ribosomal protein
31	19	29.7	20	2 CA9164	chromogranin-B - r
32	19	29.7	20	2 JP0053	ribosomal protein
33	19	29.7	20	2 JP0055	ribosomal protein
34	19	29.7	20	2 H49034	nuclear antigen EB
35	19	29.7	20	2 PH1783	T cell receptor al
36	19	29.7	20	2 T01691	hypothetical prote
37	19	29.7	20	2 AE0120	insertion element
38	19	29.7	21	2 PH1369	ig heavy chain DJ
39	18	28.1	9	2 PT0270	ig heavy chain CRD
40	18	28.1	13	4 I70075	glycophorin B (mis
41	18	28.1	14	2 PH1705	ig heavy chain V r
42	18	28.1	14	2 D61308	hemocyanin chain 5
43	18	28.1	15	2 PQ0195	Sfil-glycoprotein
44	18	28.1	15	2 PA0046	protein QAI00044 -
45	18	28.1	15	2 PQ0192	scylar glycoprotei
46	18	28.1	15	2 PH1616	ig H chain V-D-J r
47	18	28.1	15	2 S29175	D-galactose-bindin
48	18	28.1	16	2 S10807	protein kinase C i
49	18	28.1	17	2 S09607	phenylalanine-cRNA
50	18	28.1	17	2 UQ2320	hypothetical 2.1K
51	18	28.1	18	2 C56211	progesterone recep
52	18	28.1	18	2 A60118	22K protein - Lyme
53	18	28.1	18	2 A45138	arsenite oxidase I
54	18	28.1	19	2 S59717	hypothetical prote
55	18	28.1	20	2 S46205	comosain (EC 3.4.2
56	18	28.1	20	2 A20999	fructose-bisphosph
57	18	28.1	20	2 I67551	monocyte chemotact
58	18	28.1	20	2 C56385	nitrophenol 3 - Rh
59	18	28.1	20	2 A05310	apolipoprotein E -
60	18	28.1	21	2 PH1731	ig heavy chain V r
61	18	28.1	21	2 PH1730	ig heavy chain V r
62	17	26.6	7	2 PS0254	18K protein 5507 -
63	17	26.6	9	2 A33527	fructose-2,6-bisph
64	17	26.6	10	2 PN0136	pepsin (EC 3.4.23
65	17	26.6	10	2 PT0243	ig heavy chain CRD
66	17	26.6	11	2 S66606	guinoline 2-oxidor
67	17	26.6	12	2 A40763	sucrose-6-phosphat
68	17	26.6	12	2 S10624	lipovitelin - Afr
69	17	26.6	12	2 F84132	hypothetical prote
70	17	26.6	13	2 S09733	photosystem I prot
71	17	26.6	15	2 I46512	tropomn - rabbit
72	17	26.6	15	2 PQ0194	Sz-glycoprotein -
73	17	26.6	15	2 A41436	alpha-macroglobuli
74	17	26.6	16	2 S10808	protein kinase C i
75	17	26.6	16	2 B60566	cytochrome P450m51
76	17	26.6	16	2 S09732	photosystem I prot
77	17	26.6	17	1 A05168	conantokin G [vali
78	17	26.6	17	2 I46511	tropomn - rabbit
79	17	26.6	17	2 A46592	lactase-phlorizin
80	17	26.6	17	2 UQ2310	hypothetical 2.1K
81	17	26.6	19	2 PQ0409	RNA-directed RNA P
82	17	26.6	20	2 PN0133	pepsin (EC 3.4.23
83	17	26.6	20	2 S68028	iodochromine 5'-mo
84	17	26.6	20	2 S18582	hypothetical prote
85	17	26.6	20	2 I54189	galactose-1-phosph
86	17	26.6	20	2 S35921	T-cell receptor ga
87	17	26.6	20	2 S03954	acidic fibroblast
88	17	26.6	20	2 AC0269	probable trp opero
89	17	26.6	21	2 PQ0749	self-incompatibili
90	16	25.0	8	2 S70727	lpgf protein - Shi
91	16	25.0	9	2 I54379	gene NF2 protein -
92	16	25.0	12	2 PH1675	ig heavy chain V r
93	16	25.0	12	2 A34858	proteinase E - bla
94	16	25.0	13	2 PH1676	ig heavy chain V r
95	16	25.0	13	2 E60396	antigen 7H8/2 - ma
96	16	25.0	14	2 JN0389	histamine-releasin
97	16	25.0	14	2 PH1677	ig heavy chain V r
98	16	25.0	14	2 PC1215	homeotic protein E
99	16	25.0	14	2 A44920	2-halo benzate 1,2
100	16	25.0	15	2 PQ0174	scylar glycoprotei

ALIGNMENTS

RESULT 1

A1138
Isocitrate lyase (EC 4.1.3.1) - Acinetobacter calcoaceticus (fragment)
C/Species: Acinetobacter calcoaceticus
C/Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 09-Jul-2004
C/Accession: A1138
R/Hoyt, J.C.; Johnson, K.E.; Reeves, H.C.
J. Bacteriol. 173, 6844-6848, 1991
A/Title: Purification and characterization of Acinetobacter calcoaceticus isocitrate lyase
A/Reference number: A1138; MUID:92041568; PMID:1938889
A/Accession: A1138
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-15 <HOY>
A/Cross-references: UNIPROT:P28467; UNIPARC:UPI00001251F5
C/Keywords: carbon-carbon lyase; oxo-acid-lyase

Query Match 39.1%; Score 25; DB 2; Length 15;

Best Local Similarity 54.5%; Pred. No. 3.8e+02; Mismatches 4; Gaps 0;

Matches 6; Conservative 1; Indels 0;

QY 3 QNYLALVRELK 13

Db 4 QTAIDAVRELK 14

RESULT 2

S19615
globin - polychaete (Eudistylia vancouveri) (fragment)
N/Alternate names: chlorochuorin
C/Species: Eudistylia vancouveri
C/Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 09-Jul-2004
C/Accession: S19615
R/Qabar, A.N.; Stern, M.S.; Walz, D.A.; Chiu, J.T.; Tinkovich, R.; Wall, J.S.; Kapp, O.H.
J. Mol. Biol. 222, 1109-1129, 1991
A/Title: Hierarchy of globin complexes. The quaternary structure of the extracellular chain
A/Reference number: S19532; MUID:92106333; PMID:1962147
A/Accession: S19615
A/Molecule type: protein
A/Residues: 1-20 <QAB>
A/Cross-references: UNIPROT:Q7M3Q5; UNIPARC:UPI000017BD6C
A/Experimental source: plume
C/Keywords: calcium; dodecamer; heme; homotetramer; oxygen carrier

Query Match 39.1%; Score 25; DB 2; Length 20;

Best Local Similarity 50.0%; Pred. No. 5.1e+02; Mismatches 1; Indels 0;

Matches 4; Conservative 3; Indels 0;

QY 1 DKONYLAL 8

Db 12 DRQNLMS 19

RESULT 3

A20923
light meromyosin - chicken (fragment)
C/Species: Gallus gallus (chicken)
C/Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Dec-2004
C/Accession: A20923
R/Nyitrai, L.; Mocz, G.; Szilagyi, L.; Balint, M.; Lu, R.C.; Wong, A.; Gergely, J.
J. Biol. Chem. 258, 13213-13220, 1983
A/Title: The proteolytic substructure of light meromyosin.
A/Reference number: A92403; MUID:84032553; PMID:6355107
A/Accession: A20923
A/Molecule type: protein
A/Residues: 1-18 <NYI>
A/Cross-references: UNIPROT:Q8J572; UNIPARC:UPI00001775EC
C/Suprafamily: myosin motor domain homology
C/Keywords: ATP; muscle

Query Match 37.5%; Score 24; DB 2; Length 18;

Best Local Similarity 41.7%; Pred. No. 6.9e+02; Mismatches 5; Conservative 2; Mismatches 5; Indels 0;

QY 2 KONYLALVRELK 13

Db 2 KOAFTQOIRELK 13

RESULT 4

S35970
ribosomal protein L10 - Citrobacter freundii (fragment)
C/Species: Citrobacter freundii
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S35970
R/Zhyvoloup, A.
submitted to the EMBL Data Library, August 1993
A/Reference number: S35970
A/Accession: S35970
A/Molecule type: DNA
A/Residues: 1-20 <ZHY>
A/Cross-references: UNIPROT:P43448; UNIPARC:UPI0000177309; EMBL:X74448
C/Genetics:
A/Gene: rplJ
C/Suprafamily: Escherichia coli ribosomal protein L10
C/Keywords: protein biosynthesis; ribosome

Query Match 37.5%; Score 24; DB 2; Length 20;

Best Local Similarity 50.0%; Pred. No. 7.7e+02; Mismatches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DKONYLALVREL 12

Db 7 DKQALVAVSEV 18

RESULT 5

S35978
ribosomal protein L10 - Proteus vulgaris (fragment)
C/Species: Proteus vulgaris
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C/Accession: S35978
R/Zhyvoloup, A.
submitted to the EMBL Data Library, August 1993
A/Reference number: S35970
A/Accession: S35978
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-21 <ZHY>
A/Cross-references: UNIPROT:P51411; UNIPARC:UPI000016EADB; EMBL:X74446; NID:G396471; PID:G396471
A/Gene: rplJ
C/Suprafamily: Escherichia coli ribosomal protein L10
C/Keywords: protein biosynthesis; ribosome

Query Match 37.5%; Score 24; DB 2; Length 21;

Best Local Similarity 50.0%; Pred. No. 8.1e+02; Mismatches 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DKONYLALVREL 12

Db 7 DKQALVAVSEV 18

RESULT 6

A44921
hydroxyphenylacetate reductase (EC 1.1.1.81) - Methylobacterium extorquens (fragment)
C/Species: Methylobacterium extorquens
C/Date: 01-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C/Accession: A44921
R/Chistoserdova, L.V.; Lidstrom, M.E.
J. Bacteriol. 174, 71-77, 1992

A:Title: Cloning, mutagenesis, and physiological effect of a hydroxypyruvate reductase g
 A:Reference number: A44921; MUID:92104992; PMID:1729225
 A:Contents: AM1
 A:Accession: A44921
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-20 <CHI>
 A:Cross-references: UNIPARC:UPI000016P931; GB:M81443; NID:G150010; PIDN:AAA25378.1; PID:
 A:Note: sequence extracted from NCBI backbone (NCBIN:75202, NCBI:75203)
 A:Keywords: oxidoreductase

Query Match 35.9%; Score 23; DB 2; Length 20;
 Best Local Similarity 45.5%; Pred. No. 1.2e+03;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DKONYLALVRE 11
 ||: |||
 Db 9 DRESLDATVRE 19

RESULT 7

PA0015
 seed storage protein 12S 2 - Arabidopsis thaliana (fragment)
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 11-Jul-1997
 C:Accession: PA0015
 R:Kamo, M.; Kawakami, T.; Miyake, N.; Tsugita, A.
 Submitted to JIPID, July 1994
 A:Description: Separation and characterization of Arabidopsis proteins by two-dimensions
 A:Reference number: PA0001
 A:Accession: PA0015
 A:Molecule type: protein
 A:Residues: 1-14 <KAM>
 A:Cross-references: UNIPARC:UPI000017B010
 A:Experimental source: seed
 C:Keywords: pyroglyutamic acid; seed; storage protein
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 34.4%; Score 22; DB 2; Length 14;
 Best Local Similarity 36.4%; Pred. No. 1.3e+03;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 ONYALVRELK 13
 ||: |||
 Db 1 QOYLGVPEQLQ 11

RESULT 8

S49026
 ribosomal protein H525 [validated] - Haloarcula marismortui (fragment)
 C:Species: Haloarcula marismortui
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C:Accession: S49026; S63967
 R:Engemann, S.; Herfurth, E.; Briesemeister, U.; Grelle, G.; Wittmann-Liebold, B.
 Submitted to the Protein Sequence Database, November 1994
 A:Description: Cartography of ribosomal proteins of the 30S subunit from the halophilic
 A:Reference number: S49023
 A:Accession: S49026
 A:Molecule type: protein
 A:Residues: 1-18 <ENG>

A:Cross-references: UNIPROT:Q7M532; UNIPARC:UPI000017AE43
 R:Engemann, S.; Noelle, R.; Herfurth, E.; Briesemeister, U.; Grelle, G.; Wittmann-Liebold,
 B.; J. Biochem. 234, 24-31, 1995
 A:Title: Cartography of ribosomal proteins of the 30S subunit from the halophilic Haloar

A:Reference number: S63964; MUID:96096717; PMID:8529646
 A:Accession: S63967
 A:Molecule type: protein
 A:Residues: 1-18 <ENW>

A:Cross-references: UNIPARC:UPI000017AE43
 C:Keywords: blocked amino end; protein biosynthesis; ribosome

Query Match 32.8%; Score 21; DB 2; Length 18;
 Best Local Similarity 55.6%; Pred. No. 2.5e+03;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 3 ONYALVRE 11
 ||: |||
 Db 10 RNVLGPPVRE 18

RESULT 9

S71017
 hypothetical protein - Streptococcus pneumoniae (fragment)
 C:Species: Streptococcus pneumoniae
 C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 31-Dec-2004
 C:Accession: S71017
 R:Martin, B.; Sharples, G.J.; Humbert, O.; Lloyd, R.G.; Claverie, J.P.
 Mol. Microbiol. 19, 1035-1045, 1996
 A:Title: The mmsA locus of Streptococcus pneumoniae encodes a RecG-like protein involve

A:Reference number: S71015; MUID:96249697; PMID:8830261
 A:Accession: S71017
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA

A:Residues: 1-20 <MAR>
 A:Cross-references: UNIPROT:Q97PE0; UNIPROT:Q8DNU1; UNIPARC:UPI000017AC6F; EMBL:Z49988
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995
 C:Superfamily: cephalosporin-C deacetylase

Query Match 32.8%; Score 21; DB 2; Length 20;
 Best Local Similarity 57.1%; Pred. No. 2.7e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 ALVRELK 13
 ||: |||
 Db 5 ALLEELK 11

RESULT 10

S44465
 pyrrhocoriclin - Pyrrhocoris apterus
 C:Species: Pyrrhocoris apterus
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C:Accession: S44465
 R:Cociancich, S.; Dupont, A.; Hegy, G.; Lanot, R.; Holder, F.; Hetru, C.; Hoffmann, J.A.
 Biochem. J. 300, 567-575, 1994
 A:Title: Novel inducible antibacterial peptides from a hemipteran insect, the sap-suckl

A:Reference number: S44463; MUID:94271176; PMID:8002963
 A:Accession: S44465
 A:Molecule type: protein
 A:Residues: 1-20 <COC>
 A:Cross-references: UNIPROT:P37362; UNIPARC:UPI0000132E13
 C:Function:

A:Description: antibacterial protein
 A:Note: active against Gram-negative bacteria
 C:Keywords: antibacterial; hemolymph; immune response

Query Match 32.8%; Score 21; DB 2; Length 20;
 Best Local Similarity 66.7%; Pred. No. 2.7e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DKONYL 6
 ||: |||
 Db 2 DKGSYL 7

RESULT 11

PU0034
 dextransucrase (EC 2.4.1.5) - Streptococcus bovis (fragment)
 C:Species: Streptococcus bovis
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
 C:Accession: PU0034

R:Uezono, Y.; Tsumori, H.; Mukasa, H.
 Submitted to JIPID, October 1993
 A:Description: Purification and properties of glucosyltransferase synthesizing 1,6-alpha

A:Reference number: PU0034
 A:Accession: PU0034

A:Molecule type: protein

A:Residues: 1-11 <UEZ>

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: 155226

R:Weydert, A.; Daudas, P.; Caravatti, M.; Minty, A.; Bugalsky, G.; Cohen, A.; Robert, B.

J. Biol. Chem. 259, 13867-13874, 1983

A:Title: Sequential accumulation of mRNAs encoding different myosin heavy chain isoforms

in fast myosin heavy chain from mouse skeletal muscle.

A:Reference number: 155226; PMID:84061805; PMID:6196357

A:Accession: 155226

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-17 <RES>

A:Cross-references: UNIPROT:Q61932; UNIPARC:UPI00000E7F83; GB:K00986; NID:G199975; PIDN:

A:Superfamily: myosin heavy chain; myosin motor domain homology

Query Match 31.2% Score 20; DB 2; Length 11;

Best Local Similarity 36.4%; Pred. No. 2.3e+03;

Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 DKONYLALVRE 11

1 DETAVALTRE 11

RESULT 12

155226

myosin heavy chain - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: 155226

R:Weydert, A.; Daudas, P.; Caravatti, M.; Minty, A.; Bugalsky, G.; Cohen, A.; Robert, B.

J. Biol. Chem. 259, 13867-13874, 1983

A:Title: Sequential accumulation of mRNAs encoding different myosin heavy chain isoforms

in fast myosin heavy chain from mouse skeletal muscle.

A:Reference number: 155226; PMID:84061805; PMID:6196357

A:Accession: 155226

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-17 <RES>

A:Cross-references: UNIPROT:Q61932; UNIPARC:UPI00000E7F83; GB:K00986; NID:G199975; PIDN:

A:Superfamily: myosin heavy chain; myosin motor domain homology

Query Match 31.2% Score 20; DB 2; Length 17;

Best Local Similarity 27.3%; Pred. No. 3.5e+03;

Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

3 ONYLAVALRELK 13

1 RNHLRVESMQ 11

RESULT 13

E29501

fibrinopeptide A - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 09-Jul-2004

C:Accession: E29501

R:Blomback, B.; Blomback, M.; Hann, C.

unpublished results, cited by Blomback, B., in Chemotaxonomy and Ser

A:Reference number: A29501

A:Accession: E29501

A:Molecule type: protein

A:Residues: 1-17 <BLO>

A:Cross-references: UNIPROT:P14460; UNIPARC:UPI000012A764

R:Blomback, B.; Blomback, M.; Groendahl, N.J.

Acta Chem. Scand. 19, 1789-1791, 1965

A:Title: Studies on fibrinopeptides from mammals.

A:Reference number: A03118

A:Contents: annotation; confirmation of species assignment

C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfid

Query Match 31.2% Score 20; DB 2; Length 17;

Best Local Similarity 57.1%; Pred. No. 3.5e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 DKONYLA 7

5 DKGEFLA 11

RESULT 14

A35550

adrenocortical cell major secreted protein - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C:Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 09-Jul-2004

C:Accession: A35550

R:Shi, D.L.; Savona, C.; Gagnon, J.; Cochet, C.; Chambaz, E.M.; Feige, J.J.

J. Biol. Chem. 265, 2881-2887, 1990

A:Title: Transforming growth factor-beta stimulates the expression of alpha-2-macroglobu

A:Reference number: A35550; PMID:90153919; PMID:1689294

A:Accession: A35550

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-17 <SHI>

A:Cross-references: UNIPROT:Q7M2N4; UNIPARC:UPI000017C495

Query Match 31.2% Score 20; DB 2; Length 17;

Best Local Similarity 45.5%; Pred. No. 3.5e+03;

Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

2 KONYLALVREL 12

5 KPLYMVLPPL 15

RESULT 15

B53875

creatine kinase (EC 2.7.3.2) CK-I - coho salmon (fragment)

C:Species: Oncorhynchus kisutch (coho salmon)

C:Date: 26-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: B53875

R:White, K.C.; Babbitt, P.C.; Buechter, D.D.; Kenyon, G.L.

J. Protein Chem. 11, 489-494, 1992

A:Title: The principal islet of the coho salmon (Oncorhynchus kisutch) contains the BB is

A:Reference number: A53875; PMID:93080727; PMID:1449598

A:Accession: B53875

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-20 <WHI>

A:Cross-references: UNIPROT:Q9PSI4; UNIPARC:UPI00000PBF09

A:Experimental source: Brockmann body, principal islet

A>Note: sequence extracted from NCBI backbone (NCBI:P120600)

C:Superfamily: creatine kinase; creatine kinase repeat homology

C:Keywords: phosphotransferase

Query Match 31.2% Score 20; DB 2; Length 20;

Best Local Similarity 66.7%; Pred. No. 4.1e+03;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 KONYLA 7

10 KMNYSA 15

RESULT 16

A61150

2-oxoglutarate decarboxylase (EC 4.1.1.71) - Euglena gracilis (fragment)

C:Species: Euglena gracilis

C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004

C:Accession: A61150

R:Shigekawa, S.; Nakano, Y.

Arch. Biochem. Biophys. 288, 22-28, 1991

A:Title: Characterization and molecular properties of 2-oxoglutarate decarboxylase from

A:Reference number: A61150; PMID:91378443; PMID:1910306

A:Accession: A61150

A:Molecule type: protein

A:Residues: 1-20 <SHI>

A:Cross-references: UNIPROT:Q7M266; UNIPARC:UPI000017AED8

C:Keywords: carbon-carbon lyase; carboxy-lyase; homotetramer; mitochondrion

Query Match 31.2% Score 20; DB 2; Length 20;

Best Local Similarity 44.4%; Pred. No. 4.1e+03;

Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

5 YLALVRELK 13

Db 3 YKAPVKDVK 11

RESULT 17

PD0015
 A:Title: actin-binding protein - Tetrahymena pyriformis (fragment)
 C:Species: Tetrahymena pyriformis
 C>Date: 13-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004
 C:Accession: PD0015
 R:Watanabe, A.; Kuraseawa, Y.; Watanabe, Y.; Numata, O.
 J. Biochem. 123, 607-613, 1998
 A:Title: A new Tetrahymena actin-binding protein is localized in the division furrow.
 A:Reference number: PD0015; MUID:98207047; PMID:9538250
 A:Accession: PD0015
 A:Molecule type: protein
 A:Residues: 1-21 <MAT>
 A:Cross-references: UNIPROT:P81424; UNIPARC:UPI000012A412
 C:Genetics:
 A:Genetic code: SGCS
 C:Superfamily: plastin; alpha-actinin actin-binding domain homology; calmodulin repeat h
 C:Keywords: EF hand

Query Match 31.2%; Score 20; DB 2; Length 21;
 Best Local Similarity 40.0%; Pred. No. 4.3e+03;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 DKONYLALVR 10
 |||:
 Db 6 DLKHPYLIR 15

RESULT 18

S7167
 A:Title: glutathione transferase (EC 2.5.1.18) class alpha 5 - pig (fragment)
 N:Alternate names: glutathione S-transferase class alpha 5
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
 C:Accession: S7167
 R:Roitman, P.; Anglade, P.; Debrauwer, L.; Tulliez, J.
 Biochem. J. 317, 879-884, 1996
 A:Title: Characterization of pig liver glutathione S-transferases using HPLC-electrospira
 A:Reference number: S71674; MUID:96332484; PMID:8760377
 A:Accession: S7167
 A:Molecule type: protein
 A:Residues: 1-7 <ROU>
 A:Cross-references: UNIPARC:UPI00001754D3
 C:Comment: At least five species-independent classes of cytosolic glutathion transferase
 s mitochondrial form are known.
 C:Complex: dimer
 C:Function:
 A:Description: catalyzes the nucleophilic conjugation of intracellular glutathione to a
 A:Pathway: detoxification; xenobiotic metabolism
 A>Note: increased hydrophilicity of GSH-conjugates facilitates their further metabolism
 C:Superfamily: glutathione transferase
 C:Keywords: dimer; transferase

Query Match 29.7%; Score 19; DB 2; Length 7;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 NYLA 7
 |||:
 Db 4 NYIA 7

RESULT 19

I52980
 A:Title: glucocerebrosidase - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
 C:Accession: I52980; I65971

R:Reiner, O.; Wiggerson, M.; Horowitz, M.
 DNA 7, 107-116, 1988

A:Title: Structural analysis of the human glucocerebrosidase genes.
 A:Reference number: I52980; MUID:88195776; PMID:3359914
 A:Accession: I52980
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-11 <RES>
 A:Cross-references: UNIPARC:UPI000016A981; GB:M18916; NID:G183023; PIDN:AAA35878.1; PID
 A:Accession: I65971
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-11 <RE2>
 A:Cross-references: UNIPARC:UPI000016A981; GB:M18917; NID:G183025; PIDN:AAA35879.1; PID

Query Match 29.7%; Score 19; DB 2; Length 11;
 Best Local Similarity 80.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 9 VRELK 13
 |||:
 Db 7 VRELE 11

RESULT 20

S29486
 A:Title: GTP-binding protein o-rab3 - electric ray (Discothyge ommata) (fragment)
 C:Species: Discothyge ommata
 C>Date: 22-Nov-1993 #sequence_revision 27-Feb-1997 #text_change 13-Mar-1997
 C:Accession: S29486
 R:Volkmann, W.; Pevaner, J.; Elferink, L.A.; Scheller, R.H.
 FEBS Lett. 317, 53-56, 1993
 A:Title: Association of three small GTP-binding proteins with cholinergic synaptic vesic
 A:Reference number: S29485; MUID:93154521; PMID:8428634
 A:Accession: S29486
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-14 <VOL>
 A:Cross-references: UNIPARC:UPI000017BF30

Query Match 29.7%; Score 19; DB 2; Length 14;
 Best Local Similarity 42.9%; Pred. No. 4.4e+03;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 QNYLALV 9
 |||:
 Db 7 QNFNAVI 13

RESULT 21

PQ0193
 A:Title: stylar glycoprotein 3 - Peruvian tomato (fragment)
 N:Alternate names: S3-glycoprotein
 C:Species: Lycopersicon peruvianum (Peruvian tomato)
 C>Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 23-Aug-1997
 C:Accession: PQ0193; A28819
 R:Ma, S.L.; Williams, E.G.; Atkinson, A.; Anderson, M.A.; Cornish, E.C.; Grego, B.; Si
 Planta 169, 184-191, 1986
 A:Title: Style proteins of a wild tomato (Lycopersicon peruvianum) associated with expr
 A:Reference number: PQ0192
 A:Accession: PQ0193
 A:Molecule type: protein
 A:Residues: 1-15 <MAU>
 A:Cross-references: UNIPARC:UPI00001427C8
 A:Experimental source: style, strain Mill
 R:Anderson, M.A.; Cornish, E.C.; Ma, S.L.; Williams, E.G.; Hoggart, R.; Atkinson, A.;
 J.P.; Crawford, R.J.; Clarke, A.E.
 Nature 321, 38-44, 1986
 A:Title: Cloning of cDNA for a stylar glycoprotein associated with expression of self-i
 A:Reference number: A28819
 A:Accession: A28819
 A:Status: preliminary
 A:Molecule type: protein

A:Residues: 1-15 <AND>
A:Cross-references: UNIPARC:UPI00001427C8
C:Keywords: glycoprotein

Query Match 29.7%; Score 19; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 4.7e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 NYLALV 9
|:|:|
Db 3 DYQLDV 8

RESULT 22

PH0784
T-cell receptor alpha chain (F1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PH0784
R:Caranova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-II allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846; PMID:1836010
A:Accession: PH0784
A:Molecule type: mRNA
A:Residues: 1-15 <CAS>
A:Cross-references: UNIPARC:UPI000017C76B; EMBL:X60885
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 29.7%; Score 19; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 4.7e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 DKONYLAL 8
|:|:|
Db 5 DPSNNVL 12

RESULT 23

S10809
protein kinase C inhibitor KClP-1 isoform f - sheep (fragment)
N:Alternate names: probable lipocortin
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 19-Mar-1997 #sequence_revision 13-Sep-1998 #text_change 13-Sep-1998
C:Accession: S10809
R:Tokery, A.; Ellis, C.A.; Sellers, L.A.; Aitken, A.
Eur. J. Biochem. 191, 421-429, 1990
A:Title: Protein kinase C inhibitor proteins. Purification from sheep brain and sequence
A:Reference number: S10804; MUID:90345949; PMID:2143472
A:Accession: S10809
A:Molecule type: protein
A:Residues: 1-16 <TK>
A:Cross-references: UNIPARC:UPI00001758AA
A:Experimental source: brain
C:Superfamily: 14-3-3 protein

Query Match 29.7%; Score 19; DB 2; Length 16;
Best Local Similarity 55.6%; Pred. No. 5e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 DKONYLALV 9
|:|:|
Db 3 DYVRLAEV 11

RESULT 24

PH1778
T cell receptor alpha chain V region (clone 1PBL V alpha 24-5) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1778

R:Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balz, S.P.
J. Exp. Med. 178, 1-16, 1993

A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A:Reference number: PH1754; MUID:93301585; PMID:8391057
A:Accession: PH1778
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-16 <FOR>
A:Cross-references: UNIPARC:UPI000017C36C

Query Match 29.7%; Score 19; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 5e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 YLALVR 10
|:|:|
Db 1 YICVVR 6

RESULT 25

PH1781
T cell receptor alpha chain V region (clone 2DN V alpha 24-2) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1781
R:Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balz, S.P.
J. Exp. Med. 178, 1-16, 1993
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood
A:Reference number: PH1754; MUID:93301585; PMID:8391057
A:Accession: PH1781
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-16 <FOR>
A:Cross-references: UNIPARC:UPI000017C374

Query Match 29.7%; Score 19; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 5e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 YLALVR 10
|:|:|
Db 1 YICVVR 6

Search completed: January 26, 2006, 08:05:00
Job time : 9.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:47:56 ; Search time 38.6638 Seconds
(without alignments)
237.221 Million cell updates/sec

Title: US-09-662-293-7
Perfect score: 64
Sequence: 1 DKQNYLALVRELK 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 15779

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UnIProt_05.80:*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	27	42.2	20 2 Q9R5T5_PROMI	Q9R5T5 proteus mix
2	27	42.2	20 2 Q9R595_9SYNE	Q9R595 synechococc
3	26	40.6	16 2 Q4KN88_MUSSP	Q4KN88 mus spretus
4	25	39.1	15 1 ACEA_ACICA	P28467 acinetobact
5	25	39.1	20 2 Q7M3Q5_EUDVA	Q7M3Q5 eudistyllia
6	24	37.5	15 2 Q76UT2_9CAUD	Q76UT2 lactococcus
7	24	37.5	18 1 LYS_ESTAC	P82175 estigmena a
8	24	37.5	18 2 Q9D5S9_ADE04	Q9D5S9 human adeno
9	24	37.5	19 1 RL10_CITFR	P43448 citrobacter
10	24	37.5	19 2 Q4XBH7_PLACH	Q4XBH7 plasmodium
11	24	37.5	20 1 RL10_PROVU	P51411 proteus vul
12	24	37.5	20 2 Q4YD10_PLABE	Q4YD10 plasmodium
13	24	37.5	21 2 Q9L4S9_SALTY	Q9L4S9 salmoneilla
14	23	35.9	9 2 OSD4Q6_BACST	QSD4Q6 bacillus st
15	23	35.9	16 2 Q9UC18_HUMAN	Q9UC18 homo sapien
16	23	35.9	17 2 Q8WGC4_9EUC4	Q8WGC4 discorospag
17	23	35.9	18 2 Q92X12_BPARI	Q92X12 bacterioph
18	23	35.9	18 2 Q7WML5_ADE04	Q7WML5 human adeno
19	23	35.9	18 2 Q9W9C1_ADE04	Q9W9C1 human adeno
20	23	35.9	19 2 Q6L8F5_HUMAN	Q6L8F5 homo sapien
21	23	35.9	19 2 Q667U6_LITFO	Q667U6 lithobius f
22	23	35.9	19 2 Q9GPK3_9MYRI	Q9GPK3 scutigereili
23	23	35.9	19 2 Q4X122_PLACH	Q4X122 plasmodium
24	23	35.9	19 2 Q4XT43_PLACH	Q4XT43 plasmodium
25	23	35.9	20 2 Q8WGC5_9EUC4	Q8WGC5 blepharipod
26	23	35.9	20 2 Q49132_METEX	Q49132 methylobact
27	22	34.4	9 2 QSRBL7_PONRY	QSRBL7 pongo pygma
28	22	34.4	15 2 Q9TNO3_HUMAN	Q9TNO3 homo sapien
29	22	34.4	15 2 Q7R6W8_PLAYO	Q7R6W8 plasmodium
30	22	34.4	15 2 Q6QOR4_HELPY	Q6QOR4 helicobacte
31	22	34.4	19 2 Q905E3_9HIV1	Q905E3 human immun

32	22	34.4	20 2 Q8WU51_HUMAN	Q8WU51 homo sapien
33	22	34.4	20 2 Q9TWM9_OCTVU	Q9TWM9 octopus vul
34	22	34.4	20 2 Q4XG46_PLACH	Q4XG46 plasmodium
35	22	34.4	21 2 Q7RPH5_PLAYO	Q7RPH5 plasmodium
36	21	32.8	16 2 Q9RAK7_GALTE	Q9RAK7 alteromonas
37	21	32.8	16 2 Q9QY10_RAT	Q9QY10 rattus norv
38	21	32.8	17 2 Q9L8K0_ENTFA	Q9L8K0 enterococcu
39	21	32.8	17 2 Q9QVH7_9MUT1	Q9QVH7 rattus sp.
40	21	32.8	18 2 Q7M532_HALMA	Q7M532 haloarcula
41	21	32.8	18 2 Q9B2M7_HUMAN	Q9B2M7 homo sapien
42	21	32.8	18 2 Q378S2_BPRI7	Q378S2 bacterioph
43	21	32.8	19 2 Q4XGX3_PLACH	Q4XGX3 plasmodium
44	21	32.8	19 2 Q90R12_9HIV1	Q90R12 human immun
45	21	32.8	20 1 PYRRH_PYPAP	PYRRH pyrrhospis
46	21	32.8	20 2 P822S8_ASPEL	P822S8 aspergillus
47	21	32.8	20 2 Q4XN21_PLACH	Q4XN21 plasmodium
48	21	32.8	20 2 P82940_HORVU	P82940 hordeum vul
49	21	32.8	21 2 Q4XL35_PLACH	Q4XL35 plasmodium
50	21	32.8	21 2 Q5VAV3_9MARC	Q5VAV3 plagiocchila
51	21	32.8	21 2 Q5VAV5_9MARC	Q5VAV5 nipponoleje
52	21	32.8	21 2 Q5VAV7_9MARC	Q5VAV7 myricocolea
53	21	32.8	21 2 Q5VAV9_9MARC	Q5VAV9 jubula bogo
54	21	32.8	21 2 Q5VAV1_9MARC	Q5VAV1 cyclolejeun
55	21	32.8	21 2 Q5VAV3_9MARC	Q5VAV3 ceratolejeu
56	20	31.2	8 2 Q8WGC9_9EUC4	Q8WGC9 upogobia af
57	20	31.2	11 2 Q7M102_STREB	Q7M102 streptococc
58	20	31.2	12 2 Q9XNR6_PYLTI	Q9XNR6 pylatella 1
59	20	31.2	13 2 P97622_RAT	P97622 rattus norv
60	20	31.2	14 1 PA2T2_BUNCA	PA2T2 bungarus hir
61	20	31.2	14 2 Q94TW5_9EUC4	Q94TW5 pagurus car
62	20	31.2	14 2 Q863R0_PROLO	Q863R0 procyon lot
63	20	31.2	14 2 Q863R1_BASAS	Q863R1 basarriacus
64	20	31.2	14 2 Q863R2_MELUS	Q863R2 melogale mo
65	20	31.2	14 2 Q863R3_ARCCL	Q863R3 arctonyx co
66	20	31.2	14 2 Q863R4_TAXTA	Q863R4 taxidea tax
67	20	31.2	14 2 Q863R5_MELME	Q863R5 melos meles
68	20	31.2	14 2 Q863R6_ICTST	Q863R6 ictonyx str
69	20	31.2	14 2 Q863R7_GALVI	Q863R7 galictis vi
70	20	31.2	14 2 Q863R8_EIRBA	Q863R8 eira barbar
71	20	31.2	14 2 Q863R9_GULU	Q863R9 guilo guilo
72	20	31.2	14 2 Q863S0_MARPE	Q863S0 martes penn
73	20	31.2	14 2 Q863S1_MARPM	Q863S1 martes amer
74	20	31.2	14 2 Q863S2_MUSYR	Q863S2 mustela vis
75	20	31.2	14 2 Q863S3_MUSR	Q863S3 mustela fire
76	20	31.2	14 2 Q863S4_MUSR	Q863S4 mustela erm
77	20	31.2	14 2 Q863S5_PTEBR	Q863S5 pteronura b
78	20	31.2	14 2 Q863S6_LUTWA	Q863S6 lutra macul
79	20	31.2	14 2 Q863S7_LUTLU	Q863S7 lutra lutra
80	20	31.2	14 2 Q863S8_LONCO	Q863S8 lontra long
81	20	31.2	14 2 Q863S9_LONFE	Q863S9 lontra feli
82	20	31.2	14 2 Q863T0_LONCN	Q863T0 lontra cana
83	20	31.2	14 2 Q863T1_ENHJU	Q863T1 enhydra lut
84	20	31.2	14 2 Q863T2_AMBCT	Q863T2 amblyonyx ci
85	20	31.2	14 2 Q863T3_AONCA	Q863T3 aonyx capen
86	20	31.2	14 2 Q9R2Z4_CAMBE	Q9R2Z4 campylobact
87	20	31.2	14 2 Q9R2Z5_CAMBE	Q9R2Z5 campylobact
88	20	31.2	14 2 Q9W7Y9_CAMCO	Q9W7Y9 campylobact
89	20	31.2	14 2 Q9X715_CAMBE	Q9X715 campylobact
90	20	31.2	16 2 Q9LAP2_ENTFC	Q9LAP2 enterococcu
91	20	31.2	17 1 FIBA_PIG	FIBA sus scrofa
92	20	31.2	17 2 Q9HB76_HUMAN	Q9HB76 homo sapien
93	20	31.2	17 2 Q7RBC2_PLAYO	Q7RBC2 plasmodium
94	20	31.2	17 2 Q4XR88_PLACH	Q4XR88 plasmodium
95	20	31.2	17 2 Q7W2N4_BOVIN	Q7W2N4 bos taurus
96	20	31.2	17 2 Q8KHG3_STRGY	Q8KHG3 streptococc
97	20	31.2	17 2 Q8KRA3_9STRE	Q8KRA3 streptococc
98	20	31.2	17 2 Q9WW20_ENTFC	Q9WW20 enterococcu
99	20	31.2	17 2 Q9WW21_ENTFC	Q9WW21 enterococcu
100	20	31.2	17 2 Q9X515_ENTGA	Q9X515 enterococcu

ALIGNMENTS

```
RESULT 1
Q9R5T5_PROM1 PRELIMINARY; PRT; 20 AA.
ID Q9R5T5;
AC Q9R5T5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Flagellin (Fragment).
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Proteus.
OX NCBI_TaxID=584;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=91372967; PubMed=1680106;
RA Bahrani F.K., Johnson D.E., Robbins D., Mobley H.L.;
RT "Proteus mirabilis flagellin and MR/P fimbriae: isolation,
RT purification, N-terminal analysis, and serum antibody response
RT following experimental urinary tract infection.";
RL Infect. Immun. 59:3574-3580(1991).
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2234 MW; 667024216115E099 CRC64;

Query Match 42.2%; Score 27; DB 2; Length 20;
Best Local Similarity 62.5%; Pred. No. 1.3e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 NYLALVRE 11
DB 7 NYLSLVTO 14

RESULT 2
Q9R595_9SYNE PRELIMINARY; PRT; 20 AA.
ID Q9R595_9SYNE;
AC Q9R595;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Photosystem I subunit XII (Fragment).
OS Synchococcus.
OC Bacteria; Cyanobacteria; Chroococcales.
OX NCBI_TaxID=1129;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93252282; PubMed=8486290; DOI=10.1016/0378-1119(93)90618-D;
RA Muehlenhoff U., Haehnel W., Wilt H.T., Hermann R.G.;
RT "Genes encoding eleven subunits of photosystem I from the thermophilic
RT cyanobacterium Synchococcus sp.";
RL Gene 127:71-78(1993).
DR GO; GO:0009522; C:photosystem I; IEA.
DR GO; GO:0015979; P:photosynthesis; IEA.
DR InterPro; IPR010010; Pfam.
DR Pfam; PF07465; Pfam; 1.
SQ SEQUENCE 20 AA; 2102 MW; DF585D9ED9D7C512 CRC64;

Query Match 42.2%; Score 27; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 1.3e+03;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DKONYALV 9
DB 5 DTQVVALV 13

RESULT 3
Q4KN88_MUSSP PRELIMINARY; PRT; 16 AA.
ID Q4KN88_MUSSP;
AC Q4KN88;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
```

```
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE MHC class I antigen (Fragment).
GN Name-H2-Tw5;
OS Mus spretus (Western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Charchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10096;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SEB;
RA Guidry P.A., Stroyanowski I.;
RT "The Murine Family of Gut-Restricted Class Ib MHC includes
RT Alternatively Spliced Isoforms of the Proposed HLA-G Homolog,
RT Blastocyst MHC ";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY989870; AY85357.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1839 MW; 236C9069F3EC01E CRC64;

Query Match 40.6%; Score 26; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.6e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 4 NYLALVRELK 13
DB 1 DYLMNEDLK 10

RESULT 4
ACEA_ACICA STANDARD; PRT; 15 AA.
ID ACEA_ACICA;
AC P28467;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Isocitrate lyase (EC 4.1.3.1) (Isocitrase) (Isocitratase) (ICL)
DE (Fragment).
GN Name=aceA;
OS Acinetobacter calcoaceticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=471;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=92041568; PubMed=1938889;
RA Hoyt J.C., Johnson K.E., Reeves H.C.;
RT "Purification and characterization of Acinetobacter calcoaceticus
RT isocitrate lyase.";
RL J. Bacteriol. 173:6844-6848(1991).
CC -1- CATALYTIC ACTIVITY: Isocitrate = succinate + glyoxylate.
CC -1- PATHWAY: Glyoxylate bypass; first step.
CC -1- SUBUNIT: Homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the isocitrate lyase family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A41338; A41338.
CC InterPro; IPR000918; Isocit_lyase_ph.
CC PROSITE; PS00161; ISOCITRATE_LYASE; PARTIAL.
CC Direct protein sequencing; Glyoxylate bypass; Lyase;
CC Tricarboxylic acid cycle.
CC NON_TER 15
CC SEQUENCE 15 AA; 1710 MW; 83AE726B1F2F96E3 CRC64;

Query Match 39.1%; Score 25; DB 1; Length 15;
Best Local Similarity 54.5%; Pred. No. 2.3e+03;
```

Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 QNYLALVRELK 13
DB 4 QTAIDAVRELK 14

RESULT 5

Q7M305_EUDVA PRELIMINARY; PRT; 20 AA.

AC Q7M305; 16-DEC-2001 (Rel. 40, Created)
DT 01-MAR-2004 (TEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last sequence update)
DE Globin (Fragment).
OS Eudictyia vancouveri.
OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
OC Sabellidae; Sabellidae; Eudictyia.
OX NCBI_Taxid=6364;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=9210633; PubMed=1762147;
RA Gabar A.N., Stern M.S., Walz D.A., Chiu J.T., Timkovich R., Wall J.S.,
Kapp O.H., Vinogradov S.N.;
RT "Hierarchy of globin complexes. The quaternary structure of the
RT extracellular chlorocruorin of Eudictyia vancouveri.";
RL J. Mol. Biol. 222:1109-1129 (1991).
DR PIR; S19615; S19615.
FT NON_TER 1 1
FT TER 20 20
SQ SEQUENCE 20 AA; 2286 MW; 42834109F06698CB CRC64;

Query Match 39.1%; Score 25; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DKONYLAL 8
DB 12 DRONLISM 19

RESULT 6

Q76UT2_9CAUD PRELIMINARY; PRT; 15 AA.

AC Q76UT2; 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE Integrase (Fragment).
GN Nameint;
OS Lactococcus phage BKS-T.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_Taxid=11754;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96064424; PubMed=8525525;
RA Boyce J.D., Davidson B.E., Hillier A.J.;
RT "Spontaneous deletion mutants of the Lactococcus lactis temperate
RT bacteriophage BKS-T and localization of the BKS-T attP site.";
RL Appl. Environ. Microbiol. 61:4105-4109 (1995).
DR EMBL; S80308; AAB35788.2; Genomic_DNA.
FT NON_TER 1 1
SQ SEQUENCE 15 AA; 1831 MW; 12D81A642BD0B341 CRC64;

Query Match 37.5%; Score 24; DB 2; Length 15;
Best Local Similarity 41.7%; Pred. No. 3.6e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DKONYLALVREL 12
DB 4 DKOKIILMEL 15

RESULT 7

LXS_ESTAC STANDARD; PRT; 18 AA.

ID LXS_ESTAC 16-OCT-2001 (Rel. 40, Created)
AC P82175; 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Lysozyme (EC 3.2.1.17) (1,4-beta-N-acetylglucosaminidase) (Fragment).
OS Estigmenae acraea (Salt marsh moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Arctiidae; Estigmenae.
OX NCBI_Taxid=56594;
RN [1]
RP PROTEIN SEQUENCE, AND ENZYME REGULATION.
RX TISSUE=Hemocyte;
RX MEDLINE=97448947; PubMed=9303271; DOI=10.1016/S0145-305X(97)00012-8;
RA Wiltner D., Weise C., Goetz P., Wiesner A.;
RT "LPS (lipopolysaccharide)-activated immune responses in a hemocyte
RT cell line from Estigmenae acraea (Lepidoptera).";
RL Dev. Comp. Immunol. 21:323-336 (1997).
CC -1- FUNCTION: Lysozymes have primarily a bacteriolytic function; those
CC in tissues and body fluids are associated with the monocyte-
CC macrophage system and enhance the activity of immunogens (By
CC similarity).
CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-linkages between N-
CC acetylglucosaminic acid and N-acetyl-D-glucosamine residues in a
CC peptidoglycan and between N-acetyl-D-glucosamine residues in
CC chitodextrins.
CC -1- ENZYME REGULATION: By lipopolysaccharide (LPS).
CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 22 family.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC -----
CC DR InterPro; IPR001916; Glyco_hydro_22.
CC PROSITE; PS00128; LACTALBUMIN LYSOZYME, PARTIAL.
CC Antimicrobial; Bacteriolytic enzyme; Direct protein sequencing;
KM Glycosidase; Hydrolase.
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2214 MW; B229D8F5ECD7F57 CRC64;

Query Match 37.5%; Score 24; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 4.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 LVRELK 13
DB 9 LVRELK 14

RESULT 8

Q9DS99_ADE04 PRELIMINARY; PRT; 18 AA.

ID Q9DS99_ADE04 01-MAR-2001 (TEMBLrel. 16, Created)
AC Q9DS99; 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DE P23 protease (Fragment).
GN Name=p23;
OS Human adenovirus 4 (HAdV-4).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_Taxid=28280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=2-G T95-873;
RX MEDLINE=99175282; PubMed=10074533;
RA Crawford-Mikszta L.K., Nang R.N., Schnurr D.P.;
RT "Strain variation in adenovirus serotypes 4 and 7a causing acute
RT respiratory disease.";

```

RL J. Clin. Microbiol. 37:1107-1112(1999).
RN [2]
NC NUCLEOTIDE SEQUENCE.
RC STRAIN=Z-G 795-873;
RA Crawford-Mikaza L.K.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065064; AAD03661.3; -, Genomic_DNA.
DR HSSP; P03252; INLN.
DR GO; GO:0008233; F:peptidase activity; IEA.
KM Protease.
FT NON_TER
SQ SEQUENCE 18 AA; 1917 MW; 12FCE2715E7FB445 CRC64;

Query Match 37.5%; Score 24; DB 2; Length 18;
Best Local Similarity 45.5%; Pred. No. 4.3e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 DKONYLALVREL 12
Db 4 EQELKAIIVRL 14

RESULT 9
RL10_CITFR STANDARD; PRT; 19 AA.
ID P43448;
AC P43448;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE 50S ribosomal protein L10 (Fragment).
GN Name=rplJ;
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=771;
RA Zhyvoloup A.N.;
RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the ribosomal protein L10P family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X74448; CAAS2459.1; -, Genomic_DNA.
DR PIR; S35970; S35970.
DR HAMAP; MF_00362; -, 1.
DR InterPro; IPR002363; Ribosomal_L10eub.
DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
KM Ribonucleoprotein; Ribosomal protein.
FT INIT_MET 0
FT NON_TER 0
FT SEQUENCE 19 AA; 2026 MW; E20A02CD7851DB16 CRC64;

Query Match 37.5%; Score 24; DB 1; Length 19;
Best Local Similarity 50.0%; Pred. No. 4.6e+03;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DKONYLALVREL 12
Db 6 DKQALVAEVS 17

RESULT 10
Q4XBH7_PLACH PRELIMINARY; PRT; 19 AA.
AC Q4XBH7;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)

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DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC403822.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Duggett J., Trueman H.B., Mendoza J.,
RA Bidwell S.L., Rajadream M.A., Carnucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAJ01007928; CAH85746.1; -, Genomic_DNA.
KM Hypothetical protein.
FT NON_TER 1
FT SEQUENCE 19 AA; 2373 MW; 3A760616CBF95A84 CRC64;

Query Match 37.5%; Score 24; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKONYL 6
Db 14 ERQNYM 19

RESULT 11
RL10_PROVU STANDARD; PRT; 20 AA.
ID P51411;
AC P51411;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE 50S ribosomal protein L10 (Fragment).
GN Name=rplJ;
OS Proteus vulgaris.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Proteus.
OX NCBI_TaxID=585;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Zhyvoloup A.N.;
RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the ribosomal protein L10P family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X74446; CAAS2457.1; -, Genomic_DNA.
DR PIR; S35978; S35978.
DR HAMAP; MF_00362; -, 1.
DR InterPro; IPR002363; Ribosomal_L10eub.
DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
KM Ribonucleoprotein; Ribosomal protein.
FT INIT_MET 0
FT NON_TER 0
FT SEQUENCE 20 AA; 76520A02CD7851DB CRC64;

Query Match 37.5%; Score 24; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 4.8e+03;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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QY 1 DKONYALVEL 12
 DB 6 DKOAVAEVSEV 17

RESULT 12
 ID Q4YD10 PLABE PRELIMINARY; PRT; 20 AA.

AC Q4YD10;
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DE Hypothetical protein (Fragment).
 GN ORENAMES=PB406092.00.0;
 OS Plasmodium berghei.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.

NCBI_Taxid=5621;
 RN [1]

NUCLEOTIDE SEQUENCE.

RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
 RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bladwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RL transcriptomic, and proteomic analyses."
 CC Science 307:82-86(2005).

-1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.

CC EMBL; CA101006376; CA104109.1; -; Genomic_DNA.

KM Hypothetical protein. 1

FT NON TER 1
 SQ SEQUENCE 20 AA; 2501 MW; 75F9BFEC2628711 CRC64;

Query Match 37.5%; Score 24; DB 2; Length 20;
 Best Local Similarity 83.3%; Pred. No. 4.8e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 LVRELK 13
 DB 5 LVRELK 10

RESULT 13

Q9L4S9_SALTY PRELIMINARY; PRT; 21 AA.

AC Q9L4S9;
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DE Putative glycoprotein (Fragment).
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 NCBI_Taxid=602;
 RN [1]

NUCLEOTIDE SEQUENCE.

RA MEDLINE=22306558; PubMed=12420160; DOI=10.1007/s00203-002-0458-7;
 RA Rychlik I., Martin G., Methner U., Lovell M., Cardova L., Sebkova A.,
 RA Sevcik M., Damborsky J., Barrow P.A.,
 RT "Identification of Salmonella enterica serovar Typhimurium genes
 RT associated with growth suppression in stationary-phase nutrient broth
 RT cultures and in the chicken intestine."
 RL Arch. Microbiol. 178:411-420(2002).
 DR EMBL; AF68390; AAF73476.1; -; Genomic_DNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019867; C:outer membrane; IEA.
 DR GO; GO:0015288; F:porin activity; IEA.
 KW Porin.

FT NON TER 21 21
 SQ SEQUENCE 21 AA; 2340 MW; FF537CDB3287B9E2 CRC64;

Query Match 37.5%; Score 24; DB 2; Length 21;
 Best Local Similarity 62.5%; Pred. No. 5.1e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KONYALV 9
 DB 2 KAKYALVM 9

RESULT 14
 ID Q5D4Q6 BACST PRELIMINARY; PRT; 9 AA.

AC Q5D4Q6;
 DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
 DE tmRNA-encoded proteolysis-inducing peptide tag (Fragment).
 GN Name=ssrA.
 OS Bacillus stearothermophilus.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
 NCBI_Taxid=1422;
 RN [1]

NUCLEOTIDE SEQUENCE.

RA Williams K.P.;
 RT "Phylogenetic analysis of tmRNA."
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY11529; AAX12900.1; -; Genomic_DNA.
 FT NON TER 1

SQ SEQUENCE 9 AA; 935 MW; 4D46D72DCB545603 CRC64;

Query Match 35.9%; Score 23; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KONY 5
 DB 2 KONY 5

RESULT 15
 ID Q9UC18 HUMAN PRELIMINARY; PRT; 16 AA.

AC Q9UC18;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE Endozepine (Fragment).

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
 OC Homo.
 NCBI_Taxid=9606;
 RN [1]

PROTEIN SEQUENCE.

RA MEDLINE=93184488; PubMed=1292782;
 RA Apfel R., Lottspeich F., Hoppe J., Behl C., Durr G., Bogdahn U.,
 RT "Purification and analysis of growth regulating proteins secreted by a
 RT human melanoma cell line."
 RL Melanoma Res. 2:327-336(1992).
 DR HSSP; P07107; 1HB6.

SQ SEQUENCE 16 AA; 1924 MW; 9B1BDA89F501A76 CRC64;

Query Match 35.9%; Score 23; DB 2; Length 16;
 Best Local Similarity 55.6%; Pred. No. 5.8e+03;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 YLALVELK 13
 DB 3 YINKVELK 11

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RESULT 16
08WGC4_9EUC4 PRELIMINARY; PRT; 17 AA.
ID 08WGC4_9EUC4_1
AC 08WGC4_1
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE NADH dehydrogenase subunit 1 (Fragment).
OS Discosporagurus schmitti.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura; Paguroidea;
OC Paguridae; Discosporagurus.
OC NCB1_TaxID=177274;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21884466; PubMed=11886621; DOI=10.1098/rspb.2001.1886;
RA Morrison C.L., Harvey A.W., Lavery S., Tieu K., Huang Y.,
RA Cunningham C.W.;
RT "Mitochondrial gene rearrangements confirm the parallel evolution of
the crab-like form.";
RL Proc. R. Soc. Lond., B. Biol. Sci. 269:345-350(2002).
DR EMBL; AF436055; AL31626.1; -; Genomic DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER
SQ SEQUENCE 17 AA; 1878 MW; 2E40DA40F51367D7 CRC64;

Query Match 35.9%; Score 23; DB 2; Length 17;
Best Local Similarity 66.7%; Pred. No. 6.2e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NYLALV 9
Db 4 NYLLLI 9

RESULT 17
09ZX12_BPARI PRELIMINARY; PRT; 17 AA.
ID 09ZX12_BPARI_1
AC 09ZX12_1
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Putative prohead protease (Fragment).
OS Bacteriophage ARI.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OC NCB1_TaxID=66711;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98433034; PubMed=9758911; DOI=10.1159/000025351;
RA Yu S., Ding H., Seah J., Wu K., Chang Y., Chang K.S., Tam M.F.,
RA Syu W.;
RT "Characterization of a phage specific to hemorrhagic Escherichia coli
O157:H7 and disclosure of variations in host outer membrane protein
ompC";
RT J. Biomed. Sci. 5:370-382(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=ARI;
RA Syu W.J., Ding H.C., Seah J.N., Wu K.M., Yu S.L., Tam M.F.,
RA Chang Y.C.;
RA Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF022930; AAD01753.1; -; Genomic DNA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR005082; Peptidase_U9; 1.
DR Pfam; PF03420; Peptidase_U9; 1.
KW Protease.
FT NON TER
RT NON TER

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SQ SEQUENCE 17 AA; 1799 MW; A271719441BCDB19 CRC64;

Query Match 35.9%; Score 23; DB 2; Length 17;
Best Local Similarity 44.4%; Pred. No. 6.2e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 YLALVREL 13
Db 6 YMALAEAMK 14

RESULT 18
07WML5_ADE04 PRELIMINARY; PRT; 18 AA.
ID 07WML5_ADE04_1
AC 07WML5_1
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE P23 protease (Fragment).
GN Name=P23;
OS Human adenovirus 4 (HAdV-4).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OC NCB1_TaxID=28280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=CL 68578;
RX MEDLINE=99175282; PubMed=10074533;
RA Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
RT "Strain variation in adenovirus serotypes 4 and 7a causing acute
respiratory disease.";
RL J. Clin. Microbiol. 37:1107-1112(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=CL 68578;
RA Crawford-Miksza L.K.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065063; AAD03658.3; -; Genomic DNA.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000855; Peptidase_C5; 1.
DR Prodom; PD003705; Peptidase_C5; 1.
FT Protease.
FT NON TER
SQ SEQUENCE 18 AA; 1929 MW; BB3CFD4C5E7FB446 CRC64;

Query Match 35.9%; Score 23; DB 2; Length 18;
Best Local Similarity 36.4%; Pred. No. 6.6e+03;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KONYLALVREL 12
Db 4 EQELRALIRDL 14

RESULT 19
09W9C1_ADE04 PRELIMINARY; PRT; 18 AA.
ID 09W9C1_ADE04_1
AC 09W9C1_1
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE P23 protease (Fragment).
GN Name=P23;
OS Human adenovirus 4 (HAdV-4).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OC NCB1_TaxID=28280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=RI-67;
RX MEDLINE=99175282; PubMed=10074533;
RA Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
RA "Strain variation in adenovirus serotypes 4 and 7a causing acute

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RT respiratory disease.";
 RL J. Clin. Microbiol. 37:1107-1112(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=RI-67;
 RA Crawford-Mikaza L.K.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF065062; AAD03655.2; -; Genomic DNA.
 DR GO: GO:0004197; F:cysteine-type endopeptidase activity; IEA.
 DR GO: GO:0006223; F:peptidase activity; IEA.
 DR GO: GO:0006508; F:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000855; Peptidase_C5.
 DR ProDom; PD003705; Peptidase_C5; 1.
 KW Peptidase.
 FT NON_TER
 SQ SEQUENCE 18 AA; 1929 MW; BB3CPD4C5E7FB446 CRC64;
 Query Match 35.9%; Score 23; DB 2; Length 18;
 Best Local Similarity 36.4%; Pred. No. 6.6e+03;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 KNYLALVREL 12
 :|::|:
 Db 4 EQELRAIRDL 14

RESULT 20
 Q6LBF5_HUMAN
 ID Q6LBF5_HUMAN PRELIMINARY; PRT; 19 AA.
 AC Q6LBF5;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE TRA protein (Fragment).
 GN Name=CFA;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo
 NCBI_TaxID=9606;
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Liver;
 RA Sarafanov A.G.; Timofeeva M.Y., Bannikov V.M., Zakhariev V.M.,
 RT "Sequencing and primary structure analysis of a genomic sequence
 flanking the 3' terminus of human tissue plasminogen activator gene.";
 RL Mol. Biol. (Mosk.) 29:161-165(1995).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Liver;
 RA Sarafanov A.G.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X77531; CAA54669.1; -; Genomic DNA.
 DR GO: GO:0030195; P:negative regulation of blood coagulation; IEA.
 FT NON_TER
 SQ SEQUENCE 19 AA; 2342 MW; SABN0749ACF2D6A4 CRC64;
 Query Match 35.9%; Score 23; DB 2; Length 19;
 Best Local Similarity 50.0%; Pred. No. 7e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 NYLALVRE 11
 :|::|:
 Db 8 NYLDWRD 15

RESULT 21
 Q967U6_LITFO
 ID Q967U6_LITFO PRELIMINARY; PRT; 19 AA.
 AC Q967U6;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Engerlled (Fragment).
 OS Lithobius forficatus.
 OC Eukaryota; Metazoa; Arthropoda; Myriapoda; Chilopoda;
 OC Pleurostigmophora; Lithobiomorpha; Lithobiidae; Lithobius.
 NCBI_TaxID=7552;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21272202; PubMed=11378385; DOI=10.1016/S0960-9822(01)00222-6;
 RA Cook C.E., Smith M.L., Telford M.J., Bastianello A., Akam M.;
 RT "Hox genes and the phylogeny of the arthropods.";
 RL Curr. Biol. 11:759-763(2001).
 DR EMBL; AF362097; AAK51952.1; -; Genomic DNA.
 FT NON_TER
 SQ SEQUENCE 19 AA; 2339 MW; 4C6F5E9A1FE03C57 CRC64;
 Query Match 35.9%; Score 23; DB 2; Length 19;
 Best Local Similarity 83.3%; Pred. No. 7e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 LYRELK 13
 :|::|:
 Db 6 LARELK 11

RESULT 22
 Q9GPK3_9MYRI
 ID Q9GPK3_9MYRI PRELIMINARY; PRT; 19 AA.
 AC Q9GPK3;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Engerlled protein (Fragment).
 OS Scutigereila immaculata (garden symphylan).
 OC Eukaryota; Metazoa; Arthropoda; Myriapoda; Scutigereillidae;
 OC Scutigereila.
 NCBI_TaxID=146864;
 OX NCBI_TaxID=146864;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21272202; PubMed=11378385; DOI=10.1016/S0960-9822(01)00222-6;
 RA Cook C.E., Smith M.L., Telford M.J., Bastianello A., Akam M.;
 RT "Hox genes and the phylogeny of the arthropods.";
 RL Curr. Biol. 11:759-763(2001).
 DR EMBL; AF318499; AAG45179.1; -; Genomic DNA.
 FT NON_TER
 SQ SEQUENCE 19 AA; 2339 MW; 4C6F5E9A1FE03C57 CRC64;
 Query Match 35.9%; Score 23; DB 2; Length 19;
 Best Local Similarity 83.3%; Pred. No. 7e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 LYRELK 13
 :|::|:
 Db 6 LARELK 11

RESULT 23
 Q4X122_PLACH
 ID Q4X122_PLACH PRELIMINARY; PRT; 19 AA.
 AC Q4X122;
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN ORFNames=PC400809.00.0;
 OS Plasmodium chabaudi.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
 NCBI_TaxID=5825;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,

RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carnucci D.J., Yates J.R., Kafatos F.C.,
 RA Jansse C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses."; Science 307:82-86(2005).
 RL Science 307:82-86(2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL/CAJ01005631; CAH83122.1; -; Genomic_DNA.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 19 AA; 2315 MW; E6BF80132E33FD91 CRC64;
 Query Match 35.9%; Score 23; DB 2; Length 19;
 Best Local Similarity 42.9%; Pred. No. 7e+03;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 OY 2 KNYIAL 8
 DB 2 KKNYICI 8
 RESULT 24
 ID Q4XT43_PLACH PRELIMINARY; PRT; 19 AA.
 AC Q4XT43;
 DT 13-SEP-2005 (TREMBLrel. 31, Created)
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN ORFNames=PC10647.00.0;
 OS Plasmodium chabaudi.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5825;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
 RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carnucci D.J., Yates J.R., Kafatos F.C.,
 RA Jansse C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses."; Science 307:82-86(2005).
 RL Science 307:82-86(2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL/CAJ01003378; CAH79919.1; -; Genomic_DNA.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 19 AA; 2251 MW; FADCD87AB64CE02 CRC64;
 Query Match 35.9%; Score 23; DB 2; Length 19;
 Best Local Similarity 36.4%; Pred. No. 7e+03;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 OY 3 ONYLALVRELK 13
 DB 1 QELLVIOELQ 11
 RESULT 25
 ID O8WGC5_9EUCA PRELIMINARY; PRT; 20 AA.
 AC O8WGC5;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE NADH dehydrogenase subunit 1 (Fragment).

OS Blepharipoda occidentalis.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura; Hippoidea;
 OC Albundeidae; Blepharipoda.
 OX NCBI_TaxID=177216;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21884466; PubMed=11886621; DOI=10.1098/rspb.2001.1886;
 RA Morrison C.L., Harvey A.W., Lavery S., Tieu K., Huang Y.,
 RA Cunningham C.W.;
 RT "Mitochondrial gene rearrangements confirm the parallel evolution of
 RT the crab-like form."
 RL Proc. R. Soc. Lond. B. Biol. Sci. 269:345-350(2002).
 DR EMBL/AF436053; AAL31625.1; -; Genomic_DNA.
 DR GO: GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 20
 SQ SEQUENCE 20 AA; 2238 MW; 2DAF58886F21F513 CRC64;
 Query Match 35.9%; Score 23; DB 2; Length 20;
 Best Local Similarity 66.7%; Pred. No. 7.4e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 4 NYLALV 9
 DB 5 NYLILI 10
 Search completed: January 26, 2006, 08:03:51
 Job time : 41.6638 secs

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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:47:09 ; Search time 81.5172 Seconds
(without alignments)
129.360 Million cell updates/sec

Title: US-09-662-293-8
Perfect score: 124

Sequence: 1 DMAQNYKXKROQFIOSVLNNGATRQ 24

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378761 residues

Total number of hits satisfying chosen parameters: 897420

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_GeneSeq_21:*

1: geneeqp19908s:*
2: geneeqp19908s:*
3: geneeqp20008s:*
4: geneeqp2001s:*
5: geneeqp2002s:*
6: geneeqp2003as:*
7: geneeqp2003bs:*
8: geneeqp2004s:*
9: geneeqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	29.8	15	6	ABR30497 Human can
2	37	29.8	15	6	ABR31387 Human can
3	34	27.4	13	7	ADM34497 HLA bindi
4	34	27.4	13	7	ADM35730 HLA bindi
5	33.5	27.0	19	1	AAPE8118 hsc-relat
6	32	25.8	15	6	ABR30464 Human can
7	32	25.8	15	6	ABR31017 Human can
8	32	25.8	15	6	ABR30929 Human can
9	32	25.8	15	7	ADM37611 HLA bindi
10	31	25.0	9	5	ABJ01432 158P1D7 r
11	31	25.0	10	5	ABJ01921 158P1D7 r
12	31	25.0	10	5	ABJ01457 158P1D7 r
13	31	25.0	12	2	AAAI9443 Anti-Fung
14	31	25.0	12	2	AAAI9480 Anti-Fung
15	31	25.0	12	3	AAAI1988 Histactin-
16	31	25.0	14	3	ABBS6747 Human SNP
17	31	25.0	14	4	ABBS6747 Human CAR
18	31	25.0	15	6	ABG72213 Human NGF
19	31	25.0	15	2	ADM66333 Human NGF
20	31	25.0	16	2	AAW73692 M. tuberc
21	31	25.0	16	4	AAW73802 M. tuberc
22	31	25.0	16	4	AAU08157 Mycobacte
23	31	25.0	16	5	ABG78004 M. tuberc
24	31	25.0	17	4	ABBS5946 Caenor be

25	31	25.0	17	7	ADM37099 Wild-type
26	31	25.0	17	7	ADM53387 Beta-cate
27	31	25.0	17	7	ADM95021 Wild-type
28	31	25.0	17	8	ADJ78231 Peptide S
29	31	25.0	17	8	ADR31521 Beta-cate
30	31	25.0	17	9	AEA01731 Human bet
31	31	25.0	19	5	ABG96178 Cysteine-
32	31	25.0	19	5	ADM11055 Cysteine-
33	31	25.0	20	8	ADH15134 Gliadin r
34	31	25.0	20	8	ADH15661 Gliadin r
35	30	24.2	9	8	ABY01496 SARS coro
36	30	24.2	10	9	ADZ86149 SARS coro
37	30	24.2	12	2	AAV24768 Lactoferr
38	30	24.2	12	9	ADZ69939 Curvulari
39	30	24.2	13	7	ADM75353 Potential
40	30	24.2	14	9	ADY49681 Severe ac
41	30	24.2	15	6	ABR30599 Human can
42	30	24.2	15	6	ABR30928 Human can
43	30	24.2	15	6	ABR31140 Human can
44	30	24.2	15	6	ABR31256 Human can
45	30	24.2	15	6	ABR31386 Human can
46	30	24.2	15	7	ADM75913 Human MHC
47	30	24.2	15	7	ADM75938 Human MHC
48	30	24.2	15	7	ADM75962 Human MHC
49	30	24.2	15	7	ADM75981 Human Fac
50	30	24.2	15	8	ADG06417 Human B-d
51	30	24.2	15	9	ADV51686 SARS-Cov
52	30	24.2	15	9	ADV51687 SARS-Cov
53	30	24.2	15	9	ADV51690 SARS-Cov
54	30	24.2	15	9	ADV51695 SARS-Cov
55	30	24.2	15	9	ADV51692 SARS-Cov
56	30	24.2	15	9	ADV51694 SARS-Cov
57	30	24.2	15	9	ADV51688 SARS-Cov
58	30	24.2	15	9	ADV51689 SARS-Cov
59	30	24.2	15	9	ADV51691 SARS-Cov
60	30	24.2	15	9	ADV51693 SARS-Cov
61	30	24.2	15	9	ADV51696 SARS-Cov
62	30	24.2	16	7	ADD23798 Breast ca
63	30	24.2	18	4	AAK43009 Peptide s
64	30	24.2	18	4	AB91858 Antimicro
65	30	24.2	18	8	ADN03310 Exemplary
66	30	24.2	18	8	ADN032145 CD6pepti
67	30	24.2	19	6	ABP70504 Peptide c
68	30	24.2	19	9	AEA33305 SARS prot
69	30	24.2	20	8	ADH15133 Gliadin r
70	30	24.2	20	8	ADH15660 Gliadin r
71	30	24.2	20	9	ADY77534 Peptide a
72	30	24.2	21	4	AAV31984 Ubiquitin
73	29.5	23.8	14	4	AAK98489 Human peg
74	29.5	23.8	19	7	ADF14605 Rheumatoid
75	29	23.4	9	6	ABJ43855 151P3D4 c
76	29	23.4	9	6	ABJ47304 151P3D4 c
77	29	23.4	9	6	ABJ39816 151P3D4 c
78	29	23.4	9	6	ABJ44507 151P3D4 c
79	29	23.4	9	6	ABJ45095 151P3D4 c
80	29	23.4	9	6	ABJ41472 151P3D4 c
81	29	23.4	9	6	ABJ42937 151P3D4 c
82	29	23.4	9	6	ABJ42407 151P3D4 c
83	29	23.4	9	6	ABJ45886 151P3D4 c
84	29	23.4	9	6	ABJ46596 151P3D4 c
85	29	23.4	9	6	ABJ46646 151P3D4 c
86	29	23.4	9	6	ABJ49376 151P3D4 c
87	29	23.4	9	9	ADZ57400 Cytotoxic
88	29	23.4	10	4	AAK88237 Saccharom
89	29	23.4	10	6	ABJ51147 151P3D4 c
90	29	23.4	10	6	ABJ51458 151P3D4 c
91	29	23.4	10	6	ABJ51265 151P3D4 c
92	29	23.4	10	6	ABJ51288 151P3D4 c
93	29	23.4	10	6	ABJ41268 151P3D4 c
94	29	23.4	10	6	ABJ50056 151P3D4 c
95	29	23.4	10	6	ABJ53103 151P3D4 c
96	29	23.4	10	6	ABJ50479 151P3D4 c
97	29	23.4	10	6	ABJ52255 151P3D4 c

98	29	23.4	10	6	ABJ50615	ABJ50615	151P3D4 C
99	29	23.4	10	6	ABJ53745	ABJ53745	151P3D4 C
100	29	23.4	10	6	ABJ53805	ABJ53805	151P3D4 C

ALIGNMENTS

RESULT 1

ABR30497
ID ABR30497 standard; peptide; 15 AA.

XX ABR30497;

XX 19-MAY-2003 (first entry)

XX Human cancer-related protein 83P4B8 HLA peptide #1559.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;

KW human leukocyte antigen.

XX Homo sapiens.

XX MO200283921-A2.

XX 24-OCT-2002.

XX 10-APR-2002; 2002WO-US011654.

XX 10-APR-2001; 2001US-0282739P.

XX 10-APR-2001; 2001US-0283112P.

XX 25-APR-2001; 2001US-0286630P.

XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

XX PI Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of

XX PT proteins and polynucleotides, useful for therapeutic, prognostic and

XX PT diagnostic reagents for eliciting cellular or humoral immune response in

XX PT cancer patients.

XX PS Claim 13; Page 476; 1021pp; English.

XX CC The present invention relates to novel human cancer-related genes and

XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and

XX CC proteins are useful for eliciting a humoral or cellular immune response.

XX CC The genes are useful as probes and primers for the amplification and/or

XX CC detection of genes, mRNAs or their fragments, as reagents for the

XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of

XX CC directing the expression of the protein, as tools for modulating or

XX CC inhibiting the expression of genes and/or translation of transcripts, and

XX CC as therapeutic agents. The proteins and peptides are useful as

XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present

XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example

XX CC from the invention

XX SQ Sequence 15 AA;

XX Query Match

XX Best Local Similarity 29.8%; Score 37; DB 6; Length 15;

XX Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

XX ROQFIQSVLNGGATR 23

XX ||: : : ||| ||

XX 1 ROETLEQVLNRVTR 15

XX Db

XX RESULT 2

XX ABR31387

ID ABR31387 standard; peptide; 15 AA.

XX ABR31387;

XX 19-MAY-2003 (first entry)

XX Human cancer-related protein 83P4B8 HLA peptide #2449.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;

XX KW human leukocyte antigen.

XX Homo sapiens.

XX MO200283921-A2.

XX 24-OCT-2002.

XX 10-APR-2002; 2002WO-US011654.

XX 10-APR-2001; 2001US-0282739P.

XX 10-APR-2001; 2001US-0283112P.

XX 25-APR-2001; 2001US-0286630P.

XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

XX PI Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of

XX PT proteins and polynucleotides, useful for therapeutic, prognostic and

XX PT diagnostic reagents for eliciting cellular or humoral immune response in

XX PT cancer patients.

XX PS Claim 13; Page 491; 1021pp; English.

XX CC The present invention relates to novel human cancer-related genes and

XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and

XX CC proteins are useful for eliciting a humoral or cellular immune response.

XX CC The genes are useful as probes and primers for the amplification and/or

XX CC detection of genes, mRNAs or their fragments, as reagents for the

XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of

XX CC directing the expression of the protein, as tools for modulating or

XX CC inhibiting the expression of genes and/or translation of transcripts, and

XX CC as therapeutic agents. The proteins and peptides are useful as

XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present

XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example

XX CC from the invention

XX SQ Sequence 15 AA;

XX Query Match

XX Best Local Similarity 29.8%; Score 37; DB 6; Length 15;

XX Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

XX ROQFIQSVLNGGATR 23

XX ||: : : ||| ||

XX 1 ROETLEQVLNRVTR 15

XX Db

XX RESULT 3

XX ADM34497

XX ID ADM34497 standard; peptide; 13 AA.

XX AC ADM34497;

XX 10-MAR-2005 (first entry)

XX HLA binding epitope #5247.

XX Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;

XX KW MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;

KM viral disease; cancer.
 XX
 OS Unidentified.
 XX
 PN WO2003040165-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 18-OCT-2001; 2001WO-US051650.
 XX
 PR 19-OCT-2000; 2000US-0242350P.
 PR 20-APR-2001; 2001US-0285624P.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S;
 XX
 DR WPI; 2003-441519/41.
 XX
 PT New composition comprising at least one peptide having allele-specific
 PT binding motifs for HLA, useful for preventing, treating or diagnosing
 PT viral diseases and cancer.
 XX
 PS Claim 1; Page 52-379; 382pp; English.
 XX
 CC The invention relates to a composition comprising at least one peptide
 CC having an isolated, prepared epitope selected from any of the sequences
 CC from 30 lists given in the specification. Also disclosed is a method for
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a
 CC patient expressing a specific MHC class I allele by contacting cytotoxic
 CC T cells from the patient with the composition cited above. The
 CC composition comprises an epitope that is joined by an amino acid linker.
 CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
 CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
 CC binds to a complex of the HLA molecule and the epitope. Specifically
 CC claimed are peptides having allele-specific binding motifs for HLA. The
 CC compositions and methods are useful for preventing, treating or
 CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
 CC diagnostic agents for evaluating immune responses, for making antibodies
 CC and for evaluating efficacy of a vaccine. Sequences given in ADW29251-
 CC ADW37745 represent epitopes of the invention as given in Tables 2-31.
 XX
 SQ Sequence 13 AA;
 Query Match 27.4%; Score 34; DB 7; Length 13;
 Best Local Similarity 56.2%; Pred. No. 2e+02;
 Matches 9; Conservative 1; Mismatches 2; Indels 4; Gaps 1;
 QY 7 KYRQPFQSVLNNGAT 22
 DB 2 KYRQPFIL---KGAT 13
 ID ADM35730 standard; peptide; 13 AA.
 XX
 AC ADM35730;
 XX
 DT 10-MAR-2005 (first entry)
 XX
 DE HLA binding epitope #6480.
 XX
 KM Virus; cytotoxic; gene therapy; vaccine; epitope; cytotoxic T cell;
 KM MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
 KM viral disease; cancer.
 XX
 OS Unidentified.
 XX
 PN WO2003040165-A2.
 XX
 PD 15-MAY-2003.

XX
 PF 18-OCT-2001; 2001WO-US051650.
 XX
 PR 19-OCT-2000; 2000US-0242350P.
 PR 20-APR-2001; 2001US-0285624P.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S;
 XX
 DR WPI; 2003-441519/41.
 XX
 PT New composition comprising at least one peptide having allele-specific
 PT binding motifs for HLA, useful for preventing, treating or diagnosing
 PT viral diseases and cancer.
 XX
 PS Claim 1; Page 52-379; 382pp; English.
 XX
 CC The invention relates to a composition comprising at least one peptide
 CC having an isolated, prepared epitope selected from any of the sequences
 CC from 30 lists given in the specification. Also disclosed is a method for
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a
 CC patient expressing a specific MHC class I allele by contacting cytotoxic
 CC T cells from the patient with the composition cited above. The
 CC composition comprises an epitope that is joined by an amino acid linker.
 CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
 CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
 CC binds to a complex of the HLA molecule and the epitope. Specifically
 CC claimed are peptides having allele-specific binding motifs for HLA. The
 CC compositions and methods are useful for preventing, treating or
 CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
 CC diagnostic agents for evaluating immune responses, for making antibodies
 CC and for evaluating efficacy of a vaccine. Sequences given in ADW29251-
 CC ADW37745 represent epitopes of the invention as given in Tables 2-31.
 XX
 SQ Sequence 13 AA;
 Query Match 27.4%; Score 34; DB 7; Length 13;
 Best Local Similarity 56.2%; Pred. No. 2e+02;
 Matches 9; Conservative 1; Mismatches 2; Indels 4; Gaps 1;
 QY 7 KYRQPFQSVLNNGAT 22
 DB 2 KYRQPFIL---KGAT 13
 ID AAP8118 standard; protein; 19 AA.
 XX
 AC AAP8118;
 XX
 DT 25-MAR-2003 (revised)
 DT 01-JUL-2002 (revised)
 DT 08-OCT-1990 (first entry)
 XX
 DE hsc-related peptide hsc (169-187).
 XX
 KM oncogene related peptide; hsc-related.
 XX
 OS Synthetic.
 XX
 PN EP253325-A.
 XX
 PD 20-JAN-1988.
 XX
 PF 10-JUL-1987; 87EP-00109985.
 XX
 PR 11-JUL-1986; 86JP-00164331.
 PR 10-JUL-1987; 87JP-00173671.
 XX
 PA (YANA/) YANAIHARA N.

[illegible]

CC	as therapeutic agents. The proteins and peptides are useful as	
CC	therapeutic, prognostic and diagnostic reagents for cancer. The present	
CC	sequence is a human leukocyte antigen (HLA) peptide, used in an example	
CC	from the invention	
XX		
XX		
SQ	Sequence 15 AA;	
QY	10 QOFIQSVLNNGATR 23	
	: : :	
Db	1 QEILQVLNRRVTR 14	
RESULT 7		
ABR31017		
ID	ABR31017 standard; peptide; 15 AA.	
XX		
AC	ABR31017;	
XX		
DT	19-MAY-2003 (first entry)	
XX		
DE	Human cancer-related protein 83p4B8 HLA peptide #2079.	
XX		
KW	Human; cytosolic; vaccine; cancer; immune response; HLA;	
XX	human leukocyte antigen.	
XX		
OS	Homo sapiens.	
PN	WO200283921-A2.	
XX		
PD	24-OCT-2002.	
XX		
PE	10-APR-2002; 2002WO-US011654.	
PR	10-APR-2001; 2001US-0282739P.	
PR	10-APR-2001; 2001US-0283112P.	
PR	25-APR-2001; 2001US-0286630P.	
XX		
PA	(AGEN-) AGENSYS INC.	
XX		
PI	Jakovovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;	
PI	Morrison K, Morrison RK, Raitano AB;	
XX		
DR	WPI; 2003-075555/07.	
XX		
PT	New composition comprising a substance that modulates the structure of	
PT	proteins and polynucleotides, useful for therapeutic, prognostic and	
PT	diagnostic reagents for eliciting cellular or humoral immune response in	
PT	cancer patients.	
XX		
PS	Claim 13; Page 485; 1021pp; English.	
XX		
XX	The present invention relates to novel human cancer-related genes and	
CC	proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and	
CC	proteins are useful for eliciting a humoral or cellular immune response.	
CC	The genes are useful as probes and primers for the amplification and/or	
CC	detection of genes, mRNAs or their fragments, as reagents for the	
CC	diagnosis and/or prognosis of cancer, as coding sequences capable of	
CC	inhibiting the expression of the protein, as tools for modulating or	
CC	inhibiting the expression of genes and/or translation of transcripts, and	
CC	as therapeutic agents. The proteins and peptides are useful as	
CC	therapeutic, prognostic and diagnostic reagents for cancer. The present	
CC	sequence is a human leukocyte antigen (HLA) peptide, used in an example	
CC	from the invention	
XX		
XX		
SQ	Sequence 15 AA;	
Query Match	25.8%; Score 32; DB 6; Length 15;	
Best Local Similarity	42.9%; Pred. No. 4.9e+02;	
Matches	6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;	

KM cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
KW HLA.
XX
OS Homo sapiens.
XX
PN WO200216593-A2.
XX
PD 28-FEB-2002.
XX
PF 22-AUG-2001; 2001WO-US026276.
XX
PR 22-AUG-2000; 2000US-0227098P.
PR 10-APR-2001; 2001US-0282739P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
PI Chailita-Eid PM, Jakobovits A;
XX
DR WPI; 2002-425659/45.
XX
PT New compositions comprising a gene (designated 158PID7), its encoded
PT protein or their modulators, useful for treating or diagnosing cancers,
PT particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses or
humans).
XX
PS Disclosure; Page 130; 181pp; English.
XX
CC The invention relates to a novel nucleic acid, designated 158PID7. The
CC compositions are useful for treating or diagnosing cancers, particularly
CC bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
CC horses or humans). The compositions are also useful for monitoring
CC genetic abnormalities and in preparing cancer vaccines. The nucleic acid
CC of the invention can be used in gene therapy to treat the said disorders.
CC This sequence represents a human leukocyte antigen (HLA) peptide relating
CC to the 158PID7 protein of the invention
XX
SQ Sequence 9 AA:

Query Match 25.0%; Score 31; DB 5; Length 9;
Best Local Similarity 75.0%; Pred. No. 2e+06; 1; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 1;

QY 15 SLVNNGAT 22
Db |:|||||
1 SLNNGLT 8

RESULT 11
ABJ01921
ID ABJ01921 standard; peptide; 10 AA.
XX
AC ABJ01921;
XX
DT 19-SEP-2002 (first entry)
XX
DE 158PID7 related HLA peptide SEQ ID No 621.
XX
KW Cytostatic; 158PID7; cancer; bladder cancer; mouse; rat; rabbit; dog;
KW cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
KW HLA.
XX
OS Homo sapiens.
XX
PN WO200216593-A2.
XX
PD 28-FEB-2002.
XX
PF 22-AUG-2001; 2001WO-US026276.
XX
PR 22-AUG-2000; 2000US-0227098P.
PR 10-APR-2001; 2001US-0282739P.
XX

PA (AGEN-) AGENSYS INC.
XX
PI Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
PI Chailita-Eid PM, Jakobovits A;
XX
DR WPI; 2002-425659/45.
XX
PT New compositions comprising a gene (designated 158PID7), its encoded
PT protein or their modulators, useful for treating or diagnosing cancers,
PT particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses or
humans).
XX
PS Disclosure; Page 148; 181pp; English.
XX
CC The invention relates to a novel nucleic acid, designated 158PID7. The
CC compositions are useful for treating or diagnosing cancers, particularly
CC bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
CC horses or humans). The compositions are also useful for monitoring
CC genetic abnormalities and in preparing cancer vaccines. The nucleic acid
CC of the invention can be used in gene therapy to treat the said disorders.
CC This sequence represents a human leukocyte antigen (HLA) peptide relating
CC to the 158PID7 protein of the invention
XX
SQ Sequence 10 AA:

Query Match 25.0%; Score 31; DB 5; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.4e+02; 1; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 1;

QY 15 SLVNNGAT 22
Db |:|||||
2 SLNNGLT 9

RESULT 12
ABJ01457
ID ABJ01457 standard; peptide; 10 AA.
XX
AC ABJ01457;
XX
DT 19-SEP-2002 (first entry)
XX
DE 158PID7 related HLA peptide SEQ ID No 157.
XX
KW Cytostatic; 158PID7; cancer; bladder cancer; mouse; rat; rabbit; dog;
KW cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
KW HLA.
XX
OS Homo sapiens.
XX
PN WO200216593-A2.
XX
PD 28-FEB-2002.
XX
PF 22-AUG-2001; 2001WO-US026276.
XX
PR 22-AUG-2000; 2000US-0227098P.
PR 10-APR-2001; 2001US-0282739P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
PI Chailita-Eid PM, Jakobovits A;
XX
DR WPI; 2002-425659/45.
XX
PT New compositions comprising a gene (designated 158PID7), its encoded
PT protein or their modulators, useful for treating or diagnosing cancers,
PT particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses or
humans).
XX
PS Disclosure; Page 131; 181pp; English.
XX

CC The invention relates to a novel nucleic acid, designated 158PID7. The
 CC compositions are useful for treating or diagnosing cancers, particularly
 CC bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
 CC horses or humans). The compositions are also useful for monitoring
 CC genetic abnormalities and in preparing cancer vaccines. The nucleic acid
 CC of the invention can be used in gene therapy to treat the said disorders.
 CC This sequence represents a human leukocyte antigen (HLA) peptide relating
 CC to the 158PID7 protein of the invention

SO Sequence 10 AA;

Query Match 25.0%; Score 31; DB 5; Length 10;
 Best Local Similarity 75.0%; Pred. No. 4.4e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 15 SVLNGAT 22
 | : | | | | |
 Db 1 SLNNGLT 8

RESULT 13

AAW19443
 ID AAW19443 standard; peptide; 12 AA.

AC AAW19443;

DT 05-SEP-1997 (first entry)

DE Anti-fungal and anti-bacterial histatin-based peptide 13-Q2.3.9.10.

XX Candida albicans; periodontitis; caries; tooth decay; oral infection;
 KM vaginal infection; urethral infection; mucosal infection; ear infection;
 KM respiratory infection; skin infection; ophthalmic infection;
 KM bacterial disease; Streptococcus mutans; Porphyromonas gingivalis;
 KM Clostridium histolyticum.

OS Synthetic.

FT Key Location/Qualifiers
 FT Region 1..12
 FT /note= "At least one amino acid must have a D-
 configuration"

PN W09640768-A2.

PD 19-DEC-1996.

PF 07-JUN-1996; 96WO-US009374.

PR 07-JUN-1995; 95US-00481888.

PA (PERI-) PERIODONTIX INC.
 PA (UYBO-) UNIV BOSTON.

PI Oppenheim FG, Xu T, Roberts FD, Spacciapoli P, Friden PM;

DR WPI; 1997-052232/05.

PT Anti-fungal and anti-bacterial histatin-based peptide(s) - useful esp for
 PT treating Candidal infections, periodontitis and caries.

PS Disclosure; Fig 1; 72pp; English.

XX The present sequence represents peptide Q2.3.9.10, where at least one
 CC amino acid is in the D-configuration. The peptide preferably is modified
 CC by an acetyl or carbamyl addition at the N-terminus and/or amidation at
 CC the C-terminus. The peptide, based on the naturally occurring histidine-
 CC rich human histatins, have anti-fungal and anti-bacterial activity and
 CC are useful in compositions for the treatment of oral, vaginal, urethral,
 CC mucosal, respiratory, skin, ear and ophthalmic fungal or bacterial
 CC infections. It is particularly effective against local and systemic
 CC Candida albicans infection, against oral bacterial diseases such as
 CC caries and periodontitis (by inhibiting e.g. Streptococcus mutans and

CC Porphyromonas gingivalis) and against Clostridium histolyticum. The
 CC peptide has superior anti-fungal (especially anti-Candidal) and anti-
 CC bacterial activity, particularly on a weight basis, compared to the
 CC longer, naturally occurring histatins. Peptides containing D-residues are
 CC also more resistant to degradation than L-amino acid versions

SO Sequence 12 AA;

Query Match 25.0%; Score 31; DB 2; Length 12;
 Best Local Similarity 55.6%; Pred. No. 5.5e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 4 ONYKYRROOF 12
 | : | : | : | : |
 Db 3 QHNGYKROOF 11

RESULT 14

AAW19480
 ID AAW19480 standard; peptide; 12 AA.

AC AAW19480;

DT 05-SEP-1997 (first entry)

DE Anti-fungal and anti-bacterial D-amino acid peptide 113-Q2.3.9.10.

XX Candida albicans; periodontitis; caries; tooth decay; oral infection;
 KM vaginal infection; urethral infection; mucosal infection; ear infection;
 KM respiratory infection; skin infection; ophthalmic infection;
 KM bacterial disease; Streptococcus mutans; Porphyromonas gingivalis;
 KM Clostridium histolyticum.

OS Synthetic.

FT Key Location/Qualifiers
 FT Region 1..12
 FT /note= "At least one amino acid must have D-
 configuration"

PN W09640770-A2.

PD 19-DEC-1996.

PF 07-JUN-1996; 96WO-US009962.

PR 07-JUN-1995; 95US-00485273.

PA (PERI-) PERIODONTIX INC.
 PA (UYBO-) UNIV BOSTON.

PI Oppenheim FG, Xu T, Spacciapoli P, Roberts FD, Friden PM;

DR WPI; 1997-052234/05.

PT Anti-fungal and anti-bacterial D-amino acid histatins and histatin-based
 PT peptide(s) - useful esp for treating Candidal infections, periodontitis
 PT and caries.

PS Disclosure; Fig 1; 63pp; English.

XX The present sequence represents an anti-fungal and anti-bacterial D-amino
 CC acid histatin-based peptide 113-Q2.3.9.10, found in human paratoid
 CC secretion, where at least one amino acid in the peptide is in the D-
 CC configuration. The peptide is preferably modified by an acetyl or
 CC carbamyl addition at the N-terminus and/or amidation at the C-terminus.
 CC The novel D-amino acid-containing peptide, based on the naturally
 CC occurring histidine-rich human histatins, have anti-fungal and anti-
 CC bacterial activity and are useful in compositions for the treatment of
 CC oral, vaginal, urethral, mucosal, respiratory, skin, ear and ophthalmic
 CC fungal or bacterial infections. It is particularly effective against
 CC local and systemic Candida albicans infection, against oral bacterial
 CC diseases such as caries and periodontitis (by inhibiting e.g.

CC Streptococcus mutans and Porphyromonas gingivalis) and against
CC Clostridium histolyticum. The D-amino acid-containing peptide has
CC superior anti-fungal (especially anti-candidal) and anti-bacterial
CC activity, particularly on a weight basis, compared to the natural L-
CC amino acid forms of histatin and histatin-based peptides. The presence
CC of D-residues also makes the peptides more resistant to degradation than
CC corresponding L-amino acid versions
XX
SQ Sequence 12 AA;
Query Match 25.0%; Score 31; DB 2; Length 12;
Best Local Similarity 55.6%; Pred. No. 5.5e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
DY 4 ONYKYRROOF 12
Db 3 QHNGYKQOF 11
RESULT 15
AAB11993
ID AAB11993 standard; peptide: 12 AA.
XX
AC AAB11993;
XX
DT 24-NOV-2000 (first entry)
XX
DE Histatin-related peptide, P-113-KR2.3.9.10Q.
XX
KM Histatin-related peptide; cystic fibrosis; Pseudomonas aeruginosa;
KM antibiotic resistance; pulmonary infection; antibacterial; antibiotic.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 12 /note= "C-terminal amide"
XX
PN WO200040204-A2.
XX
PD 13-JUL-2000.
XX
PF 07-JAN-2000; 2000WO-US000480.
XX
PR 08-JAN-1999; 99US-00226666.
XX
PA (PERI-) PERIODONTIX INC.
XX
PI Spacelapoli P, Rothstein DM, Friden PM;
XX
DR WPI: 2000-465852/40.
XX
PT Treating cystic fibrosis and combating Pseudomonas and other pulmonary
PT infections in a mammal comprises administering histatin or a fragment of
PT it.
XX
PS Example 6; Page 13; 27pp; English.
XX
CC The invention relates to treating cystic fibrosis via the administration
CC of a histatin, a fragment of histatin, or a histatin-related peptide. The
CC peptide that is administered contains between 8 and 20 amino acids and
CC has the sequence: X1-X2-X3-X4-X5-X6-X7-X8-X9-X10-X11-X12-X13-X14-X15-X16-
CC X17-X18-X19-X20-X21-X22-X23 where X1 is Asp or absent; X2 is Ser or
CC absent; X3 is His or absent; X4 is Ala, His, Leu or absent; X5 is Lys,
CC Gln, Arg, Orn, or another basic amino acid; X6 is Arg, Gln, Lys, or
CC another basic amino acid; X7 is His, Phe, Tyr Leu, or another hydrophobic
CC amino acid; X8 is His, Phe, Tyr Leu, or another hydrophobic amino acid;
CC X9 is Gly, Lys, Arg, Ser, or a basic amino acid; X10 is Tyr; X11 is Lys,
CC His, Phe, Leu, or another hydrophobic amino acid; X12 is Lys, Gln, Arg,
CC Orn, or another basic amino acid; X13 is Lys, Gln, Arg, Orn, another
CC basic amino acid, or absent; X14 is Phe or absent X15 is His, Phe, Tyr,
CC Leu, another hydrophobic amino acid, or absent; X16 is Gln or absent; X17

CC is Lys or absent; X18 is His or absent; X19 is His or absent; X20 is Ser
CC or absent; X21 is His or absent; X22 is Arg or absent; and X23 is Gly or
CC absent. Optionally, the peptide may contain at least one modification
CC selected from an N-terminal acyl addition, an N-terminal carbamyl
CC addition and a C-terminal amide addition. Histatin, histatin fragments
CC and histatin-related peptides have activity against Pseudomonas
CC aeruginosa. They may therefore be used to combat Pseudomonas infections
CC and other pulmonary infections in cystic fibrosis patients. Such
CC infections are often resistant to the antibiotics normally used to treat
CC pulmonary infections. Sequences AAB11985-B11993 represent histatin-
CC related peptides used in the exemplifications of the invention. With the
CC exception of P-113-Q2.3.9.10 (AAB11988), all these peptides showed
CC activity against Pseudomonas aeruginosa
XX
SQ Sequence 12 AA;
Query Match 25.0%; Score 31; DB 3; Length 12;
Best Local Similarity 55.6%; Pred. No. 5.5e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
DY 4 ONYKYRROOF 12
Db 3 QHNGYKQOF 11
RESULT 16
AAB11988
ID AAB11988 standard; peptide: 12 AA.
XX
AC AAB11988;
XX
DT 24-NOV-2000 (first entry)
XX
DE Histatin-related peptide, P-113-Q2.3.9.10.
XX
KM Histatin-related peptide; cystic fibrosis; Pseudomonas aeruginosa;
KM antibiotic resistance; pulmonary infection; antibacterial; antibiotic.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 12 /note= "C-terminal amide"
XX
PN WO200040204-A2.
XX
PD 13-JUL-2000.
XX
PF 07-JAN-2000; 2000WO-US000480.
XX
PR 08-JAN-1999; 99US-00226666.
XX
PA (PERI-) PERIODONTIX INC.
XX
PI Spacelapoli P, Rothstein DM, Friden PM;
XX
DR WPI: 2000-465852/40.
XX
PT Treating cystic fibrosis and combating Pseudomonas and other pulmonary
PT infections in a mammal comprises administering histatin or a fragment of
PT it.
XX
PS Example 5; Page 12; 27pp; English.
XX
CC The invention relates to treating cystic fibrosis via the administration
CC of a histatin, a fragment of histatin, or a histatin-related peptide. The
CC peptide that is administered contains between 8 and 20 amino acids and
CC has the sequence: X1-X2-X3-X4-X5-X6-X7-X8-X9-X10-X11-X12-X13-X14-X15-X16-
CC X17-X18-X19-X20-X21-X22-X23 where X1 is Asp or absent; X2 is Ser or
CC absent; X3 is His or absent; X4 is Ala, His, Leu or absent; X5 is Lys,
CC Gln, Arg, Orn, or another basic amino acid; X6 is Arg, Gln, Lys, or
CC another basic amino acid; X7 is His, Phe, Tyr Leu, or another hydrophobic

CC amino acid; X8 is His, Phe, Tyr Leu, or another hydrophobic amino acid;
 CC X9 is Gly, Lys, Arg, Ser, or a basic amino acid; X10 is Tyr; X11 is Lys,
 CC His, Phe, Leu, or another hydrophobic amino acid; X12 is Lys, Gln, Arg,
 CC Orn, or another basic amino acid; X13 is Lys, Gln, Arg, Orn, another
 CC basic amino acid, or absent; X14 is Phe or absent; X15 is His, Phe, Tyr,
 CC Leu, another hydrophobic amino acid, or absent; X16 is Glu or absent; X17
 CC is Lys or absent; X18 is His or absent; X19 is His or absent; X20 is Ser
 CC or absent; X21 is His or absent; X22 is Arg or absent; and X23 is Gly or
 CC absent. Optionally, the peptide may contain at least one modification
 CC selected from an N-terminal acyl addition, an N-terminal carbamyl
 CC addition and a C-terminal amide addition. Histatin, histatin fragments
 CC and histatin-related peptides have activity against *Pseudomonas*
 CC aeruginosa. They may therefore be used to combat *Pseudomonas* infections
 CC and other pulmonary infections in cystic fibrosis patients. Such
 CC infections are often resistant to the antibiotics normally used to treat
 CC pulmonary infections. Sequences ABB11985-B11993 represent histatin-
 CC related peptides used in the exemplifications of the invention. With the
 CC exception of the present sequence, all these peptides showed activity
 CC against *Pseudomonas aeruginosa*
 XX

SO Sequence 12 AA;

Query Match 25.0%; Score 31; DB 3; Length 12;
 Best Local Similarity 55.6%; Pred. No. 5.5e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 QNTKYRQF 12
 : : : : :
 Db 3 QHNGYKQF 11

RESULT 17

ABBS6747
 ID ABB56747 standard; peptide; 14 AA.

AC ABB56747;
 DT 05-MAR-2002 (first entry)
 DE Human SNP related amino acid sequence SEQ ID NO:1112.
 XX
 KM Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;
 KM immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;
 KM autoimmune disease; inflammation; cancer; nervous system disease;
 KM infection; polymorphic protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200138586-A2.
 XX
 PD 31-MAY-2001.
 XX
 PF 22-NOV-2000; 2000WO-US032311.
 XX
 PR 24-NOV-1999; 99US-0167383P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA, Leach M;
 XX
 DR WPI; 2001-355949/37.
 XX
 PT Isolated human nucleic acids comprising one or more single nucleotide
 PT polymorphisms, useful for treating a subject suffering from a pathology,
 PT e.g., autoimmune diseases, ascribed to the presence of a sequence
 PT polymorphism.
 XX
 PS Claim 1; Page 636; 674pp; English.
 XX
 CC ABL0010 to ABL01104 represent human nucleic acid oligonucleotides
 CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531
 CC to ABB56903 represent human peptides encoded by some of the SNP
 CC oligonucleotides. The sequences from the present invention can have

CC immunosuppressive, cytostatic, antiinflammatory, neuroprotective and
 CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides
 CC and antibodies from the present invention can be used for treating a
 CC subject suffering from, at risk for, or suspected of, suffering from a
 CC pathology ascribed to the presence of a sequence polymorphism. The
 CC pathology may be autoimmune diseases, inflammation, cancer, diseases of
 CC the nervous system, and infection by pathogenic microorganisms. The SNPs
 CC are also useful for determining which forms of a characterized
 CC polymorphism are present in individuals. The antibodies may be used in
 CC the detection, quantitation and/or cellular or tissue localisation of a
 CC polymorphic protein (e.g., for use in measuring levels of the polymorphic
 CC protein within appropriate physiological samples)
 XX

SO Sequence 14 AA;

Query Match 25.0%; Score 31; DB 4; Length 14;
 Best Local Similarity 60.0%; Pred. No. 6.5e+02;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 DMAQNTKYRQ 10
 : : : : :
 Db 4 DRTANVYRQ 13

RESULT 18

ABG72213
 ID ABG72213 standard; peptide; 15 AA.

AC ABG72213;
 DT 14-FEB-2003 (first entry)
 DE Human CARD-12 peptide used to raise CARD-12 antibodies.
 XX
 KM Human; caspase recruitment domain-12; CARD-12; apoptosis; transgenic;
 KM inflammatory disorder; immune disorder; Crohn's disease;
 KM reactive arthritis; insulin-dependent diabetes; multiple sclerosis;
 KM contact dermatitis; psoriasis; graft versus host disease; sarcoidosis;
 KM graft rejection; atopic condition; asthma; allergic rhinitis;
 KM gastrointestinal allergy; food allergy; eosinophilia; conjunctivitis;
 KM glomerular nephritis; viral infection; bacterial infection;
 KM Alzheimer's disease; Parkinson's disease; retinitis pigmentosa;
 KM Huntington's disease; anaemia; myocardial infarction; stroke; cancer;
 KM cytostatic; antiinflammatory; immunosuppressive; neuroprotective;
 KM dermatological; nephrotoxic; ophthalmological; cardiac;
 KM cerebroprotective; immunogen.
 XX
 OS Homo sapiens.
 XX
 PN WO200285939-A1.
 XX
 PD 31-OCT-2002.
 XX
 PF 24-APR-2002; 2002WO-US013009.
 XX
 PR 24-APR-2001; 2001US-00841739.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Bertin J;
 XX
 DR WPI; 2003-093096/08.
 XX
 PT Novel caspase recruitment domain-12, CARD-12, polypeptide useful for
 PT treating inflammatory disorders and immune disorders e.g., Crohn's
 PT disease, diabetes, multiple sclerosis, Hashimoto's thyroiditis and
 PT Grave's disease.
 XX
 PS Example 3; Page 18; 112pp; English.
 XX
 CC The present invention relates to the isolation of human caspase
 CC recruitment domain-12 (CARD-12), and the polynucleotide sequence encoding
 CC it. The CARD family of proteins are involved in apoptosis. The invention

CC also discloses CARD-12 fusion proteins, antigenic peptides, anti-CARD-12
CC antibodies, recombinant expression vectors, host cells containing these
CC expression vectors, and non-human transgenic animals. CARD-12 polypeptide
CC and polynucleotide sequences are useful for diagnosing and treating
CC inflammatory and immune disorders such as Crohn's disease, reactive
CC arthritis, Lyme disease, insulin-dependent diabetes, multiple sclerosis,
CC Hashimoto's thyroiditis, Grave's disease, contact dermatitis, psoriasis,
CC graft rejection, graft versus host disease, sarcoidosis, atopic
CC conditions (e.g. asthma, allergies, allergic rhinitis, gastrointestinal
CC allergies, food allergies), eosinophilia, conjunctivitis, glomerular
CC nephritis, certain pathogen susceptibility such as helminthic
CC infections (e.g. leishmaniasis), viral infections (e.g. human
CC immunodeficiency virus (HIV)), bacterial infections (e.g. tuberculosis,
CC lepromatous leprosis), arthritis, Alzheimer's disease, Parkinson's disease,
CC retinitis pigmentosa, Huntington's disease, anemia, myocardial
CC infarction, stroke, and cancer. The present sequence representing a
CC peptide of human CARD-12 is used to raise CARD-12 antibodies in rabbits
CC
CC
SQ Sequence 15 AA;

Query Match 25.0%; Score 31; DB 6; Length 15;
Best Local Similarity 54.5%; Pred. No. 7.1e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 8 YRQQFIGSVLN 18
:|:|:|:|
Db 2 WRQSLQSVKN 12

RESULT 19
ADM86333
ID ADM86333 standard; peptide; 15 AA.

XX ADM86333;
XX
XX 21-APR-2005 (first entry)

XX Human NGF receptor targeted peptide SEQ ID NO:11, retro-inverso form.

XX NGF; nerve growth factor; cytosstatic; cancer; decontamination;
XX analyte detection; screening; neoplasm.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1..15 /note="All D-form residues"

XX US2005027457-A1.

XX 03-FEB-2005.

XX 11-FEB-2004; 2004US-00777829.

XX 24-JAN-2000; 2000US-00490701.

XX 23-JAN-2001; 2001US-00767460.

XX (MAND/) MANDELL A J.

XX (SELZ/) SELZ K A.

XX (SHLE/) SHLESINGER M F.

XX Mandell AJ, Selz KA, Shlesinger MF;

XX WPI; 2005-151359/16.

XX Novel isolated peptide comprising retro-inverso amino acid sequence of

XX peptide, useful for diagnosing or treating cancer.

XX Claim 1; Page: 50pp; English.

XX The invention relates to novel retro-inverso peptides or peptide-like

XX molecules which have a high probability of binding to and/or otherwise

XX modulating the function of polypeptides and/or proteins, and to methods

CC for designing such peptides or peptide-like molecules. Certain peptides
CC CC The invention have cytostatic activity, depending on their polypeptide
CC target. A retro-inverso peptide of the invention is useful for diagnosing
CC or treating cancer, or for detecting contaminants in water, food or soil
CC samples. The present sequence represents a retro-inverso form of a
CC peptide designed to target the human nerve growth factor (NGF) receptor.
CC Note: The present sequence is not shown in the specification, but was
CC derived from ADM86234.

XX Sequence 15 AA;

Query Match 25.0%; Score 31; DB 9; Length 15;
Best Local Similarity 62.5%; Pred. No. 7.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 DMAONTKY 8
|:|:|:|
Db 7 DTAENHRY 14

RESULT 20
AAW73692
ID AAW73692 standard; peptide; 16 AA.

XX AAW73692;
XX
XX 24-MAR-1999 (first entry)

XX M. tuberculosis antigen clone ORF-1 peptide 1-16.

XX Antigen; M.tuberculosis protein; immunotherapy; tuberculosis; diagnosis;

XX infection.

XX Mycobacterium tuberculosis.

XX MO9853076-A2.

XX 26-NOV-1998.

XX 20-MAY-1998; 98MO-US010514.

XX 20-MAY-1997; 97US-00858998.

XX 05-MAY-1998; 98US-00073009.

XX (CORI-) CORIXA CORP.

XX Alderson MR, Dillon DC, Skeiky YAM, Campos-Neco A;

XX WPI; 1999-045315/04.

XX New isolated Mycobacterium tuberculosis antigens - used to develop

XX products for the prevention, treatment and diagnosis of tuberculosis

XX infection.

XX Example 1; Page 55; 104pp; English.

XX This sequence represents an immunogenic portion of a Mycobacterium

XX tuberculosis antigen of the invention. The polypeptides are useful for

XX immunotherapy to treat or prevent tuberculosis (especially in humans);

XX e.g. they can be included with an acceptable carrier in pharmaceutical

XX compositions or included in vaccines, and administered to induce

XX protective immunity in a patient against M. tuberculosis. Tuberculosis is

XX a chronic, infectious disease generally caused by M. tuberculosis

XX infection, and if left untreated typically results in serious

XX complications and death. Fusion proteins containing the antigen, or DNA

XX molecules can similarly be included with an acceptable carrier in

XX pharmaceutical compositions or in vaccines and administered as above. The

XX polypeptides are also useful for diagnosis of tuberculosis, by contacting

XX dermal cells with at least one polypeptide and detecting an immune

XX response (especially induction) on the patient's skin. Inhibiting the

XX spread of tuberculosis requires vaccination and accurate diagnosis, since

XX antibiotic therapy may not be effective due to the existence of an

XX asymptomatic but contagious stage and to patient non-compliance. The

Query Match	25.0%;	Score 31;	DB 2;	Length 16;
Best Local Similarity	33.3%;	Pred. No. 7.6e+02;		
Matches	5;	Conservative	4;	Indels 0;
		Mismatches		Gaps 0;

```
QY      5 NYKRYQQFIQSVLNN 19
      ||::|||::|
Db      2 NYEQQEQAASQQILSS 16
```

RESULT 22	
AAU08157	
ID AU08157	standard; peptide; 16 AA

DE Mycobacterium tuberculosis overlapping peptide ORF-1-16.

KW Tuberculosis; Mycobacterium infection; gene therapy; anti bacterial

05 Mycobacterium tuberculosis

PN WO200162893-A2.

PF 26-FEB-2001; 2001WO-US005992.

PR 25-FEB-2000; 2000US-0185037P.

PR 08-AUG-2000; 2000US-0223828P.

PA (CORI-) CORIXA CORP.

PI Campos-Neto A, Skeiky Y, Ovendale P, Jen S, Lodes M;

DR WPI; 2001-536638/59.

PT An isolated polypeptide comprising a *Mycobacterium* antigen, e.g., from
PT *Mycobacterium tuberculosis*, useful in a vaccine for enhancing an immune
PT response to and inhibiting development of a *Mycobacterium* infection.

PS Example 1; Page 127; 161pp; English

CC The presensitization relates to the isolation of Mycobacterium
CC tuberculois antigen polypeptides (e.g. Tb224) and the nucleic acids
CC encoding them. The invention describes compounds and methods for the
CC diagnosis of tuberculois or for inducing protective immunity against
CC tuberculois. The compounds comprise at least one immunogenic portion of
CC one or more Mycobacterium proteins and nucleic acid molecules encoding
CC such polypeptides. The Mycobacterium proteins and nucleic acid molecules
CC encoding them can be used in diagnostic kits for the detection of
CC Mycobacterium infection in patients and biological samples. The compounds
CC of the invention and antibodies directed against the Mycobacterium
CC proteins may be used in vaccines for immunisation against Mycobacterium
CC infections. The nucleic acids encoding the Mycobacterium proteins may
CC be used in gene therapy. AAU08147-AAU08158 represent peptides (ORF-1-1
CC to ORF-1-17) which overlap to the open reading frame ORF-1
XX
XQ Sequence 16 AA;

```
RESULT 23
ABG78004
ID ABG78004 standard; peptide; 16 AA.
XX
AC ABG78004;
XX
DT 15-NOV-2002 (first entry)
XX
DE M. tuberculosis CD4+ antigen ORF-1.1-1-17 peptide #16.
XX
KM Antigen; CD4+; infectious disease; tumour; tuberculosis;
XX autoimmune disease; Leishmaniasis; dendritic cell; T cell.
XX
OS Mycobacterium tuberculosis.
XX
PN US2002081579-A1.
XX
PD 27-JUN-2002.
XX
PF 13-FEB-1998; 98US-00023588.
XX
PR 13-FEB-1998; 98US-00023588.
XX
PA (POT)/ POTTER J E R.
XX
PI Skeiky YAW, Dillon DC, Alderson MR;
XX
DR WPI; 2002-617730/66.
XX
PT Identifying DNAs encoding CD4+ T cell stimulating antigens, for isolating
PT new CD4+ T cell-stimulating antigens associated with e.g. infections,
PT comprises measuring the levels of interferon-gamma production or cell
PT proliferation.
XX
PS Example 2; Page 33; 46pp; English.
XX
CC The invention relates to identifying DNA sequences that encode CD4+ T
CC cell stimulating antigens or antigens containing antibody epitopes
CC comprising determining the level of CD4+ T cell stimulation when incubated
CC with dendritic cells that have been exposed with a host cell transformed
CC with a plasmid suspected of containing a DNA sequence that encodes a CD4+
CC T cell stimulating antigen. Also included are (1) an isolated DNA
CC sequence consisting of DNA sequences isolated using the new method, their
CC complement or DNA sequences that hybridise to them; (2) an expression
CC vector comprising (1); (3) a host cell transformed with the expression
CC vector of (2); and (4) a polypeptide comprising an immunogenic portion of
CC antigen, or a variant of the antigen that differs only in conservative
CC substitutions and/or modifications, where the antigen comprises an amino
CC acid sequence encoded by (1). The method is useful for identifying and
CC isolating new antigens that stimulate CD4+ T cells. In particular, the
CC method is useful for isolating antigens associated with any disorder in
CC which the stimulation of CD4+ T cells is believed to play a role in the
CC body's immune response, e.g. CD4+ T cell-stimulating antigens associated
CC with infectious disease agents such as Mycobacterium tuberculosis or
CC Leishmaniasis, tumour tissue, or autoimmune disorders. The present method
CC is less technically difficult and less time-consuming than prior methods.
CC The present method is also more suitable for high-throughput use. The
CC present sequence represents an overlapping peptide derived from a CD4+ T
CC cell-stimulating antigen from M. tuberculosis
XX
SQ Sequence 16 AA;
XX
Query Match 25.0%; Score 31; DB 5; Length 16;
Best Local Similarity 33.3%; Pred. No. 7.6e+02;
Matches 5; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 5 NYKXROQFIQSVLN 19
||:|:|:|:|:|:|
Db 2 NYEOQEQNSQOILSS 16
```

```
RESULT 24
AAB85946
```

```
ID AAB85946 standard; peptide; 17 AA.
XX
AC AAB85946;
XX
DT 30-NOV-2001 (first entry)
XX
DE Castor bean 2S small subunit protein fragment.
XX
KM Nadin gene; promoter; Brassica; phenotype; transcription; EA9; 3H11;
XX 2A11; alpha-amylase.
XX
OS Ricinus communis.
XX
PN US6281410-B1.
XX
PD 28-AUG-2001.
XX
PF 15-JAN-1999; 99US-00232861.
XX
PR 31-JUL-1986; 86US-00891529.
PR 26-MAY-1987; 87US-00054369.
PR 28-JUL-1987; 87US-00078538.
PR 25-JAN-1988; 88US-00147781.
PR 15-MAR-1988; 88US-00168190.
PR 29-APR-1988; 88US-00188361.
PR 02-NOV-1988; 88US-00267885.
PR 21-MAY-1990; 90US-00526123.
PR 09-JUL-1990; 90US-00550804.
PR 10-AUG-1993; 93US-00105852.
PR 07-JUN-1995; 95US-00484941.
PR 07-MAR-1997; 97US-00812665.
XX
PA (CALJ ) CALGENE LLC.
XX
PI Knauf VC, Kridl JC;
XX
DR WPI; 2001-564354/63.
XX
PT Obtaining a plant that produces a seed with a modified phenotype or
PT altering a seed phenotype, comprises transforming a plant cell with a DNA
PT construct consisting of operably linked components in the direction of
PT transcription.
XX
PS Example 9; Fig 6; 68pp; English.
XX
CC The invention provides a method for obtaining a plant which produces at
CC least one seed having a modified phenotype. The method involves
CC transforming a host plant cell with a DNA construct which consists of
CC operably linked components in the direction of transcription, a promoter
CC region from a Brassica plant gene, a DNA sequence of interest other than
CC the native coding sequence, and a transcription termination region. The
CC method is useful for obtaining plants having modified phenotype or for
CC altering the phenotype of a plant seed or tissue. The DNA constructs are
CC used in manipulating plant cells to provide for regulated transcription,
CC such as light inducible transcription, in a plant tissue or plant part of
CC interest at particular stages of plant growth or in response to external
CC control. These constructs are also used for modulation of expression of
CC endogenous products as well as production of exogenous products in the
CC seed. Sequences AAB85941-47 represent fragments of storage proteins used
CC in comparison studies with the storage protein 2A11
XX
SQ Sequence 17 AA;
XX
Query Match 25.0%; Score 31; DB 4; Length 17;
Best Local Similarity 46.2%; Pred. No. 8.2e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 4 QNYKYROQFIQSV 16
||:|:|:|:|:|:|
Db 2 QNLRQCEYIQOV 14
```

```
RESULT 25
```

Search completed: January 26, 2006, 07:57:58
Job time : 84.5172 secs

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ADM37099
ID ADM37099 standard; peptide; 17 AA.
XX
AC ADM37099;
XX
DT 03-JUN-2004 (first entry)
XX
DE Wild-type Betacatenin 34-50.
XX
KM Beta-catenin; AKT kinase; kinase; phosphorylation substrate;
XX kinase recognition domain; E3 binding region.
XX
OS Unidentified.
XX
PN US2003170611-A1.
XX
PD 11-SEP-2003.
XX
PF 09-MAR-2002; 2002US-00093840.
XX
PR 09-MAR-2002; 2002US-00093840.
XX
PA (CARD/) CARDONE M H.
XX (YAFF/) YAFFE M.
XX
PI Cardone MH, Yaffe M;
XX
DR WPI; 2003-863752/80.
XX
PT Identifying a molecule capable of modulating a kinase activity in situ
XX using a substrate with an altered kinase recognition domain and an
XX associated label is useful in drug discovery.
XX
PS Disclosure; Fig 3b; 25pp; English.
XX
CC The invention relates to identifying a molecule capable of modulating a
XX kinase activity in situ, comprising exposing a candidate molecule to a
XX cell comprising a phosphorylation substrate associated with a detectable
XX label and having a kinase recognition domain altered to be recognised by
XX a kinase that does not recognise the substrate in its unaltered state,
XX and determining whether the candidate molecule causes a change in an
XX expression of the label. Also included are a molecule capable of
XX modulating activity of at least one kinase in situ identified by the
XX claimed method, a fusion protein (comprising an E3 binding region, a
XX kinase recognition domain and a green fluorescent protein, where the
XX kinase recognition domain is the domain of beta-catenin, HIV protein VPU,
XX p27, Bcl-2 or c-Jun), a fusion protein (comprising an E3 binding region,
XX a kinase recognition domain and an enzyme capable of producing a
XX detectable enzymatic product, where the kinase recognition domain is the
XX domain of beta-catenin, HIV protein VPU, p27, Bcl-2 or c-Jun), an
XX isolated genetic molecule encoding one of the above fusion proteins, a
XX vector capable of expressing the above genetic molecule and a cell
XX transfected with the above vector. Expression of the label requires
XX phosphorylation of the phosphorylation substrate by the kinase. The
XX kinase recognition domain is altered to include a consensus recognition
XX motif for the kinase (e.g. AKT kinase). The invention is useful to study
XX kinase activity in situ and to screen for molecules that modulate kinase
XX activities in situ, for example in drug discovery. The invention allows
XX for information on multiple kinases to be provided simultaneously, which
XX prior art does not provide. The present sequence is the wild-type region
XX of Beta-catenin, which may be mutated to an AKT (not defined)
XX phosphorylation site.
XX
SQ Sequence 17 AA;
XX
Query Match 25.0%; Score 31; DB 7; Length 17;
Best Local Similarity 35.7%; Pred. No. 8.2e+02;
Matches 5; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 9 RQOFQSGVLNNGAT 22
Db 4 QQSYLDGSHSGAT 17

```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:50:06 ; Search time 22.5517 Seconds
(without alignments)
87.985 Million cell updates/sec

Title: US-09-662-293-8

Perfect score: 124
Sequence: 1 DMAQNYKRRQFIQSVMNGATRG 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 229350

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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2: /cgn2_6/ptodata/1/1aa/6_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/PTCUS_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/R_COMB.pep: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	25.0	9	2	US-09-935-430-132
2	31	25.0	10	2	US-09-935-430-157
3	31	25.0	10	2	US-09-935-430-621
4	31	25.0	12	1	US-08-973-563A-37
5	31	25.0	12	1	US-08-973-559-37
6	31	25.0	12	1	US-09-226-666-14
7	31	25.0	14	2	US-08-505-250-14
8	31	25.0	14	2	US-08-505-250-14
9	31	25.0	16	2	US-09-073-009-49
10	31	25.0	16	2	US-09-073-010-49
11	30	24.2	12	2	US-09-462-118-30
12	30	24.2	18	2	US-09-623-548A-1034
13	30	24.2	18	2	US-09-657-276-1034
14	30	24.2	18	1	PCT-US93-03748-1
15	28.5	23.0	18	1	US-08-816-105A-14
16	28	22.6	10	2	US-09-935-430-180
17	28	22.6	10	2	US-09-935-430-425
18	28	22.6	12	2	US-09-411-706-6
19	28	22.6	13	2	US-09-935-032-6
20	28	22.6	13	2	US-09-543-940-9
21	28	22.6	15	1	US-07-918-181A-20
22	28	22.6	15	1	US-08-231-575-20
23	28	22.6	15	4	PCT-US93-06928-20
24	28	22.6	16	1	US-08-346-849-58
25	28	22.6	16	1	US-08-346-849-58
26	28	22.6	16	1	US-08-934-222-60
27	28	22.6	16	1	US-08-934-402-60
28	28	22.6	16	1	US-09-207-621-60
29	28	22.6	16	1	US-08-293-284A-58
30	28	22.6	16	1	US-08-293-284A-58
31	28	22.6	16	1	US-08-532-818-60
32	28	22.6	16	2	US-09-231-797-60
33	28	22.6	16	2	US-08-934-224-60
34	28	22.6	16	2	US-08-934-224-60
35	28	22.6	16	2	US-08-934-223-60
36	28	22.6	16	2	US-09-413-992-60
37	28	22.6	16	2	US-08-898-300-58
38	28	22.6	16	2	US-08-898-300-58
39	28	22.6	16	2	US-08-824-513-58
40	28	22.6	16	2	US-08-824-513-58
41	28	22.6	21	1	US-08-280-373B-5
42	27	21.8	9	2	US-09-935-430-114
43	27	21.8	9	2	US-09-935-430-130
44	27	21.8	9	2	US-09-935-430-492
45	27	21.8	10	2	US-08-159-339A-932
46	27	21.8	10	2	US-08-159-339A-992
47	27	21.8	12	1	US-07-598-416-1
48	27	21.8	12	1	US-08-441-818-1
49	27	21.8	12	1	US-08-973-563A-36
50	27	21.8	12	1	US-08-973-559-36
51	27	21.8	12	1	US-08-628-183-1
52	27	21.8	12	2	US-09-226-666-13
53	27	21.8	14	1	US-08-082-849B-19
54	27	21.8	14	4	PCT-US94-01624-19
55	27	21.8	15	2	US-09-009-953-129
56	27	21.8	16	1	US-08-480-190-58
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58	27	21.8	16	2	US-09-171-705-15
59	27	21.8	16	2	US-09-009-953-187
60	27	21.8	16	2	US-08-475-399A-58
61	27	21.8	16	2	US-09-311-784A-315
62	27	21.8	16	2	US-08-077-255A-58
63	27	21.8	16	2	US-09-657-757-16
64	27	21.8	16	4	PCT-US93-07545-58
65	27	21.8	17	1	US-08-467-420A-10
66	27	21.8	17	1	US-08-470-110A-10
67	27	21.8	17	1	US-08-667-769A-10
68	27	21.8	17	1	US-08-940-371-10
69	27	21.8	17	2	US-08-637-647-10
70	27	21.8	17	2	US-09-563-222C-26
71	27	21.8	17	2	US-09-830-748B-11
72	27	21.8	17	2	US-10-700-740-10
73	27	21.8	17	4	PCT-US95-17082A-10
74	27	21.8	21	2	US-09-674-674D-45
75	27	21.8	21	2	US-09-674-674D-49
76	26.5	21.4	20	1	US-08-107-676-22
77	26.5	21.4	20	2	US-09-295-820-22
78	26	21.0	10	1	US-08-406-530-1
79	26	21.0	10	1	US-08-556-597-1
80	26	21.0	10	2	US-09-270-542-30
81	26	21.0	11	1	US-08-471-033-16
82	26	21.0	11	1	US-08-471-044-16
83	26	21.0	11	1	US-08-463-483A-16
84	26	21.0	11	1	US-08-471-046A-16
85	26	21.0	11	1	US-08-378-566B-16
86	26	21.0	11	1	US-08-378-566B-16
87	26	21.0	11	1	US-08-766-858A-44
88	26	21.0	11	1	US-08-469-334-14
89	26	21.0	11	2	US-09-300-529-16
90	26	21.0	11	2	US-09-333-336A-16
91	26	21.0	11	2	US-09-333-336A-16
92	26	21.0	11	2	US-09-402-036-16
93	26	21.0	11	2	US-09-904-226-16
94	26	21.0	12	1	US-08-392-973A-2
95	26	21.0	12	1	US-08-973-563A-29
96	26	21.0	12	1	US-08-973-563A-29
97	26	21.0	12	2	US-08-933-235-9
98	26	21.0	12	2	US-09-147-208-20
99	26	21.0	12	2	US-08-469-260A-40
100	26	21.0	12	2	US-09-434-476A-19

ALIGNMENTS

```
RESULT 1
US-09-935-430-132
; Sequence 132, Application US/09935430
; Patent No. 6863892
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-ELD, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/09/935,430
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 132
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-132

Query Match          25.0%; Score 31; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      15 SVLNNGAT 22
      |:|||||
Db      1 SLNNGLT 8

RESULT 2
US-09-935-430-157
; Sequence 157, Application US/09935430
; Patent No. 6863892
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-ELD, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/09/935,430
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 157
; LENGTH: 10
; TYPE: PRT
```

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-157

Query Match          25.0%; Score 31; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 79;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      15 SVLNNGAT 22
      |:|||||
Db      2 SLNNGLT 9

RESULT 3
US-09-935-430-621
; Sequence 621, Application US/09935430
; Patent No. 6863892
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-ELD, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/09/935,430
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 621
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-621

Query Match          25.0%; Score 31; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 79;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      15 SVLNNGAT 22
      |:|||||
Db      2 SLNNGLT 9

RESULT 4
US-08-973-563A-37
; Sequence 37, Application US/08973563A
; Patent No. 5885965
; GENERAL INFORMATION:
; APPLICANT: Oppenheim, Frank G.
; APPLICANT: Xu, Tao
; APPLICANT: Spacciopoli, Peter
; APPLICANT: Roberts, F. D.
; APPLICANT: Friden, Philip M.
; TITLE OF INVENTION: Anti-Fungal D-Amino Acid Histatin-Based
; TITLE OF INVENTION: Peptides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millica Drive
; CITY: Lexington
; STATE: MA
```



```

; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973.563A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,273
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: PER95-02A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..12
; OTHER INFORMATION: /note="At least one amino acid
; OTHER INFORMATION: must have a D configuration."
; US-08-973-563A-37

Query Match 25.0%; Score 31; DB 1; Length 12;
Best Local Similarity 55.6%; Pred. No. 98;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 QNYKYRQOF 12
DB 3 QHHGYKQOF 11

RESULT 5
US-08-973-559-37
; Sequence 37, Application US/08973559
; Patent No. 5912230
; GENERAL INFORMATION:
; APPLICANT: OPENHEIM, FRANK G.
; APPLICANT: XU, TAO
; APPLICANT: ROBERTS, F. D.
; APPLICANT: SPACCIAPOLI, PETER
; APPLICANT: FRIDEN, PHILIP M.
; TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial
; TITLE OF INVENTION: Histatin-Based Peptides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Miltia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973.559
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 514
```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/481,888
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: PER95-01A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-973-559-37

Query Match 25.0%; Score 31; DB 1; Length 12;
Best Local Similarity 55.6%; Pred. No. 98;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 QNYKYRQOF 12
DB 3 QHHGYKQOF 11

RESULT 6
US-09-226-666-14
; Sequence 14, Application US/09226666A
; Patent No. 6528488
; GENERAL INFORMATION:
; APPLICANT: Spacciapoli, Peter
; APPLICANT: Rochstein, David M.
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: METHOD FOR TREATING CYSTIC FIBROSIS
; FILE REFERENCE: 50032/007001
; CURRENT APPLICATION NUMBER: US/09/226,666A
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from Homo sapiens
; US-09-226-666-14

Query Match 25.0%; Score 31; DB 2; Length 12;
Best Local Similarity 55.6%; Pred. No. 98;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 QNYKYRQOF 12
DB 3 QHHGYKQOF 11

RESULT 7
US-08-505-250-14
; Sequence 14, Application US/08505250
; Patent No. 6183983
; GENERAL INFORMATION:
; APPLICANT: Sato, Haruya
; APPLICANT: Yamamoto, Keiji
; APPLICANT: Suzuki, Kokichi
; APPLICANT: Ikeda, Masahiro
; APPLICANT: Sakagami, Masahiro
; APPLICANT: Taniguchi, Makoto
; TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
; FILE REFERENCE: 110-511
; CURRENT APPLICATION NUMBER: US/08/505,250
```

```

TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Coumbia Center, 701 Fifth Ave.
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,009
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.441C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Mycobacterium tuberculosis
US-09-073-009-49

Query Match 25.0%; Score 31; DB 2; Length 16;
Best Local Similarity 33.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

OY 5 NYKYRQOFIOSVLNN 19
||::||::||:
Db 2 NYEQEQASQIILSS 16

RESULT 10
US-09-073-010-49
; Sequence 49, Application US/09073010
; Patent No. 6613881
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Campos-Neto, Antonio
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS OF TUBERCULOSIS AND
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 Coumbia Center, 701 Fifth Ave.
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,010
; FILING DATE: 05-MAY-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.440C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
; US-09-073-010-49

Query Match      25.0%; Score 31; DB 2; Length 16;
Best Local Similarity 33.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY      5  NNYKROQFGSVLNN 19
| : : | : : |
Db      2  NYEQOEQASQOILSS 16

RESULT 11
US-09-462-118-30
; Sequence 30, Application US/09462118
; Patent No. 6610833
; GENERAL INFORMATION:
; APPLICANT: Rodman, Toby C.
; TITLE OF INVENTION: Monoclonal Human Natural Antibodies
; FILE REFERENCE: 4436/1C074-US1
; CURRENT APPLICATION NUMBER: US/09/462.118
; CURRENT FILING DATE: 1999-12-18
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Human
; US-09-462-118-30

Query Match      24.2%; Score 30; DB 2; Length 12;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      2  MAONYKXRO 10
| : : | : : |
Db      1  LAENYKXSOQ 9

RESULT 12
US-09-623-548A-1034
; Sequence 1034, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623.548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
```

```

; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1034
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-09-623-548A-1034

Query Match      24.2%; Score 30; DB 2; Length 18;
Best Local Similarity 41.7%; Pred. No. 2.3e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      3  AONYKROQFTQ 14
| : : | : : |
Db      7  AASHYONQFVQ 18

RESULT 13
US-09-657-276-1034
; Sequence 1034, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657.276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1034
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-09-657-276-1034

Query Match      24.2%; Score 30; DB 2; Length 18;
Best Local Similarity 41.7%; Pred. No. 2.3e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      3  AONYKROQFTQ 14
| : : | : : |
Db      7  AASHYONQFVQ 18

RESULT 14
PCT-US93-03748-1
; Sequence 1, Application PC/TUS9303748
; GENERAL INFORMATION:
; APPLICANT: Howard, Russell J.
; APPLICANT: Leung, Lawrence L.K.
; TITLE OF INVENTION: Modulation of Thrombospondin-CD36 Interactions
```

```

      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/816,105A
      FILING DATE: 14-MAR-1997
      CLASSIFICATION: 435
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: DE 19625269.5
      FILING DATE: 25-JUN-1996
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: DE 19611252.4
      FILING DATE: 22-MAR-1996
      ATTORNEY/AGENT INFORMATION:
      NAME: Kurt G. Briscoe
      REGISTRATION NUMBER: 33,141
      REFERENCE/DOCKET NUMBER: Bayer 9814-KGB
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (914) 332-1700
      TELEFAX: (914) 332-1844
      INFORMATION FOR SEQ ID NO: 14:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 18 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
US-08-816-105A-14

Query Match          23.0%; Score 28.5; DB 1; Length 18;
Best Local Similarity 42.1%; Pred. No. 4.1e+02;
Matches      8; Conservative      3; Mismatches      7; Indels      1; Gaps      1;

QY      5 NYKXROQFIQSVLNNGATR 23
      :| | | | :| | | |
Db      1 DYLYEQDLI-TFLDNQDTR 18

RESULT 16
US-09-935-430-180
: Sequence 180; Application US/09935430
: Patent No. 6863892
: GENERAL INFORMATION:
: APPLICANT: FARIS, MARY
: APPLICANT: HUBERT, RENE
: APPLICANT: RAITANO, ARTHUR
: APPLICANT: APAR, DANIEL
: APPLICANT: LEVIN, BLANA
: APPLICANT: CHALITTA-EID, PIA
: APPLICANT: JAKOBOVITZ, AYA
: TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
: TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
: TITLE OF INVENTION: OTHER CANCERS
: FILE REFERENCE: 51158-20050.00
: CURRENT APPLICATION NUMBER: US/09/935,430
: CURRENT FILING DATE: 2001-08-22
: PRIOR APPLICATION NUMBER: 60/227,098
: PRIOR FILING DATE: 2000-08-22
: PRIOR APPLICATION NUMBER: 60/282,739
: PRIOR FILING DATE: 2001-04-10
: NUMBER OF SEQ ID NOS: 700
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 180
: LENGTH: 10
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-180

Query Match          22.6%; Score 28; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches      6; Conservative      1; Mismatches      2; Indels      0; Gaps      0;

QY      12 FQISVLNNG 20
      | | | | |
Db      1 FQISVLNNG 9

```

RESULT 17
US-09-935-430-425
; Sequence 425, Application US/09935430
; Patent No. 6663892
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: APAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLOVITZ, PIA
; APPLICANT: JAKOBOWITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/09/935.430
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 425
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-425

Query Match 22.6%; Score 28; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 12 FIOVLNNG 20
| : : : : :
Db 1 FOLSLNNG 9

RESULT 18
US-09-411-706-6
; Sequence 6, Application US/09411706
; Patent No. 6312956
; GENERAL INFORMATION:
; APPLICANT: Lane, Kirk B.
; TITLE OF INVENTION: NUCLEAR TARGETED PEPTIDE NUCLEIC ACID OLIGOMER
; FILE REFERENCE: 3765
; CURRENT APPLICATION NUMBER: US/09/411.706
; CURRENT FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus NLS
; OTHER INFORMATION: peptide
US-09-411-706-6

Query Match 22.6%; Score 28; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 6 YKYRQGF 12
| : : : : :
Db 5 YKYRPEY 11

RESULT 19

US-09-935-032-6
; Sequence 6, Application US/09935032
; Patent No. 6623966
; GENERAL INFORMATION:
; APPLICANT: Lane, Kirk B.
; TITLE OF INVENTION: NUCLEAR TARGETED PEPTIDE NUCLEIC ACID OLIGOMER
; FILE REFERENCE: 3765
; CURRENT APPLICATION NUMBER: US/09/935.032
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US/09/411.706
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus NLS
; OTHER INFORMATION: peptide
US-09-935-032-6

Query Match 22.6%; Score 28; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 6 YKYRQGF 12
| : : : : :
Db 5 YKYRPEY 11

RESULT 20
US-09-543-940-9
; Sequence 9, Application US/09543940
; Patent No. 6613742
; GENERAL INFORMATION:
; APPLICANT: Huang, Ziwei
; APPLICANT: Luo, Zhaowen
; APPLICANT: Zhou, Naimeing
; APPLICANT: Luo, Jiansong
; TITLE OF INVENTION: Chemokine-Derived Synthetic Peptides
; FILE REFERENCE: 8321-40
; CURRENT APPLICATION NUMBER: US/09/543.940
; CURRENT FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,106
; PRIOR FILING DATE: 1999-04-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide containing segment from C-terminal region
; OTHER INFORMATION: of human SDF-1 protein
US-09-543-940-9

Query Match 22.6%; Score 28; DB 2; Length 13;
Best Local Similarity 33.3%; Pred. No. 3.4e+02;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 7 KYRQFIQSVLN 18
| : : : : :
Db 2 KWIQVEYDEKALN 13

RESULT 21
US-07-918-181A-20
; Sequence 20, Application US/07918181A
; Patent No. 5338833
; GENERAL INFORMATION:
; APPLICANT: Fowlkes, Dana M.

TITLE OF INVENTION: C-Terminal IL-6 Muteins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/918,181A
FILING DATE: 23-JUL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sheets, Eric J.
REGISTRATION NUMBER: 30,326
REFERENCE/DOCKET NUMBER: FOM-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
US-07-918-181A-20
Query Match 22.6%; Score 28; DB 1; Length 15;
Best Local Similarity 53.3%; Pred. No. 4e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
QY 10 QQFIQSVLNGATRO 24
Db 2 QEFLOSSLR--ALRQ 14
RESULT 22
US-08-231-575-20
Sequence 20, Application US/08231575
Patent No. 5565336
GENERAL INFORMATION:
APPLICANT: Fowikes, Dana M.
TITLE OF INVENTION: C-Terminal IL-6 Muteins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,575
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/918,181
FILING DATE: 23-JUL-1992

ATTORNEY/AGENT INFORMATION:
NAME: Sheets, Eric J.
REGISTRATION NUMBER: 30,326
REFERENCE/DOCKET NUMBER: FOM-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
US-08-231-575-20
Query Match 22.6%; Score 28; DB 1; Length 15;
Best Local Similarity 53.3%; Pred. No. 4e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
QY 10 QQFIQSVLNGATRO 24
Db 2 QEFLOSSLR--ALRQ 14
RESULT 23
PCT-US93-06928-20
Sequence 20, Application PC/TUS9306928
GENERAL INFORMATION:
APPLICANT: Fowikes, Dana M.
TITLE OF INVENTION: Carboxy Terminal IL-6 Muteins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 11014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06928
FILING DATE: 19930723
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/918,181
FILING DATE: 23-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: FOM-2-T
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
PCT-US93-06928-20

Query Match 22.6%; Score 28; DB 1; Length 15;
Best Local Similarity 53.3%; Pred. No. 4e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 10 QOPIQSYLVNNGATRO 24
DB 2 QEFLOSSLR--ALRQ 14

RESULT 24

US-08-346-849-58
Sequence 58, Application US/08346849
Patent No. 5670483

GENERAL INFORMATION:

APPLICANT: Zhang, Shuguang
APPLICANT: Lockshin, Curtis
APPLICANT: Rich, Alexander
APPLICANT: Holmes, Todd
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESSES:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173-4799

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,849
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28 DECEMBER 1992
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-6008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-346-849-58

Query Match 22.6%; Score 28; DB 1; Length 16;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 NYKYROOF 12
DB 2 NYQYNYOY 9

RESULT 25

US-08-346-849-59
Sequence 59, Application US/08346849
Patent No. 5670483

GENERAL INFORMATION:

APPLICANT: Zhang, Shuguang
APPLICANT: Lockshin, Curtis
APPLICANT: Rich, Alexander

APPLICANT: Holmes, Todd
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESSES:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173-4799

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,849
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28 DECEMBER 1992
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-6008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-346-849-59

Query Match 22.6%; Score 28; DB 1; Length 16;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 NYKYROOF 12
DB 4 NYQYNYOY 11

Search completed: January 26, 2006, 08:07:00
Job time : 23.7184 secs

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OM protein - protein search, using sw model

Run on: January 26, 2006, 08:04:12 : Search time 78 seconds
(without alignments)
128.563 Million cell updates/sec

Title: US-09-662-293-8
Perfect score: 124
Sequence: 1 DMAQNYKRYROQFIQSVLNGATRRQ 24

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 369445

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA Main:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	26.6	17	4	US-10-057-789-250 Sequence 250, App
2	33	26.6	17	4	US-10-212-628-250 Sequence 250, App
3	31	25.0	9	3	US-09-935-430-132 Sequence 132, App
4	31	25.0	9	4	US-10-277-292-132 Sequence 132, App
5	31	25.0	9	4	US-10-280-340-132 Sequence 132, App
6	31	25.0	9	5	US-10-990-137-132 Sequence 132, App
7	31	25.0	10	3	US-09-935-430-157 Sequence 157, App
8	31	25.0	10	3	US-09-935-430-621 Sequence 621, App
9	31	25.0	10	4	US-10-277-292-157 Sequence 157, App
10	31	25.0	10	4	US-10-277-292-621 Sequence 621, App
11	31	25.0	10	4	US-10-280-340-157 Sequence 157, App
12	31	25.0	10	4	US-10-280-340-621 Sequence 621, App
13	31	25.0	10	5	US-10-990-137-157 Sequence 157, App
14	31	25.0	10	5	US-10-990-137-621 Sequence 621, App
15	31	25.0	12	3	US-09-226-666-14 Sequence 14, App
16	31	25.0	14	5	US-10-813-638-1312 Sequence 1312, App
17	31	25.0	16	3	US-09-073-009-49 Sequence 49, App
18	31	25.0	16	3	US-09-023-588-49 Sequence 49, App
19	31	25.0	16	3	US-09-793-306-49 Sequence 49, App
20	30	24.2	10	5	US-10-936-237-11 Sequence 11, App
21	30	24.2	12	4	US-10-247-946-30 Sequence 30, App
22	30	24.2	12	4	US-10-251-526-30 Sequence 30, App
23	30	24.2	15	6	US-11-009-460-104 Sequence 104, App
24	30	24.2	18	4	US-10-197-954-35 Sequence 35, App
25	30	24.2	18	5	US-10-760-085-35 Sequence 35, App
26	30	24.2	18	6	US-11-066-697-1034 Sequence 1034, App
27	30	24.2	19	5	US-10-479-166-17 Sequence 17, App
28	29	23.4	16	5	US-10-656-721-13 Sequence 13, App
29	29	23.4	17	5	US-10-837-269-156 Sequence 156, App
30	29	23.4	17	5	US-10-837-269-157 Sequence 157, App
31	29	23.4	19	5	US-10-837-269-157 Sequence 157, App
32	29	23.4	19	5	US-10-837-269-160 Sequence 160, App
33	29	23.4	21	3	US-09-853-830-45 Sequence 45, App
34	29	23.4	21	4	US-10-139-146-3 Sequence 3, App
35	29	23.4	21	4	US-10-139-973-14 Sequence 14, App
36	29	23.4	21	4	US-10-438-729-45 Sequence 45, App
37	28.5	23.0	17	4	US-10-471-220-47 Sequence 47, App
38	28.5	23.0	21	4	US-10-745-069-37 Sequence 37, App
39	28.5	23.0	21	4	US-10-768-288A-37 Sequence 37, App
40	28.5	23.0	21	4	US-10-768-325A-37 Sequence 37, App
41	28.5	23.0	21	5	US-10-869-649-37 Sequence 37, App
42	28	22.6	10	3	US-09-935-430-180 Sequence 180, App
43	28	22.6	10	3	US-09-935-430-425 Sequence 425, App
44	28	22.6	10	4	US-10-277-292-180 Sequence 180, App
45	28	22.6	10	4	US-10-277-292-425 Sequence 425, App
46	28	22.6	10	4	US-10-280-340-180 Sequence 180, App
47	28	22.6	10	4	US-10-280-340-425 Sequence 425, App
48	28	22.6	10	5	US-10-990-137-180 Sequence 180, App
49	28	22.6	13	5	US-10-990-137-425 Sequence 425, App
50	28	22.6	13	5	US-10-222-703A-867 Sequence 867, App
51	28	22.6	15	4	US-10-203-915A-248 Sequence 248, App
52	28	22.6	15	4	US-10-203-915A-249 Sequence 249, App
53	28	22.6	15	5	US-10-886-773-130 Sequence 130, App
54	28	22.6	15	5	US-10-886-773-131 Sequence 131, App
55	28	22.6	15	5	US-10-505-929-525 Sequence 525, App
56	28	22.6	15	5	US-10-505-929-526 Sequence 526, App
57	28	22.6	15	5	US-10-505-929-527 Sequence 527, App
58	28	22.6	15	5	US-10-505-929-528 Sequence 528, App
59	28	22.6	15	5	US-10-505-929-529 Sequence 529, App
60	28	22.6	15	5	US-10-505-929-530 Sequence 530, App
61	28	22.6	15	5	US-10-505-929-531 Sequence 531, App
62	28	22.6	16	4	US-10-390-472-58 Sequence 58, App
63	28	22.6	16	4	US-10-390-472-59 Sequence 59, App
64	28	22.6	16	6	US-11-065-970-19 Sequence 19, App
65	28	22.6	17	5	US-10-996-316-170 Sequence 170, App
66	28	22.6	17	6	US-11-036-098-10 Sequence 10, App
67	28	22.6	20	5	US-10-482-284A-68 Sequence 68, App
68	28	22.6	20	5	US-10-690-376-111 Sequence 111, App
69	28	22.6	21	5	US-10-505-929-584 Sequence 584, App
70	27.5	22.2	18	4	US-10-685-898-99 Sequence 99, App
71	27.5	22.2	20	6	US-11-107-086-35 Sequence 35, App
72	27	21.8	9	3	US-09-935-430-114 Sequence 114, App
73	27	21.8	9	3	US-09-935-430-130 Sequence 130, App
74	27	21.8	9	4	US-09-935-430-192 Sequence 192, App
75	27	21.8	9	4	US-10-062-257-9 Sequence 9, App
76	27	21.8	9	4	US-10-277-292-114 Sequence 114, App
77	27	21.8	9	4	US-10-277-292-130 Sequence 130, App
78	27	21.8	9	4	US-10-277-292-492 Sequence 492, App
79	27	21.8	9	4	US-10-280-340-114 Sequence 114, App
80	27	21.8	9	4	US-10-280-340-132 Sequence 132, App
81	27	21.8	9	4	US-10-280-340-192 Sequence 192, App
82	27	21.8	9	5	US-10-280-440-430 Sequence 430, App
83	27	21.8	9	5	US-10-865-478-133 Sequence 133, App
84	27	21.8	9	5	US-10-990-137-114 Sequence 114, App
85	27	21.8	9	5	US-10-990-137-130 Sequence 130, App
86	27	21.8	9	5	US-10-990-137-492 Sequence 492, App
87	27	21.8	12	3	US-09-226-666-13 Sequence 13, App
88	27	21.8	14	5	US-10-953-901-594 Sequence 594, App
89	27	21.8	14	4	US-10-103-395-129 Sequence 129, App
90	27	21.8	16	3	US-09-775-805-8 Sequence 8, App
91	27	21.8	16	4	US-10-103-395-187 Sequence 187, App
92	27	21.8	16	4	US-10-371-525-315 Sequence 315, App
93	27	21.8	16	4	US-10-371-525-315 Sequence 315, App
94	27	21.8	16	4	US-10-371-525-315 Sequence 315, App
95	27	21.8	16	4	US-10-371-525-315 Sequence 315, App
96	27	21.8	16	4	US-10-753-339-8 Sequence 8, App
97	27	21.8	17	3	US-09-563-222-26 Sequence 26, App
98	27	21.8	17	3	US-09-995-529-70 Sequence 70, App
99	27	21.8	17	3	US-09-995-529-76 Sequence 76, App
100	27	21.8	17	3	US-09-995-529-76 Sequence 76, App

ALIGNMENTS

RESULT 1

```

US-10-057-789-250
; Sequence 250, Application US/10057789
; Publication No. US20030082522A1
; GENERAL INFORMATION:
; APPLICANT: Paul Haynes
; APPLICANT: Jing Wei
; APPLICANT: John Yates
; APPLICANT: Nancy Andon
; TITLE OF INVENTION: DIFFERENTIAL LABELLING FOR QUANTITATIVE
; TITLE OF INVENTION: ANALYSIS OF COMPLEX PROTEIN MIXTURES
; FILE REFERENCE: NADII 022A
; CURRENT APPLICATION NUMBER: US/10/057,789
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/264,576
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/305,232
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 250
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 4
; OTHER INFORMATION: Xaa = Modified Cysteine
US-10-057-789-250

```

Query Match	26.6%;	Score 33;	DB 4;	Length 17;
Best Local Similarity	43.8%;	Pred. No. 3.6e+02;		
Matches	7;	Conservative	2;	Mismatches 7;
				Indels 0;
				Gaps 0;

QY 8 YRQDFIQSVLNGATR 23
| | | | | :
Db 2 YTXQFVDMVLPTALK 17

RESULT 2

```

US-10-212-628-250
? Sequence 250, Application US/10212628
? Publication No. US20030087329A1
? GENERAL INFORMATION:
? APPLICANT: Paul Haynes
? APPLICANT: John Yates
? APPLICANT: Jing Wei
? APPLICANT: Nancy Andon
? TITLE OF INVENTION: DIFFERENTIAL LABELLING FOR QUANTITATIVE
? TITLE OF INVENTION: ANALYSIS OF COMPLEX PROTEIN MIXTURES
? FILE REFERENCE: NAD1.022CP1
? CURRENT APPLICATION NUMBER: US/10/212,628
? CURRENT FILING DATE: 2002-08-01
? PRIOR APPLICATION NUMBER: US 60/264,576
? PRIOR FILING DATE: 2001-01-26
? PRIOR APPLICATION NUMBER: US 60/305,232
? PRIOR FILING DATE: 2001-07-13
? PRIOR APPLICATION NUMBER: US 10/057,789
? PRIOR FILING DATE: 2002-01-25
? NUMBER OF SEQ ID NOS: 311
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 250
? LENGTH: 17
? TYPE: PRT
? ORGANISM: Saccharomyces cerevisiae
? FEATURE:
? NAME/KEY: VARIANT
? LOCATION: 4

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OTHER INFORMATION: Xaa = Modified Cysteine
US-10-212-628-250

Query Match	26.6%	Score 33;	DB 4;	Length 17;
Best Local Similarity	43.8%	Pred. No. 3.6e+02;		
Matches	7;	Conservative	2;	Mismatches 7;
				Indels 0;
				Gaps 0;

QY 8 YRQQFIQSVLNNGATR 23
| | | | | :
Db 2 YTXQFVDMVLPLNTALK 17

RESULT 3

```

US-09-935-430-132
; Sequence 132. Application US/09935430
; Publication No. US20030017466A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RATTANO, ARTHUR
; APPLICANT: APAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TTLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/09/935.430
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 132
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Peptide motif
US-09-935-430-132

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Query Match	25.0%	Score 31;	DB 3;	Length 9;
Best Local Similarity	75.0%;	Pred. No. 1.7e+06;		
Matches	6;	Conservative	1;	Mismatches 1;
				Indels 0;
				Gaps 0;

QY	15	SVLNGCAT	22
		:	
Db	1	SLNNGLT	8

RESULT 4

US-10-277-292-132
 Sequence 132. Application US/10277292
 Publication No. US20030199470A1
 GENERAL INFORMATION:
 APPLICANT: FARIS, MARY
 APPLICANT: HUBERT, RENE
 APPLICANT: RAITANO, ARTHUR
 APPLICANT: APAR, DANIEL
 APPLICANT: LEVIN, ELANA
 APPLICANT: CHALOVITZ, PIA
 APPLICANT: JAKOBOVITZ, AYA
 TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
 TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
 TITLE OF INVENTION: OTHER CANCERS
 FILE REFERENCE: 51158-20050.00
 CURRENT APPLICATION NUMBER: US/10/277.292
 CURRENT FILING DATE: 2002-10-21
 PRIOR APPLICATION NUMBER: US/09/935.430
 PRIOR FILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: 60/227,098
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/282,739
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 700
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 132
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-132

Query Match 25.0%; Score 31; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 15 SVLNNGAT 22
|:|||||
Db 1 SLNNGLT 8

RESULT 5
US-10-280-340-132
Sequence 132, Application US/10280340
Publication No. US20030207835A1
GENERAL INFORMATION:
APPLICANT: FARIS, MARY
APPLICANT: HUBERT, RENE
APPLICANT: RATTANO, ARTHUR
APPLICANT: APEAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: CHALILITA-EID, PIA
APPLICANT: JAKOBOVITZ, AVA
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
TITLE OF INVENTION: OTHER CANCERS
FILE REFERENCE: 51158-20050.00
CURRENT APPLICATION NUMBER: US/10/280,340
CURRENT FILING DATE: 2002-10-25
PRIOR APPLICATION NUMBER: US/09/935,430
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227,098
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/282,739
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 700
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 132
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-132

Query Match 25.0%; Score 31; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 15 SVLNNGAT 22
|:|||||
Db 1 SLNNGLT 8

RESULT 6
US-10-990-137-132
Sequence 132, Application US/10990137
Publication No. US20050227253A1
GENERAL INFORMATION:
APPLICANT: FARIS, MARY
APPLICANT: HUBERT, RENE

APPLICANT: RATTANO, ARTHUR
APPLICANT: APEAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: CHALILITA-EID, PIA
APPLICANT: JAKOBOVITZ, AVA
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
TITLE OF INVENTION: OTHER CANCERS
FILE REFERENCE: 511582005003
CURRENT APPLICATION NUMBER: US/10/990,137
CURRENT FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: 09/935,430
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 60/227,098
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 700
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 132
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-990-137-132

Query Match 25.0%; Score 31; DB 5; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 15 SVLNNGAT 22
|:|||||
Db 1 SLNNGLT 8

RESULT 7
US-09-935-430-157
Sequence 157, Application US/09935430
Publication No. US20030017466A1
GENERAL INFORMATION:
APPLICANT: FARIS, MARY
APPLICANT: HUBERT, RENE
APPLICANT: RATTANO, ARTHUR
APPLICANT: APEAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: CHALILITA-EID, PIA
APPLICANT: JAKOBOVITZ, AVA
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
TITLE OF INVENTION: OTHER CANCERS
FILE REFERENCE: 51158-20050.00
CURRENT APPLICATION NUMBER: US/09/935,430
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227,098
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/282,739
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 700
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 157
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-157

Query Match 25.0%; Score 31; DB 3; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 15 SVLNNGAT 22

Db 1 SLINNGLT 8

RESULT 8

US-09-935-430-621
; Sequence 621, Application US/09935430
; Publication No. US20030017466A1
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALILITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 621
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-621

Query Match 25.0%; Score 31; DB 3; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 15 SVLNNGAT 22
|:|||||
Db 2 SLINNGLT 9

RESULT 9

US-10-277-292-157
; Sequence 157, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALILITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 157
; LENGTH: 10

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-157

Query Match 25.0%; Score 31; DB 4; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 15 SVLNNGAT 22
|:|||||
Db 1 SLINNGLT 8

RESULT 10

US-10-277-292-621
; Sequence 621, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALILITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 621
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-621

Query Match 25.0%; Score 31; DB 4; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 15 SVLNNGAT 22
|:|||||
Db 2 SLINNGLT 9

RESULT 11

US-10-280-340-157
; Sequence 157, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALILITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 157
; LENGTH: 10

```

FILE REFERENCE: 51158-20050.00
CURRENT APPLICATION NUMBER: US/10/280.340
CURRENT FILING DATE: 2002-10-25
PRIORITY APPLICATION NUMBER: US/09/935.430
PRIORITY FILING DATE: 2001-08-22
PRIORITY APPLICATION NUMBER: 60/227,098
PRIORITY FILING DATE: 2000-08-22
PRIORITY APPLICATION NUMBER: 60/282,739
PRIORITY FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 700
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 157
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-157

```

```

Query Match      25.0%; Score 31; DB 4; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      15 SVLNNGAT 22
      |||||
Db      1 SLNNGLT 8

```

```

RESULT 12
US-10-280-340-621
Sequence 621, Application US/10280340
Publication No. US20030207835A1
GENERAL INFORMATION:
APPLICANT: PARIS, MARY
APPLICANT: HUBERT, RENE
APPLICANT: RAITANO, ARTHUR
APPLICANT: APAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: CHALLITA-EID, PIA
APPLICANT: JAKOBOWITZ, AYA
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
FILE REFERENCE: 51158-20050.00
CURRENT APPLICATION NUMBER: US/10/280.340
CURRENT FILING DATE: 2002-10-25
PRIORITY APPLICATION NUMBER: US/09/935.430
PRIORITY FILING DATE: 2001-08-22
PRIORITY APPLICATION NUMBER: 60/227,098
PRIORITY FILING DATE: 2000-08-22
PRIORITY APPLICATION NUMBER: 60/282,739
PRIORITY FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 700
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 621
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-621

```

```

Query Match      25.0%; Score 31; DB 4; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      15 SVLNNGAT 22
      |||||
Db      2 SLNNGLT 9

```

```

RESULT 13
US-10-990-137-157

```

```

Sequence 157, Application US/10990137
Publication No. US20050227253A1
GENERAL INFORMATION:
APPLICANT: PARIS, MARY
APPLICANT: HUBERT, RENE
APPLICANT: RAITANO, ARTHUR
APPLICANT: APAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: CHALLITA-EID, PIA
APPLICANT: JAKOBOWITZ, AYA
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
FILE REFERENCE: 511582005003
CURRENT APPLICATION NUMBER: US/10/990.137
CURRENT FILING DATE: 2004-11-15
PRIORITY APPLICATION NUMBER: 09/935,430
PRIORITY FILING DATE: 2001-08-22
PRIORITY APPLICATION NUMBER: 60/282,739
PRIORITY FILING DATE: 2001-04-10
PRIORITY APPLICATION NUMBER: 60/227,098
PRIORITY FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 700
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 157
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-990-137-157

```

```

Query Match      25.0%; Score 31; DB 5; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      15 SVLNNGAT 22
      |||||
Db      1 SLNNGLT 8

```

```

RESULT 14
US-10-990-137-621
Sequence 621, Application US/10990137
Publication No. US20050227253A1
GENERAL INFORMATION:
APPLICANT: PARIS, MARY
APPLICANT: HUBERT, RENE
APPLICANT: RAITANO, ARTHUR
APPLICANT: APAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: CHALLITA-EID, PIA
APPLICANT: JAKOBOWITZ, AYA
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
FILE REFERENCE: 511582005003
CURRENT APPLICATION NUMBER: US/10/990.137
CURRENT FILING DATE: 2004-11-15
PRIORITY APPLICATION NUMBER: 09/935,430
PRIORITY FILING DATE: 2001-08-22
PRIORITY APPLICATION NUMBER: 60/282,739
PRIORITY FILING DATE: 2001-04-10
PRIORITY APPLICATION NUMBER: 60/227,098
PRIORITY FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 700
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 621
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

```

US-10-990-137-621

Query Match 25.0%; Score 31; DB 5; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 15 SVLNNGAT 22

Db 2 SLNNGLT 9

RESULT 15
US-09-226-666-14
Sequence 14, Application US/09226666A
Patent No. US20020077282A1

GENERAL INFORMATION:
APPLICANT: Spacciapoli, Peter
APPLICANT: Rothstein, David M.
APPLICANT: Fridgen, Phillip M.
TITLE OF INVENTION: METHOD FOR TREATING CYSTIC FIBROSIS
FILE REFERENCE: 50032/007001
CURRENT APPLICATION NUMBER: US/09/226,666A
CURRENT FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Derived from Homo sapiens
US-09-226-666-14

Query Match 25.0%; Score 31; DB 3; Length 12;
Best Local Similarity 55.6%; Pred. No. 5.1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 QNYKYROOF 12

Db 3 QHGYKQOF 11

RESULT 16
US-10-813-638-1312
Sequence 1312, Application US/10813638
Publication No. US20040235026A1

GENERAL INFORMATION:
APPLICANT: Shinkets, Richard A.
APPLICANT: Leach, Martin D.
TITLE OF INVENTION: NUCLEIC ACIDS CONTAINING SINGLE NUCLEIC ACID POLYMORPHISMS AND ME
FILE REFERENCE: 15966-599
CURRENT APPLICATION NUMBER: US/10/813,638
CURRENT FILING DATE: 2004-03-29
PRIOR APPLICATION NUMBER: 60/163,783
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 1468
SOFTWARE: Curagen Patent Formatter Version 0.9
SEQ ID NO 1312
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (7)...(0)
OTHER INFORMATION: cSNP translation
US-10-813-638-1312

Query Match 25.0%; Score 31; DB 5; Length 14;
Best Local Similarity 60.0%; Pred. No. 6.1e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 DMAQNYKYRQ 10

Db 4 DRTANVXYRQ 13

RESULT 17
US-09-073-009-49
Sequence 49, Application US/09073009
Patent No. US20010012888A1

GENERAL INFORMATION:
APPLICANT: Alderson, Mark
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neco, Antonio
TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Ave.
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104

TUBERCULOSIS AND ME

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,009
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mark, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.441C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 49:

SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Mycobacterium tuberculosis
US-09-073-009-49

Query Match 25.0%; Score 31; DB 3; Length 16;
Best Local Similarity 33.3%; Pred. No. 7e+02;
Matches 5; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 5 NYKYRQFIQSVLNN 19

Db 2 NYEQEQASQOILIS 16

RESULT 18
US-09-023-588-49
Sequence 49, Application US/09023588
Patent No. US20020081579A1

GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark R.
TITLE OF INVENTION: METHOD FOR THE ISOLATION OF NOVEL ANTIGENS
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington

Query Match	25.0%	Score 31;	DB 3;	Length 16;
Best Local Similarity	33.3%	Pred. No. 7e+02;		
Matches	5;	Conservative	6;	Mismatches 4;
				Indels 0;
				Gaps 0;

```

RESULT 22
US-10-251-526-30
; Sequence 30, Application US/10251526
; Publication No. US20030144486A1
;
GENERAL INFORMATION
;
APPLICANT: Rodman, Tody C.
;
TITLE OF INVENTION: Monoclonal Human Natural Antibodies
;
FILE REFERENCE: 4436/1C074-US1
;
CURRENT APPLICATION NUMBER: US/10/251,526
;
CURRENT FILING DATE: 2002-09-20
;
PRIOR APPLICATION NUMBER: US/09/462,118

```

;; PRIOR FILING DATE: 1999-12-18
;; NUMBER OF SEQ ID NOS: 36
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 30
;; LENGTH: 12
;; TYPE: PRT
;; ORGANISM: Human
US-10-251-526-30

Query Match 24.2%; Score 30; DB 4; Length 12;
Best Local Similarity 55.6%; Pred. No. 7.4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 AONVXYRQFIQ 10
|::|::|::|
Db 1 LAENVKSOQ 9

RESULT 23
US-11-009-460-104
; Sequence 104, Application US//11009460
; Publication No. US20050181459A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: CARTER, Graham
; TITLE OF INVENTION: METHOD FOR MAPPING AND ELIMINATING
; TITLE OF INVENTION: T-CELL EPITOPES
; FILE REFERENCE: MER-135
; CURRENT APPLICATION NUMBER: US/11/009,460
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: PCT/EP03/06110
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: EP02012919.3
; PRIOR FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential T-cell Epitopes
US-11-009-460-104

Query Match 24.2%; Score 30; DB 6; Length 15;
Best Local Similarity 43.8%; Pred. No. 9.5e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 4; Gaps 1;

OY 8 YROQFIOSVLNCGATR 23
|::|::|::|::|
Db 2 YKSGY----LNNGPQR 13

RESULT 24
US-10-197-954-35
; Sequence 35, Application US//10197954
; Publication No. US20030119021A1
; GENERAL INFORMATION:
; APPLICANT: K"ster, Hubert
; APPLICANT: Siddiqi, Suhail
; APPLICANT: Little, Daniel
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 24743-2305
; CURRENT APPLICATION NUMBER: US//10/197,954
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 60/306,019
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/314,123
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/363,433

;; PRIOR FILING DATE: 2002-03-11
;; NUMBER OF SEQ ID NOS: 149
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 35
;; LENGTH: 18
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-197-954-35

Query Match 24.2%; Score 30; DB 4; Length 18;
Best Local Similarity 41.7%; Pred. No. 1.2e+03;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 3 AONVXYRQFIQ 14
|::|::|::|::|
Db 7 AASHIYONQFVQ 18

RESULT 25
US-10-760-085-35
; Sequence 35, Application US//10760085
; Publication No. US20050042771A1
; GENERAL INFORMATION:
; APPLICANT: Hubert, K"ster
; APPLICANT: Daniel Paul Little
; APPLICANT: Suhail Mahmood Siddiqi
; APPLICANT: Matthew Peter Grealish
; APPLICANT: Subramaniam Marappan
; APPLICANT: Chester Frederick Haseman III
; APPLICANT: Ping Yip
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 24743-2309
; CURRENT APPLICATION NUMBER: US/10/760,085
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: 60/441,398
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-760-085-35

Query Match 24.2%; Score 30; DB 5; Length 18;
Best Local Similarity 41.7%; Pred. No. 1.2e+03;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 3 AONVXYRQFIQ 14
|::|::|::|::|
Db 7 AASHIYONQFVQ 18

Search completed: January 26, 2006, 08:38:35
Job time : 79 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 08:05:12 : Search time 4.55172 Seconds
(without alignments)
57.099 Million cell updates/sec

Title: US-09-662-293-8
Perfect score: 124
Sequence: 1 DMAQNYKXROQFIQSVLNGATRQ 24

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 37628

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

Published Applications NA New:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PTCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	26.6	19	7	US-11-033-039-1123 Sequence 1123, App
2	30	24.2	13	6	US-10-511-559-255 Sequence 255, App
3	29.5	23.8	15	6	US-10-511-559-75 Sequence 75, App
4	28	22.6	11	7	US-11-045-024-2254 Sequence 110, App
5	28	22.6	11	7	US-11-045-024-2254 Sequence 2254, App
6	28	22.6	11	7	US-11-045-024-2254 Sequence 9528, App
7	28	22.6	13	6	US-10-945-674A-77 Sequence 77, App
8	28	22.6	15	7	US-11-045-024-13293 Sequence 13293, App
9	27	21.8	9	7	US-11-111-463-12 Sequence 12, App
10	27	21.8	13	6	US-10-511-559-454 Sequence 254, App
11	27	21.8	15	7	US-11-022-562-43 Sequence 43, App
12	27	21.8	15	7	US-11-022-562-44 Sequence 44, App
13	27	21.8	15	7	US-11-106-932-114 Sequence 114, App
14	27	21.8	15	7	US-11-045-024-13006 Sequence 13006, App
15	27	21.8	15	7	US-11-045-024-13016 Sequence 13016, App
16	27	21.8	16	6	US-10-973-977-8 Sequence 8, App
17	27	21.8	17	7	US-11-145-861-215 Sequence 8, App
18	27	21.8	19	7	US-11-033-039-1125 Sequence 1125, App
19	27	21.8	20	7	US-11-022-562-249 Sequence 249, App
20	27	21.8	20	7	US-11-022-562-250 Sequence 250, App
21	26	21.0	19	6	US-10-503-575-329 Sequence 329, App
22	26	21.0	20	7	US-11-196-400-16 Sequence 16, App
23	26	20.2	9	7	US-11-041-893-54 Sequence 54, App
24	25	20.2	12	7	US-11-054-515-2823 Sequence 2823, App
25	25	20.2	13	6	US-10-511-559-256 Sequence 256, App

26	25	20.2	13	6	US-10-511-559-257 Sequence 257, App
27	25	20.2	19	6	US-10-503-575-203 Sequence 203, App
28	25	20.2	19	6	US-10-880-238-115 Sequence 115, App
29	25	20.2	20	6	US-10-485-788A-600 Sequence 600, App
30	24	19.4	8	7	US-11-045-024-1054 Sequence 1054, App
31	24	19.4	9	7	US-11-111-463-13 Sequence 13, App
32	24	19.4	9	7	US-11-033-039-615 Sequence 615, App
33	24	19.4	10	6	US-10-501-411A-321 Sequence 321, App
34	24	19.4	11	7	US-11-045-024-1387 Sequence 1387, App
35	24	19.4	12	7	US-11-069-834-16 Sequence 16, App
36	24	19.4	13	7	US-11-145-861-197 Sequence 197, App
37	24	19.4	14	7	US-11-033-039-121 Sequence 121, App
38	24	19.4	14	7	US-11-152-697-41 Sequence 41, App
39	24	19.4	15	7	US-11-045-024-13015 Sequence 13015, App
40	24	19.4	15	7	US-11-045-024-13069 Sequence 13069, App
41	24	19.4	16	7	US-11-033-039-123 Sequence 123, App
42	24	19.4	17	6	US-10-665-658-44 Sequence 44, App
43	24	19.4	17	6	US-10-834-397-196 Sequence 196, App
44	24	19.4	17	7	US-11-007-428-4 Sequence 4, App
45	24	19.4	18	6	US-10-509-787A-92 Sequence 92, App
46	24	19.4	18	7	US-11-054-515-2795 Sequence 2795, App
47	24	19.4	19	6	US-10-503-575-282 Sequence 282, App
48	24	19.4	19	6	US-10-503-575-283 Sequence 283, App
49	24	19.4	19	6	US-10-503-575-284 Sequence 284, App
50	24	19.4	19	7	US-11-212-443-153 Sequence 153, App
51	24	19.4	20	7	US-11-022-562-292 Sequence 292, App
52	24	19.4	20	7	US-11-022-562-293 Sequence 293, App
53	24	19.4	20	7	US-11-026-403-74 Sequence 74, App
54	23.5	19.0	16	7	US-11-125-837-13 Sequence 13, App
55	23.5	19.0	20	6	US-10-518-599-21 Sequence 21, App
56	23	18.5	9	7	US-11-045-024-13662 Sequence 13662, App
57	23	18.5	9	7	US-11-136-079-652 Sequence 652, App
58	23	18.5	10	7	US-11-045-024-2026 Sequence 2026, App
59	23	18.5	10	7	US-11-045-024-6448 Sequence 6448, App
60	23	18.5	10	7	US-11-045-024-9521 Sequence 9521, App
61	23	18.5	11	7	US-11-045-024-1389 Sequence 1389, App
62	23	18.5	11	7	US-11-045-024-1190 Sequence 1190, App
63	23	18.5	16	6	US-10-929-888-445 Sequence 445, App
64	23	18.5	17	6	US-10-507-662-4 Sequence 4, App
65	23	18.5	17	6	US-10-665-558-41 Sequence 41, App
66	23	18.5	17	7	US-11-102-743-9 Sequence 9, App
67	23	18.5	19	6	US-10-503-575-140 Sequence 140, App
68	23	18.5	19	6	US-10-503-575-215 Sequence 215, App
69	23	18.5	19	6	US-10-503-575-313 Sequence 313, App
70	23	18.5	19	7	US-11-212-443-155 Sequence 155, App
71	23	18.5	20	6	US-10-939-890-148 Sequence 148, App
72	23	18.5	20	6	US-10-467-657-8826 Sequence 8826, App
73	22.5	18.1	15	7	US-11-045-024-13464 Sequence 13464, App
74	22.5	18.1	19	6	US-10-503-575-237 Sequence 237, App
75	22.5	18.1	20	6	US-10-623-155-413 Sequence 413, App
76	22.5	18.1	20	6	US-10-623-155-524 Sequence 524, App
77	22.5	18.1	20	6	US-10-501-411A-218 Sequence 218, App
78	22.5	18.1	20	6	US-10-501-411A-252 Sequence 252, App
79	22	17.7	7	7	US-11-097-749-11 Sequence 11, App
80	22	17.7	8	7	US-11-045-024-3574 Sequence 3574, App
81	22	17.7	8	7	US-11-045-024-10656 Sequence 10656, App
82	22	17.7	8	7	US-11-045-024-12478 Sequence 12478, App
83	22	17.7	9	7	US-11-026-403-26 Sequence 26, App
84	22	17.7	9	7	US-11-136-079-648 Sequence 648, App
85	22	17.7	10	6	US-10-467-657-8944 Sequence 8944, App
86	22	17.7	10	6	US-10-467-657-8944 Sequence 8944, App
87	22	17.7	11	7	US-11-035-546-18 Sequence 18, App
88	22	17.7	12	7	US-11-021-441-100 Sequence 100, App
89	22	17.7	12	7	US-11-152-666-264 Sequence 264, App
90	22	17.7	13	6	US-10-511-559-504 Sequence 504, App
91	22	17.7	14	6	US-10-503-575-79 Sequence 79, App
92	22	17.7	16	7	US-11-226-325-9 Sequence 9, App
93	22	17.7	17	6	US-10-834-397-203 Sequence 203, App
94	22	17.7	18	6	US-10-503-575-77 Sequence 77, App
95	22	17.7	19	6	US-10-503-575-177 Sequence 177, App
96	22	17.7	20	6	US-10-939-890-147 Sequence 147, App
97	22	17.7	20	6	US-10-485-788A-585 Sequence 585, App
98	22	17.7	20	7	US-11-022-562-191 Sequence 191, App

99 22 17.7 20 7 US-11-094-142-34 Sequence 34, Appl
100 22 17.7 20 7 US-11-166-412-154 Sequence 154, App

ALIGNMENTS

RESULT 1
US-11-033-039-1123

Sequence 1123, Application US/11033039
Publication No. US20060002947A1

GENERAL INFORMATION:

APPLICANT: HUMPHREYS, ROBERT

APPLICANT: XU, MINZHEN

TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES

FILE REFERENCE: REF-2017US01

CURRENT APPLICATION NUMBER: US/11/033,039

CURRENT FILING DATE: 2005-01-11

PRIOR APPLICATION NUMBER: 10/245,871

PRIOR FILING DATE: 2002-09-17

PRIOR APPLICATION NUMBER: 10/197,000

PRIOR FILING DATE: 2002-07-17

PRIOR APPLICATION NUMBER: 09/396,813

PRIOR FILING DATE: 1999-09-14

NUMBER OF SEQ ID NOS: 1452

SOFTWARE: PatentIn version 3.3

SEQ ID NO 1123

LENGTH: 19

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

FEATURE:

NAME/KEY: MOD_RES

LOCATION: (5)..(5)

OTHER INFORMATION: Ava

US-11-033-039-1123

Query Match

Best Local Similarity 26.6%; Score 33; DB 7; Length 19;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 MAONKYR 9

Db 3 MKXNYKR 10

RESULT 2
US-10-511-559-255

Sequence 255, Application US/10511559

Publication No. US20050256304A1

GENERAL INFORMATION:

APPLICANT: JONES, Tim

APPLICANT: BAKER, Matthew

APPLICANT: CARR, Francis, J.

TITLE OF INVENTION: MODIFIED FACTOR VIII

FILE REFERENCE: MER-133

CURRENT APPLICATION NUMBER: US/10/511,559

CURRENT FILING DATE: 2004-10-15

PRIOR APPLICATION NUMBER: PCT/EP03/04063

PRIOR FILING DATE: 2003-04-17

PRIOR APPLICATION NUMBER: EP 02008712.8

PRIOR FILING DATE: 2002-04-18

PRIOR APPLICATION NUMBER: EP 03006554.4

PRIOR FILING DATE: 2003-03-24

NUMBER OF SEQ ID NOS: 1147

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 255

LENGTH: 13

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-255

Query Match 24.2%; Score 30; DB 6; Length 13;
Best Local Similarity 43.8%; Pred. No. 34;
Matches 7; Conservative 2; Mismatches 3; Indels 4; Gaps 1;

OY 8 YROOFIOSVINGNATR 23
Db 1 YKSQY---LNNGPQR 12

RESULT 3
US-10-511-559-75

Sequence 75, Application US/10511559

Publication No. US20050256304A1

GENERAL INFORMATION:

APPLICANT: JONES, Tim

APPLICANT: BAKER, Matthew

APPLICANT: CARR, Francis, J.

TITLE OF INVENTION: MODIFIED FACTOR VIII

FILE REFERENCE: MER-133

CURRENT APPLICATION NUMBER: US/10/511,559

CURRENT FILING DATE: 2004-10-15

PRIOR APPLICATION NUMBER: PCT/EP03/04063

PRIOR FILING DATE: 2003-04-17

PRIOR APPLICATION NUMBER: EP 02008712.8

PRIOR FILING DATE: 2002-04-18

PRIOR APPLICATION NUMBER: EP 03006554.4

PRIOR FILING DATE: 2003-03-24

NUMBER OF SEQ ID NOS: 1147

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 75

LENGTH: 15

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Epitope of human Factor VIII

US-10-511-559-75

Query Match

Best Local Similarity 24.2%; Score 30; DB 6; Length 15;

Matches 7; Conservative 2; Mismatches 3; Indels 4; Gaps 1;

OY 8 YROOFIOSVINGNATR 23

Db 2 YKSQY---LNNGPQR 13

RESULT 4
US-10-503-575-110

Sequence 110, Application US/10503575

Publication No. US20050244823A1

GENERAL INFORMATION:

APPLICANT: Drijfhout, Jan Wouter

APPLICANT: Van Veelen, Petrus Antonius

APPLICANT: Konig, Frits

TITLE OF INVENTION: NOVEL EPIPTOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHOD

FILE REFERENCE: 2799/72843-PCT-US

CURRENT APPLICATION NUMBER: US/10/503,575

CURRENT FILING DATE: 2004-08-04

PRIOR APPLICATION NUMBER: PCT/NL03/00077

PRIOR FILING DATE: 2003-02-04

PRIOR APPLICATION NUMBER: EP 02075456.0

PRIOR FILING DATE: 2002-02-04

NUMBER OF SEQ ID NOS: 340

SOFTWARE: PatentIn version 3.1

SEQ ID NO 110

LENGTH: 19

TYPE: PRT

ORGANISM: Homo sapiens

US-10-503-575-110


```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: SDF-1 CXCR4 receptor antagonist analogue
; OTHER INFORMATION: C-terminal residues 55-67 linked by -(CH-2)-n-
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = leu linked via -(CH-2)-n-, where n = 1 to 20.
; OTHER INFORMATION: to the C-terminal amino acid of any one of SEQ ID NOS:76,
; OTHER INFORMATION: 78, 87-94, 103-110, and 117-122
US-10-945-674A-77

Query Match          22.6%; Score 28; DB 6; Length 13;
Best Local Similarity 33.3%; Pred. No. 70;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      7 KYRQQTQSVLN 18
      |:::|
Db      2 KMQEYLEKALN 13

RESULT 8
US-11-045-024-13293
; Sequence 13293, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esreban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT FILING DATE: 2005-01-28
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13293
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13293

Query Match          22.6%; Score 28; DB 7; Length 15;
Best Local Similarity 45.5%; Pred. No. 82;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      11 QFIQSVLNNGA 21
      |:::|
Db      3 QLIBALLDTGA 13
```

```

RESULT 9
US-11-111-463-12
; Sequence 12, Application US/11111463
; Publication No. US20050261196A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Jerrold R.
; APPLICANT: Mccarty, Randall J.
; APPLICANT: McKay, Derek
; TITLE OF INVENTION: MYOSIN LIGHT CHAIN KINASE INHIBITORS AND METHODS OF USE
; FILE REFERENCE: 092234-9030-US01
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: US/11/111,463
; PRIOR FILING DATE: 2004-04-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-111-463-12

Query Match          21.8%; Score 27; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.8e+04;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      4 QNYKYRQ 11
      |:::|
Db      2 KKVKYRRK 9

RESULT 10
US-10-511-559-254
; Sequence 254, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: US/10/511,559
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: EP 03006554.4
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 254
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-254

Query Match          21.8%; Score 27; DB 6; Length 13;
Best Local Similarity 46.2%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 4; Gaps 1;

QY      8 YRQFIQSVLNNG 20
      |:::|
Db      3 YKSGY-----LNG 11

RESULT 11
```

```
US-11-022-562-43
; Sequence 43, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
; FILE REFERENCE: DEN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; PRIOR FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
US-11-022-562-43

Query Match      21.8%; Score 27; DB 7; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY      15 SVLNNGATRQ 24
Db      5 SAUSEGATPQ 14

RESULT 12
US-11-022-562-44
; Sequence 44, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
; FILE REFERENCE: DEN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; PRIOR FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
US-11-022-562-44

Query Match      21.8%; Score 27; DB 7; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY      15 SVLNNGATRQ 24
Db      1 SAUSEGATPQ 10

RESULT 13
US-11-106-932-114
; Sequence 114, Application US/11106932
; Publication No. US20050260697A1
; GENERAL INFORMATION:
; APPLICANT: WANG, KA-WANG KEVIN
; APPLICANT: HAYES, RONALD
; APPLICANT: LIT, MING CHEN
```

```
APPLICANT: OLI, MONIKA
; TITLE OF INVENTION: PROTEOLYTIC MARKERS AS DIAGNOSTIC BIOMARKERS FOR CANCER, ORGAN
; TITLE OF INVENTION: INJURY AND MUSCLE REHABILITATION/EXERCISE OVERTRAINING
; FILE REFERENCE: 5853-549-1
; CURRENT APPLICATION NUMBER: US/11/106,932
; CURRENT FILING DATE: 2005-04-15
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 114
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-932-114

Query Match      21.8%; Score 27; DB 7; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY      15 SVLNNGATRQ 24
Db      2 SEMVNGATEQ 11

RESULT 14
US-11-045-024-13006
; Sequence 13006, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060, 0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13006
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13006

Query Match      21.8%; Score 27; DB 7; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY      15 SVLNNGATRQ 24
Db      1 SAUSEGATPQ 10
```

```
Db          2  SALSEGATPQ 11

RESULT 15
US-11-045-024-13016
; Sequence 13016, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13016
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13016

Query Match          21.8%; Score 27; DB 7; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY          15  SVLNNGATRQ 24
Db          6  SALSEGATPQ 15

RESULT 16
US-10-973-977-8
; Sequence 8, Application US/10973977
; Publication No. US20060008467A1
; GENERAL INFORMATION:
; APPLICANT: HAYNES, BARTON F.
; APPLICANT: LIAO, HUA-XIN
; APPLICANT: LETVIN, NORMAN
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE
; FILE REFERENCE: 1579-942
; CURRENT FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: 09/775,805
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/497,497
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 107

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-973-977-8

Query Match          21.8%; Score 27; DB 6; Length 16;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY          15  SVLNNGATRQ 24
Db          5  SALSEGATPQ 14

RESULT 17
US-11-145-861-215
; Sequence 215, Application US/11145861
; Publication No. US20060014138A1
; GENERAL INFORMATION:
; APPLICANT: Chinnaiyan, Arul
; APPLICANT: Wang, Xiaoju
; TITLE OF INVENTION: Phage Microarray Profiling of the Humoral Response to Disease
; FILE REFERENCE: UM-09899
; CURRENT FILING DATE: 2005-06-06
; NUMBER OF SEQ ID NOS: 464
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 215
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-145-861-215

Query Match          21.8%; Score 27; DB 7; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY          10  QQFIQSVLNN 19
Db          2  KQILSSVLNS 11

RESULT 18
US-11-033-039-1125
; Sequence 1125, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: US/11/033,039
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1125
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (5)..(5)
```

OTHER INFORMATION: Ava
US-11-033-039-1125

Query Match 21.8%; Score 27; DB 7; Length 19;
Best Local Similarity 38.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 9 RQGFIOQSVLNNGA 21
DB 2 RMXKLDQVYVNONA 14

RESULT 19
US-11-022-562-249
Sequence 249, Application US/11022562
Publication No. US20050249742A1
GENERAL INFORMATION:
APPLICANT: Ruprecht, Ruth M.
APPLICANT: Shisong, Jiang
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
FILE REFERENCE: DEN-043CN
CURRENT FILING DATE: 2004-12-22
PRIORITY FILING DATE: 2003-06-27
PRIORITY FILING DATE: 2003-06-27
PRIORITY FILING DATE: 2002-06-27
NUMBER OF SEQ ID NOS: 340
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 249
LENGTH: 20
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
US-11-022-562-249

Query Match 21.8%; Score 27; DB 7; Length 20;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 15 SVLNNGATQ 24
DB 3 SALSEGATPQ 12

RESULT 20
US-11-022-562-250
Sequence 250, Application US/11022562
Publication No. US20050249742A1
GENERAL INFORMATION:
APPLICANT: Ruprecht, Ruth M.
APPLICANT: Shisong, Jiang
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
FILE REFERENCE: DEN-043CN
CURRENT FILING DATE: 2004-12-22
PRIORITY FILING DATE: 2003-06-27
PRIORITY FILING DATE: 2003-06-27
PRIORITY FILING DATE: 2002-06-27
NUMBER OF SEQ ID NOS: 340
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 250
LENGTH: 20
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
US-11-022-562-250

Query Match 21.8%; Score 27; DB 7; Length 20;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 15 SVLNNGATQ 24
DB 3 SALSEGATPQ 12

RESULT 21
US-10-503-575-329
Sequence 329, Application US/10503575
Publication No. US20050244823A1
GENERAL INFORMATION:
APPLICANT: Drifhout, Jan Mouter
APPLICANT: van Veele, Petrus Antonius
TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHO
FILE REFERENCE: 2799/72843-PCT-US
CURRENT FILING DATE: 2004-08-04
PRIORITY FILING DATE: 2003-02-04
PRIORITY FILING DATE: 2003-02-04
PRIORITY FILING DATE: 2002-02-04
NUMBER OF SEQ ID NOS: 340
SOFTWARE: PatentIn version 3.1
SEQ ID NO 329
LENGTH: 19
TYPE: PRT
ORGANISM: Homo sapiens
US-10-503-575-329

Query Match 21.0%; Score 26; DB 6; Length 19;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 7 KYRQGFIOQSVLN 18
DB 3 RMXKLDQVYVNONA 14

RESULT 22
US-11-196-400-16
Sequence 16, Application US/11196400
Publication No. US20050287166A1
GENERAL INFORMATION:
APPLICANT: DRUTHE, PIERRE
APPLICANT: DAUBERSIES, PIERRE
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
FILE REFERENCE: 200773USODIV
CURRENT FILING DATE: 2005-08-04
PRIORITY FILING DATE: 2005-08-04
PRIORITY FILING DATE: 2000-12-22
PRIORITY FILING DATE: 1998-02-06
PRIORITY FILING DATE: 1998-02-06
PRIORITY FILING DATE: 1996-06-12
PRIORITY FILING DATE: 1995-06-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.3
SEQ ID NO 16
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Peptide
US-11-196-400-16

Query Match 21.0%; Score 26; DB 7; Length 20;
Best Local Similarity 36.4%; Pred. No. 2.4e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 9 RQGFIOQSVLN 19

Db 9 KENIIDNLLNN 19

RESULT 23

US-11-041-893-54
; Sequence 54, Application US/11041893
; Publication No. US2006002941A1
; GENERAL INFORMATION:
; APPLICANT: Mahdraz, Gregory G.
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
; FILE REFERENCE: 100123.401
; CURRENT APPLICATION NUMBER: US/11/041,893
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/616,855
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/538,713
; PRIOR FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-11-041-893-54

Query Match 20.2%; Score 25; DB 7; Length 9;
Best Local Similarity 62.5%; Pred. No. 5.8e+04;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 14 QSVLNNGA 21
Db 1 QAVANGGA 8

RESULT 24

US-11-054-515-2823
; Sequence 2823, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blyls
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2823
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2823

Query Match 20.2%; Score 25; DB 7; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DMAQVYKY 8
Db 1 DMKVYKY 8

RESULT 25

US-10-511-559-256
; Sequence 256, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CAR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 0306554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 256
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-256

Query Match 20.2%; Score 25; DB 6; Length 13;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 17 LNNGATR 23
Db 4 LNNGPQR 10

Search completed: January 26, 2006, 08:39:06
Job time : 4.55172 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:48:50 : Search time 12 Seconds
(without alignments)
192.434 Million cell updates/sec

Title: US-09-662-293-8
Perfect score: 124
Sequence: 1 DMAQNYKXROOFIQSVLNGATRG 24

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 4071

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR 80:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	24.2	20	2	T50757
2	28	22.6	10	2	S4282
3	27	21.8	21	2	C56817
4	26	21.0	12	2	PH0771
5	26	21.0	17	2	J02330
6	25	20.2	17	2	J02310
7	25	20.2	19	2	A44239
8	25	20.2	20	2	S18582
9	25	20.2	20	2	S03508
10	24	19.4	10	2	F44644
11	24	19.4	18	2	B57789
12	23	19.0	9	2	C36730
13	23	18.5	14	2	F48394
14	23	18.5	15	2	S72217
15	23	18.5	15	2	JN0730
16	23	18.5	20	2	S00494
17	23	18.5	20	2	S00028
18	22	17.7	9	2	D58503
19	22	17.7	12	2	S10624
20	22	17.7	12	2	PH0746
21	22	17.7	17	2	PS0454
22	22	17.7	18	2	PH0768
23	22	17.7	20	2	S17461
24	22	17.7	20	2	JN0142
25	22	17.7	20	2	D42842
26	22	17.7	20	2	S35970
27	22	17.7	20	2	A54519
28	22	17.7	20	2	S28779
29	22	17.7	21	2	S35978

30	22	17.7	21	2	P00257	microbial serine p
31	22	17.7	21	2	S57568	T cell receptor V-
32	22	17.7	21	2	S69350	4-hydroxybenzoate
33	21.5	17.3	19	2	B60977	14-3-3 protein hom
34	21	16.9	7	2	A38081	amine oxidase (cop
35	21	16.9	9	2	PC7076	spectrin alpha cha
36	21	16.9	11	2	S42587	cellf protein - Esc
37	21	16.9	11	2	A32428	amine oxidase (cop
38	21	16.9	15	2	PH1329	Ig heavy chain DJ
39	21	16.9	15	2	A56049	urinary tract ston
40	21	16.9	15	2	S33781	acetylcholine synth
41	21	16.9	16	2	S10807	protein kinase C i
42	21	16.9	17	2	S48655	glutathione dehydr
43	21	16.9	18	2	PH1368	Ig heavy chain DJ
44	21	16.9	19	2	PH1313	Ig heavy chain DJ
45	21	16.9	21	2	S71602	recombination prot
46	21	16.9	21	2	T06566	ribulose-bisphosph
47	20	16.1	10	2	S28055	cytochrome b559 co
48	20	16.1	10	2	F41839	ribosomal protein
49	20	16.1	10	2	S30348	clotting protein -
50	20	16.1	10	2	JN0025	mosaic - sea urchi
51	20	16.1	10	2	A44871	monodehydroascorba
52	20	16.1	11	2	C59151	protein-tyrosine k
53	20	16.1	11	2	S23306	substance P - Ala
54	20	16.1	13	2	A33208	calreticulin, hepa
55	20	16.1	13	2	S29488	GMP-binding protei
56	20	16.1	13	2	S47362	T-cell antigen rec
57	20	16.1	13	2	G44644	neurotoxin-associ
58	20	16.1	14	2	S39932	S-allele-associate
59	20	16.1	14	2	S39931	S-allele-associate
60	20	16.1	15	2	B33208	calreticulin, uer
61	20	16.1	15	2	S32677	nitrogenase cofact
62	20	16.1	15	2	P00182	scylar glycoprotei
63	20	16.1	15	2	G60977	protein 425 - Cal1
64	20	16.1	16	2	PH1588	Ig H chain V-D-J r
65	20	16.1	17	2	PD0005	very-high-density
66	20	16.1	18	2	T73024	T cell receptor be
67	20	16.1	18	2	A38890	11k protein 5306 f
68	20	16.1	19	2	S00495	hemocyanin chain I
69	20	16.1	19	2	T50329	wc-repeat protein
70	20	16.1	19	2	A33361	CAMP-regulated pho
71	20	16.1	20	2	A53875	creatine kinase (E
72	20	16.1	20	2	S46205	comosasin (EC 3.4.2
73	20	16.1	20	2	S46204	ananasin (EC 3.4.22
74	20	16.1	20	2	S00493	hemocyanin chain I
75	20	16.1	20	2	A48394	major fat-globule
76	20	16.1	20	2	S17501	glutaminase - Alca
77	20	16.1	20	2	P00544	capsid protein VP5
78	20	16.1	20	2	S33291	lipopolysaccharide
79	20	16.1	21	2	S78574	protein kinase C i
80	20	16.1	21	2	A60420	lens intrinsinc mem
81	20	16.1	21	2	PC4443	cytochrome c3 - De
82	19.5	15.7	19	2	B53145	high conductance c
83	19.5	15.7	21	2	E44101	calmodulin, vasoc
84	19	15.3	11	2	S35490	type II site-speci
85	19	15.3	12	2	I39390	acetylcholine rece
86	19	15.3	13	2	PC1149	equinactoxin 1A - 8
87	19	15.3	13	2	S47361	T-cell antigen rec
88	19	15.3	14	1	QMWAP	poliicetes mastopara
89	19	15.3	14	2	S39930	S-allele-associate
90	19	15.3	14	2	PT0210	T-cell receptor al
91	19	15.3	14	2	EC7079	unidentified 27.2K
92	19	15.3	15	2	PQ0174	ethylar glycoprotei
93	19	15.3	15	2	PQ0175	ethylar glycoprotei
94	19	15.3	15	2	S00706	actin - sea urchin
95	19	15.3	15	2	PH1314	Ig heavy chain DJ
96	19	15.3	15	2	PQ0073	T-cell receptor be
97	19	15.3	15	2	PT0096	pyruvate dehydroge
98	19	15.3	17	2	PH0769	T-cell receptor be
99	19	15.3	17	2	S16144	spova protein - Ba
100	19	15.3	17	2	B31435	adherence lectin 1

ALIGNMENTS

RESULT 1

T50757

pufk protein [imported] - Rhodobacter sphaeroides

C:Species: Rhodobacter sphaeroides

C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004

C:Accession: T50757

R:Choudhary, M.; Kaplan, S.

Nucleic Acids Res. 28, 862-867, 2000

A:Title: DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroides 2

A:Reference number: 225222; MUID:20115911; PMID:10648776

A:Accession: T50757

A:Status: preliminary; translated from GE/EMBL/DBD

A:Molecule type: DNA

A:Residues: 1-20 <CHO>

A:Cross-references: UNIPROT:Q53121; UNIPARC:UPI00001329F3; EMBL:AF195122; PIDN:AAF24301.

A:Experimental source: strain 2.4.1

C:Genetics:

A:Gene: pufk

Query Match

Best Local Similarity 24.2%; Score 30; DB 2; Length 20;

Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 9 RQRFIQSVLNNNG 20

DB 8 RHQHVASVLRSG 19

RESULT 2

S42282

paraportal crystal protein cryIIb - Bacillus thuringiensis plasmid (fragment)

N:Alternate names: delta-endotoxin

C:Species: Bacillus thuringiensis

C:Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 24-Jul-1998

C:Accession: S42282

R:Crickmore, N.; Wheeler, V.C.; Ellar, D.J.

Mol. Gen. Genet. 242, 365-368, 1994

A:Title: Use of an operon fusion to induce expression and crystallisation of a Bacillus

A:Reference number: S42282; MUID:94150472; PMID:7906381

A:Accession: S42282

A:Molecule type: protein

A:Residues: 1-10 <CR>

A:Cross-references: UNIPARC:UPI000017ACD4

A:Experimental source: subsp. galleriae 916

C:Genetics:

A:Gene: cryIIb

C:Keywords: delta-endotoxin

Query Match

Best Local Similarity 22.6%; Score 28; DB 2; Length 10;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 13 IQSVLNNNG 20

DB 1 MNTVLNNG 8

RESULT 3

C56817

photosystem I protein Psal - Synechococcus sp. (PCC 6301) (fragment)

C:Species: Synechococcus sp.

C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 18-Aug-1995

C:Accession: C56817

R:Li, N.; Warren, P.V.; Golbeck, J.H.; Frank, G.; Zuber, H.; Bryant, D.A.

Biochim. Biophys. Acta 1059, 215-225, 1991

A:Title: Polypeptide composition of the Photosystem I complex and the Photosystem I core

A:Reference number: A56817; MUID:91355213; PMID:1653017

A:Accession: C56817

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-21 <LII>

A:Cross-references: UNIPARC:UPI0000132581

A:Note: sequence extracted from NCBI backbone (NCBIP:57972)

C:Genetics:

A:Gene: psal

Query Match

Best Local Similarity 21.8%; Score 27; DB 2; Length 21;

Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 14 QSVLNNNGATRPQ 24

DB 2 QDVIANNGTAE 12

RESULT 4

PH0771

T-cell receptor beta chain (P55.1.1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999

C:Accession: PH0771

R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilesky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A:Title: T cell receptor genes in a series of class I major histocompatibility complex-r

allelic exclusion and antigen-specific repertoire.

A:Reference number: PH0746; MUID:92078846; PMID:1836010

A:Accession: PH0771

A:Molecule type: mRNA

A:Residues: 1-12 <CAS>

A:Cross-references: UNIPARC:UPI0000115FBE; EMBL:X60865; NID:953624; PIDN:CAA43255.1; PID

A:Experimental source: T lymphocyte

C:Keywords: T-cell receptor

Query Match

Best Local Similarity 21.0%; Score 26; DB 2; Length 12;

Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 AQNVYKROQF 12

DB 2 ASSFOYQYRF 11

RESULT 5

JQ2320

hypothetical 2.1k protein - potato chloroplast

C:Species: chloroplast Solanum tuberosum (potato)

C:Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004

C:Accession: JQ2320; JQ2315

R:Kawagoe, Y.; Kikuta, Y.

Theor. Appl. Genet. 81, 13-20, 1991

A:Title: Chloroplast DNA evolution in potato (Solanum tuberosum L.).

A:Reference number: JQ2306

A:Accession: JQ2320

A:Molecule type: DNA

A:Residues: 1-17 <KWL>

A:Cross-references: UNIPROT:Q7M2E3; UNIPARC:UPI000017B0C3

A:Experimental source: cv. W553-4

A:Accession: JQ2315

A:Molecule type: DNA

A:Residues: 1-17 <KWL>

A:Cross-references: UNIPARC:UPI000017B0C3

A:Experimental source: cv. 150

C:Genetics:

A:Gene: chloroplast

C:Keywords: chloroplast

Query Match

Best Local Similarity 21.0%; Score 26; DB 2; Length 17;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 MAQNYKXR 9

Db 1 MKNYSYK 8

RESULT 6

QJ0210

hypothetical 2.1k protein - tomato chloroplast (strain Toko)

C:Species: chloroplast Lycopersicon esculentum (tomato)

C>Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004

C:Accession: J02310

R:Kawagoe, Y.; Kikuta, Y.

Theor. Appl. Genet. 81, 13-20, 1991

A:Title: Chloroplast DNA evolution in potato (Solanum tuberosum L.).

A:Reference number: J02306

A:Accession: J02310

A:Molecule type: DNA

A:Residues: 1-17 <KAM>

A:Cross-references: UNIPROT:Q7M2E9, UNIPARC:UPI0000178098

A:Experimental source: strain Toko

C:Genetics:

A:Genome: chloroplast

C:Keywords: chloroplast

Query Match 20.2%; Score 25; DB 2; Length 17;

Best Local Similarity 50.0%; Pred. No. 1.7e+03;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 MAQNYKTR 9

Db 1 MKPNYSYK 8

RESULT 7

A44239

amine oxidase (copper-containing) (EC 1.4.3.6), kidney - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C:Accession: A44239

R:Turner, S.M.; Patsic, M.M.; Scaman, C.H.; Smith, A.J.; Brown, D.E.; Dooley, D.M.; Mure,

Biochemistry 31, 12147-12154, 1992

A:Title: Identification of topaquinine and its consensus sequence in copper amine oxidase

A:Reference number: A44239; PMID:1457410

A:Accession: A44239

A:Molecule type: protein

A:Residues: 1-7, 'X', '9-19 <JAN>

A:Cross-references: UNIPROT:Q9TRK6, UNIPARC:UPI000008701B; PIDN:AA824426.1; PID:9261360

A:Experimental source: kidney

A>Note: sequence extracted from NCBI backbone (NCBIP:119897)

A>Note: we show one of the unidentified residues as tyrosine forming the topaquinine pro

C:Superfamily: amiloride-binding protein

C:Keywords: oxidoreductase; quinoprotein; topaquinine

F/B/Modified site: topaquinine (Tyr) #status experimental

Query Match 20.2%; Score 25; DB 2; Length 19;

Best Local Similarity 55.6%; Pred. No. 1.9e+03;

Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 NYKYRQPT 13

Db 7 NYDYIXDFI 15

RESULT 8

S18582

hypothetical protein K (puG 3' region) - Rhodobacter sphaeroides

C:Species: Rhodobacter sphaeroides

C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 03-May-1994

C:Accession: S18582; S32855

R:Hunter, C.N.; McGlynn, P.; Ashby, M.K.; Burgess, J.G.; Olsen, J.D.

Mol. Microbiol. 5, 2649-2661, 1991

A:Title: DNA sequencing and complementation/deletion analysis of the bchA-puf operon reg

C:Reference number: S18580; PMID:92140030; PMID:1779756

A:Accession: S18582

A>Status: preliminary

A:Molecule type: DNA
A:Residues: 1-20 <HUN>
A:Cross-references: UNIPARC:UPI000017AB8B; EMBL:X68795

Query Match

Best Local Similarity 20.2%; Score 25; DB 2; Length 20;

Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 9 RQPTQSVLNG 20

Db 8 RHNHVASVLRSG 19

RESULT 9

S03508

T-cell receptor alpha chain J region (19) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 05-Nov-1999

C:Accession: S03508

R:Minoto, A.; Mjolsness, S.; Hood, L.

Nature 316, 832-836, 1995

A:Title: Genomic organization of the genes encoding mouse T-cell receptor alpha-chain.

A:Reference number: S03503; PMID:85296332; PMID:2993908

A:Accession: S03508

A:Molecule type: DNA

A:Residues: 1-20 <WIN>

A:Cross-references: UNIPARC:UPI0000115262; EMBL:X03058; NID:954521; PIDN:CAA26865.1; PI

A>Note: this sequence was determined from the germline gene

C:Keywords: T-cell receptor

Query Match 20.2%; Score 25; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 2e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NYKY 8

Db 5 NYKY 8

RESULT 10

F44644

neurotoxin-associated protein type B Hn+ 35k chain, band 3a - Clostridium botulinum (fr

C:Species: Clostridium botulinum

C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004

C:Accession: F44644

R:Somers, E.; DasGupta, B.R.

J. Protein Chem. 10, 415-425, 1991

A:Title: Clostridium botulinum types A, B, C1, and E produce proteins with or without h

A:Reference number: A44644; PMID:92143938; PMID:11781887

A:Contents: type B

A:Accession: F44644

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <SOM>

A:Cross-references: UNIPROT:Q9RSN6; UNIPARC:UPI0000082EFF

A>Note: sequence extracted from NCBI backbone (NCBIP:83787)

C:Keywords: hemagglutinin

Query Match 19.4%; Score 24; DB 2; Length 10;

Best Local Similarity 57.1%; Pred. No. 1.4e+03;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 13 IQSVLNN 19

Db 1 IQNVLND 7

RESULT 11

B57789

kidney stone matrix protein - human (fragment)

C:Species: Homo sapiens (hmn)

C>Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 23-Feb-1996

A:Accession: B57789

R:Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, February 1996
A:Description: The proteins of gallbladder stones.
A:Reference number: A57789
A:Accession: B57789
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <BIN>
A:Cross-references: UNIPARC:UPI000017C28A
A:Experimental source: urate calcium oxalate kidney stone

Query Match 19.4%; Score 24; DB 2; Length 18;
Best Local Similarity 36.4%; Pred. No. 2.5e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 5 NYKTRQPIQS 15
| : : ||
Db 4 NVKFTGEIVQS 14

RESULT 12
C36730
hutu protein - Klebsiella pneumoniae (fragment)
C:Species: Klebsiella pneumoniae
C:Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 08-Oct-1999
C:Accession: C36730
R:Schwacha, A.; Bender, R.A.
J. Bacteriol. 172, 5477-5481, 1990
A:Title: Nucleotide sequence of the gene encoding the repressor for the histidine utilia
A:Reference number: A36730; MUID:90368611; PMID:2203754
A:Accession: C36730
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-9 <SCH>
A:Cross-references: UNIPARC:UPI000012CEC3; GB:M34604; NID:G149203; PIDN:AAA25076.1; PID:

Query Match 19.0%; Score 23.5; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

OY 2 MAQNYKXRRQ 10
| : : ||||
Db 1 MSQS-KYRQ 8

RESULT 13
F48394
glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (fr
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C:Accession: F48394
R:Mahter, J.H.; Benghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A:Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
II-like sequences.
A:Reference number: A48394; MUID:93250576; PMID:8485470
A:Accession: F48394
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <MAT>
A:Cross-references: UNIPARC:UPI000014C319
A:Experimental source: milk
A:Note: sequence extracted from NCBI backbone (NCBI:111455)
C:Keywords: glycoprotein

Query Match 18.5%; Score 23; DB 2; Length 14;
Best Local Similarity 36.4%; Pred. No. 2.8e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 13 IQSVLNNGATR 23
| : : ||||
Db 4 VTXTVTOGASR 14

RESULT 14
S72217
D-arabinose 1-dehydrogenase [NAD(P)] (EC 1.1.1.117) - yeast (Candida albicans) (fragment)
C:Species: Candida albicans
C:Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 03-Jun-2002
C:Accession: S72217
R:Kim, S.T.; Huh, W.K.; Kim, J.Y.; Hwang, S.W.; Kang, S.O.
Biochim. Biophys. Acta 1297, 1-8, 1996
A:Title: D-arabinose dehydrogenase and biosynthesis of erythroascorbic acid in Candida al
A:Reference number: S72217; MUID:96439039; PMID:8841374
A:Accession: S72217
A:Molecule type: protein
A:Residues: 1-14 <KIM>
A:Cross-references: UNIPARC:UPI000017CDB9
C:Keywords: oxidoreductase

Query Match 18.5%; Score 23; DB 2; Length 14;
Best Local Similarity 62.5%; Pred. No. 2.8e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 13 IQSVLNNG 20
| : : ||||
Db 7 IDPXLNNG 14

RESULT 15
JN0730
hypothetical 1.7k protein - phage SP1
N:Alternate names: hypothetical protein 42.1
C:Species: phage SP1
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C:Accession: JN0730
R:Chai, S.; Srepan, U.; Lueder, G.; Trautner, T.A.; Alonso, J.C.
Gene 129, 41-49, 1993
A:Title: Sequence analysis of the left end of the Bacillus subtilis bacteriophage SP1 g
A:Reference number: JN0729; MUID:93328123; PMID:8335259
A:Accession: JN0730
A:Molecule type: DNA
A:Residues: 1-15 <CHA>
A:Cross-references: UNIPARC:UPI000017A84E; EMBL:X65941

Query Match 18.5%; Score 23; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 16 VLNNG 20
| : : ||||
Db 1 MLNNG 5

RESULT 16
S00494
hemocyanin chain II - Japanese spiny lobster (fragment)
C:Species: Panulirus japonicus (Japanese spiny lobster)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C:Accession: S00494
R:Makino, N.; Kimura, S.
Eur. J. Biochem. 173, 423-430, 1988
A:Title: Subunits of Panulirus japonicus hemocyanin. 1. Isolation and properties.
A:Reference number: S00492; MUID:88196131; PMID:3360019
A:Accession: S00494
A:Molecule type: protein
A:Residues: 1-20 <MAK>
A:Cross-references: UNIPROT:P82312; UNIPARC:UPI000012C37C
A:Superfamily: hemocyanin
C:Keywords: copper; hemolymph; hexamer; oxygen carrier

Query Match 18.5%; Score 23; DB 2; Length 20;
Best Local Similarity 29.4%; Pred. No. 4e+03;
Matches 5; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 2 MAQNYKTRQPIQSVLN 18

Db 3 VASSTAHKQDINHLD 19

RESULT 17

PS0028
Flagellar motor switch protein flbd - Escherichia coli (fragment)
C/Species: Escherichia coli
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 18-Jun-1993
C/Accession: PS0028
R/Malakoti, J.; Komeda, Y.; Matsumura, P.
J. Bacteriol. 171, 2728-2734, 1989
A/Title: DNA sequence analysis, gene product identification, and localization of flagellin
A/Reference number: PS0027; PMID:8921963; PMID:2651416
A/Accession: PS0028
A/Molecule type: DNA
A/Residues: 1-20 <MAL>
A/Cross-references: UNIPARC:UPI000017AA3D
C/Genetics:
A/Gene: flbd

Query Match 18.5%; Score 22; DB 2; Length 20;
Best Local Similarity 62.5%; Pred. No. 4e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 17 LNNGATRG 24
Db 1 MNHATVQ 8

RESULT 18

D58503
translation elongation factor EF-Tu - unidentified bacterium (fragment)
C/Species: unidentified bacterium
C/Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004
C/Accession: D58503
R/Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, October 1996
A/Description: The proteins of kidney and gallbladder stones.
A/Reference number: A58501
A/Accession: D58503
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-9 <BIN>
A/Cross-references: UNIPROT:Q7M151, UNIPARC:UPI000017827D
A/Experimental source: human bile and stones
C/Superfamily: translation elongation factor Tu; translation elongation factor Tu homolog
C/Keywords: GTP binding

Query Match 17.7%; Score 22; DB 2; Length 9;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 YRQGF 12
Db 2 YRQGF 6

RESULT 19

S10624
lipovitelin - African clawed frog
C/Species: Xenopus laevis (African clawed frog)
C/Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
C/Accession: S10624
R/Wallace, R.A.; Hoch, K.L.; Carnavall, O.
J. Mol. Biol. 213, 407-409, 1990
A/Title: Placement of small lipovitelin subunits within the vitellogenin precursor in X
A/Reference number: S10624; PMID:9027895; PMID:2352275
A/Accession: S10624
A/Molecule type: protein
A/Residues: 1-12 <WAL>
A/Cross-references: UNIPARC:UPI000017BF94

Query Match 17.7%; Score 22; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 YRQGF 12
Db 6 YRQGF 10

RESULT 20

PH0746
T-cell receptor beta chain (B28) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C/Accession: PH0746
R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A/Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A/Reference number: PH0746; PMID:92078846; PMID:1836010
A/Accession: PH0746
A/Molecule type: mRNA
A/Residues: 1-12 <CAS>
A/Cross-references: UNIPARC:UPI0000115FA5; EMBL:X60837; NID:950098; PIDN:CAA43230.1; PI
A/Experimental source: T lymphocyte
C/Keywords: T-cell receptor

Query Match 17.7%; Score 22; DB 2; Length 12;
Best Local Similarity 40.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 AONKYRQGF 12
Db 2 ASSSRYEQYF 11

RESULT 21

PS0454
38k protein 3129 - rice (strain Nihonbare) (fragment)
C/Species: Oryza sativa (rice)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Mar-1995
C/Accession: PS0454
R/Tsugita, A.
submitted to JIPID, April 1993
A/Reference number: PS0206
A/Accession: PS0454
A/Molecule type: protein
A/Residues: 1-17 <TSU>
A/Cross-references: UNIPARC:UPI000017B100
A/Experimental source: leaf, chloroplast, stem
A/Note: molecular weight 38k, pI 5.9

Query Match 17.7%; Score 22; DB 2; Length 17;
Best Local Similarity 80.0%; Pred. No. 4.9e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 NGATR 23
Db 11 NGXTR 15

RESULT 22

PH0768
T-cell receptor beta chain (M2) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C/Accession: PH0768
R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A/Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A/Reference number: PH0746; PMID:92078846; PMID:1836010
A/Accession: PH0768

A;Molecule type: mRNA
A;Residues: 1-18 <CAS>
A;Cross-references: UNIPARC:UPI0000115FBB; EMBL:X60862; NID:552972; PIDN:CAA4325.1; PIR:PIR000001
A;Experimental source: T lymphocyte
C;Keywords: T-cell receptor

Query Match	17.7%	Score 22	DB 2	Length 18
Best Local Similarity	42.9%	Pred. No. 5.2e+03		
Matches	3	Conservative	2	Mismatches 2; Indels 0; Gaps 0;

QY	6	YKYRQOF	12
	:	:	:
Db	10	FNYAEQF	16

RESULT 23
S17461
flavodoxin B - Azotobacter chroococcum (fragment)
C:Species: Azotobacter chroococcum
C:Date: 19-Mar-1997 #sequence_revision 30-Jan-1998 #text_change 09-Jul-2004
C:Accession: S17461
R:Baby, S.; Barker, P.D.; Hill, H.A.O.; Sanghera, G.S.; Dunbar, B.; Ashby, G.A.; Eady,
Biochem. J. 277, 113-119, 1991
A:Title: Direct electrochemistry of two genetically distinct Flavodoxins isolated from *A.
A:Reference number: S16929; MUID:91315397; PMID:1859358*
A:Accession: S17461
A:Molecule type: protein
A:Residues: 1-20 <BAG>
A:Cross-references: UNIPROT:O9R5U5; UNIPARC:UPI0000086F94
A:Superfamily: Flavodoxin; flavodoxin homology
C:Keywords: electron transfer; flavoprotein; FMN
F:5-20/Domain: flavodoxin homology (fragment) <FLX>
F:9-14/Region: FMN-phosphate binding #status predicted

Query Match	17.7%;	Score 22;	DB 2;	Length 20;
Best Local Similarity	57.1%;	Pred. No. 5.8e+03;		
Matches	4;	Conservative	1;	Mismatches 2;
				Indels 0;
				Gaps 0;

QY	18	NNGATRQ	24
		:	
Db	10	NTGKTRK	16

RESULT 24
JA0142
proteinase inhibitor DE-3 - coral tree (fragment)
C:Species: Erythrina corallodendron (coral tree)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: JA0142
R:Joubert, F.J.
Phytochemistry 27, 1297-1300, 1988
A:Title: Purification and properties of proteinase inhibitors from Erythrina corallodendron
A:Reference number: JA0142
A:Accession: JA0142
A:Molecule type: protein
A:Residues: 1-20 <JOU>
A:Cross-references: UNIPROT:P07475; UNIPARC:UPI00001763AB
A:Note: proteinase inhibitor DE-3 has an estimated molecular weight of 20K
C:Superfamily: plant Kunitz-type proteinase inhibitor
C:Keywords: proteinase inhibitor

Query Match	17.7%	Score 22;	DB 2;	Length 20;
Best Local Similarity	57.1%;	Pred. No. 5.8e+03;		
Matches	4;	Conservative	1;	Mismatches 2;
			Indels	0;
			Gaps	0;

Qy	16	VLNNGAT	22
		:	
Db	9	VWQNGGT	15

RESULT 25
D42842
antifungal 2S storage albumin large chain - radish (fragment)

C:Species: *Raphanus sativus* (radish)
C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #ext_change 31-Dec-2004
C:Accession: D42842
R:Terras, F.R.; Schoofs, H.M.; De Bolle, M.F.; Van Leuven, F.; Rees, S.B.; Vanderleyden, J. Biol. Chem. 267, 15301-15309, 1992
A:Title: Analysis of two novel classes of plant antifungal proteins from radish (*Raphanus*
A:Reference number: A42842; MUID:92348373; PMID:1639777
A:Accession: D42842
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <TR>
A:Cross-references: UNIPROT:Q9S8V7; UNIPARC:UPI00000A93E6
A:Experimental source: seed
A:Note: sequence extracted from NCBI backbone (NCBIP.109925)
C:Superfamily: Alpha amylase inhibitor

Query Match	17.7%	Score 22;	DB 2;	Length 20;
Best Local Similarity	31.2%	Pred. No. 5.8e+03;		
Matches	5;	Conservative	2;	Mismatches 9;
				Indels 0;
				Gaps 0

```
QY      4 QNYKYRQQFIQSVLNN 19
      | : | : ||
Db      2 QGPQQRPLLQCCNN 17
```

Search completed: January 26, 2006, 08:05:01
Job time : 13 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:47:56 : Search time 71.3793 Seconds
(without alignments)
237.221 Million cell updates/sec

Title: US-09-662-293-8
Perfect score: 124
Sequence: 1 DMAQNYKYRQOFISVLNNGATRQ 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 216443 seqs, 70528306 residues

Total number of hits satisfying chosen parameters: 15779

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Uniprot 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	25.8	20	2	Q4YK5_PLABE
2	32	25.8	20	2	P81074_BACCE
3	30	24.2	15	2	Q9S8A2_HELAN
4	30	24.2	20	1	PURK_RHOSH
5	29	23.4	20	2	Q4YB5_PLABE
6	29	23.4	21	2	Q7RBF8_PLAYO
7	29	23.4	21	2	Q7RKZ7_PLAYO
8	28.5	23.0	19	2	Q38371_BPMG2
9	28	22.6	17	2	Q7BVD5_BORBU
10	28	22.6	21	2	Q9R5K0_STRPY
11	27.5	22.2	20	2	Q9R5E1_AERHY
12	27	21.8	16	1	HTPG_ACICA
13	27	21.8	18	2	Q4Z714_PLABE
14	27	21.8	19	2	Q9TWY2_LEIME
15	27	21.8	19	2	Q4X617_PLACH
16	27	21.8	17	2	Q4YB5_PLABE
17	26	21.0	17	2	Q7M2E3_SOLTU
18	26	21.0	18	2	Q9TRD8_RABIT
19	26	21.0	21	2	Q4Y571_PLACH
20	25	20.2	9	2	Q9BVF9_HUMAN
21	25	20.2	16	2	Q5G554_BALMU
22	25	20.2	17	2	Q9UM85_HUMAN
23	25	20.2	17	2	Q7M2E9_LYCES
24	25	20.2	17	2	Q9S8Y3_LUPAR
25	25	20.2	18	2	Q9TW6_APLCA
26	25	20.2	18	2	Q8B133_TATY6
27	25	20.2	19	2	Q60F81_CARCR
28	25	20.2	20	2	Q4XN21_PLACH
29	25	20.2	20	2	Q4XWC8_PLACH
30	25	20.2	20	2	Q64619_RAT
31	25	20.2	21	2	Q5BWH5_SCHUA

32	25	20.2	21	2	Q7RPC3_PLAYO	Q7RPC3 plasmodium
33	24	19.4	10	2	Q9R5N6_CLOBO	Q9R5N6 clostridium
34	24	19.4	15	2	Q5K607_CRACO	Q5K607 crassostrea
35	24	19.4	15	2	Q9MBU7_VIRIRU	Q9MBU7 vibrio phag
36	24	19.4	15	2	Q7BVD5_BORBU	Q7BVD5 borrelia bu
37	24	19.4	16	2	Q7RG27_PLASMODIUM	Q7RG27 plasmodium
38	24	19.4	17	2	Q4Y9B8_PLABE	Q4Y9B8 plasmodium
39	24	19.4	18	2	Q8VNI9_PSPAT	Q8VNI9 haemophilus
40	24	19.4	19	2	Q4XOC6_PLACH	Q4XOC6 plasmodium
41	24	19.4	19	2	Q9QUN1_PSWRI	Q9QUN1 ractus sp.,
42	24	19.4	20	2	Q4Y4K7_PLACH	Q4Y4K7 plasmodium
43	24	19.4	20	2	Q4YQNH_PLABE	Q4YQNH plasmodium
44	24	19.4	21	2	Q9U400_DROXY	Q9U400 drosophila
45	24	19.4	21	2	Q11811_SHIYI	Q11811 human immun
46	23.5	19.0	9	1	HUTU_KIRAE	P12381 krebsiella
47	23.5	19.0	17	2	Q4XN35_PLACH	Q4XN35 plasmodium
48	23	18.5	13	2	Q7PD99_PLAYO	Q7PD99 plasmodium
49	23	18.5	13	2	Q50L81_9DIPR	Q50L81 drosophila
50	23	18.5	13	2	Q79D25_PREDI	Q79D25 fremyella d
51	23	18.5	14	2	Q50176_DROAN	Q50176 drosophila
52	23	18.5	15	2	Q6LC05_PSEAE	Q6LC05 pseudomonas
53	23	18.5	16	2	Q50L70_9DIPR	Q50L70 drosophila
54	23	18.5	16	2	Q50L82_9DIPR	Q50L82 drosophila
55	23	18.5	17	2	Q7R8F8_PLAYO	Q7R8F8 plasmodium
56	23	18.5	17	2	Q7RAG5_PLAYO	Q7RAG5 plasmodium
57	23	18.5	18	2	Q7SCI4_NEUCR	Q7SCI4 neurospora
58	23	18.5	19	2	Q4X3T4_PLACH	Q4X3T4 plasmodium
59	23	18.5	19	2	Q4X3V6_PLACH	Q4X3V6 plasmodium
60	23	18.5	20	1	HGY2_PANDA	P82312 panuilius j
61	23	18.5	20	2	Q9TWN5_THESE	Q9TWN5 theileria s
62	23	18.5	20	2	Q50L73_DROVA	Q50L73 drosophila
63	23	18.5	20	2	Q4XVG2_PLACH	Q4XVG2 plasmodium
64	23	18.5	20	2	Q4Y9Y2_PLABE	Q4Y9Y2 plasmodium
65	23	18.5	21	2	Q4X4U6_PLACH	Q4X4U6 plasmodium
66	23	18.5	21	2	Q4XJY0_PLACH	Q4XJY0 plasmodium
67	23	18.5	21	2	Q4YQZ6_PLABE	Q4YQZ6 plasmodium
68	23	18.5	21	2	Q4YS28_PLABE	Q4YS28 plasmodium
69	23	18.5	21	2	Q4Z1S7_PLABE	Q4Z1S7 plasmodium
70	23	18.5	21	2	Q4Z540_PLABE	Q4Z540 plasmodium
71	23	18.5	21	2	Q66MQ2_9H1Y1	Q66MQ2 human immun
72	22.5	18.1	19	2	Q9F6J8_YERPE	Q9F6J8 yersinia pe
73	22	17.7	9	2	Q7M151_9BACT	Q7M151 undentifite
74	22	17.7	9	2	Q765Y9_CHICK	Q765Y9 gallus gall
75	22	17.7	11	2	Q5GUT3_COXBU	Q5GUT3 coxiella bu
76	22	17.7	11	2	Q5GUT3_COXBU	Q5GUT3 coxiella bu
77	22	17.7	12	2	Q5EGT6_ANACL	Q5EGT6 anas crecca
78	22	17.7	12	2	Q5EGT8_ANACL	Q5EGT8 anas clypea
79	22	17.7	12	2	Q5EGT9_ANADI	Q5EGT9 anas discor
80	22	17.7	12	2	Q5EGU0_ANAAC	Q5EGU0 anas acuta
81	22	17.7	12	2	Q5EGU1_AIXSP	Q5EGU1 aix sponaa
82	22	17.7	12	2	Q5EGU6_ANAST	Q5EGU6 anas strepe
83	22	17.7	12	2	Q5EGU9_ANAPA	Q5EGU9 anas falcac
84	22	17.7	12	2	Q5EGV6_ANAPB	Q5EGV6 anas pemeio
85	22	17.7	12	2	Q5EGW1_ANAPM	Q5EGW1 anas americ
86	22	17.7	12	2	Q5EGW3_ANAST	Q5EGW3 anas sibila
87	22	17.7	14	2	Q6EUD7_CAPHI	Q6EUD7 capra hircu
88	22	17.7	14	2	Q9SM55_BOVIN	Q9SM55 bos taurus
89	22	17.7	15	1	ESTB_SCHGA	P81011 schizaphis
90	22	17.7	15	2	Q4YCG5_PLABE	Q4YCG5 plasmodium
91	22	17.7	16	2	Q96TR0_HUMAN	Q96TR0 homo sapien
92	22	17.7	16	2	Q91923_SHITO	Q91923 shigella bo
93	22	17.7	16	2	Q91925_SHITL	Q91925 shigella fl
94	22	17.7	16	2	Q91927_SHISO	Q91927 shigella so
95	22	17.7	17	2	Q91937_SHISO	Q91937 shigella so
96	22	17.7	17	2	Q9UCF0_HUMAN	Q9UCF0 homo sapien
97	22	17.7	17	2	Q5MBK4_TYMAN	Q5MBK4 tymanoctom
98	22	17.7	17	2	Q76N86_RAT	Q76N86 ractus norv
99	22	17.7	18	2	Q71UR5_HUMAN	Q71UR5 homo sapien
100	22	17.7	18	2	Q9Z1Y8_SHIYNE	Q9Z1Y8 gryon sp. c

ALIGNMENTS

OY	3	AONTKYRQOFTQSUN	18
	:	:	:
db	3	SSGVVFINLFIOKIN	18

Query Match 25.8% Score 32; DB 2; Length 20;
Beat Local Similarity 37.5% Pred. NO. 8.2e+02;
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

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RESULT 1
ID QAYIKS_PLABE PRELIMINARY; PRT; 20 AA.
AC QAYIKS;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB40245.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxId=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churche C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Randreadm M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrall B., Turner C.M.R., Waters A.P., Stiden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
transcriptomic, and proteomic analyses.";
RL Science 307:82-86 (2005).
CC -! CAUTION: The sequence shown here is derived from an
EMBL/genbank/dbj whole genome shotgun (WGS) entry which is
preliminary data.
CC DR EMBL: CAAT01004758; CAT1260.1; -, Genomic_DNA.
KW KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 20 AA; 2282 MW; AF1P9EC9C0CFE6FA CRC64;

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RESULT 2			
ID	PS3074_BACCE	PRT;	20 AA.
AC	PS3074_BACCE PRELIMINARY;		
AC	PS3074;		
DT	01-OCT-2001 (TREMBLrel, 18, Created)		
DT	01-OCT-2001 (TREMBLrel, 18, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel, 25, Last annotation update)		
DE	60 kDa chaperonin (Protein Cpn60) (groEL protein) (Fragment).		
OS	Bacillus cereus.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;		
OC	Bacillus cereus group.		
OX	NCBI_TaxID=1396;		
RN	[1]		
RP	PROTEIN SEQUENCE, AND INDUCTION.		
RC	STRAIN=NCIMB 11796;		
RA	Browne N., Dowds B.C.A.;		
RL	Submitted (JUL-2001) to Swiss-Prot.		
CC	-1- FUNCTION: Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions (By similarity).		
CC	-1- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of 7 subunits (By similarity).		
CC	-1- INDUCTION: By heat shock.		
CC	-1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.		
DR	GO: 0005524; F:ATP binding; IEA.		
DR	GO: 00051082; F:unfolded protein binding; IEA.		
DR	GO: 0006457; P:protein folding; IEA.		
DR	GO: 0006966; P:response to unfolded protein; IEA.		
DR	InterPro: IPR001844; Chaperin Cpn60.		
DR	PROSITE; PS00296; CHAPERONIN_CPN60; PARTIAL.		
KW	ATP-binding; Chaperone; Heat shock.		
FT	NON TER 20 20		

SQ	SEQUENCE	20 AA;	2307 MW;	OAC2E3646264AAR03 CRC64;
	Query Match	25.8%;	Score 32;	DB 2; Length 20;
	Best Local Similarity	46.7%;	Pred. No. 8.2e+02;	
	Matches	7; Conservative	4; Mismatches	4; Indels
OY		3 AONKYRQQFIQSVL 17		
	: : : : :			
DB		1 AKNIKFSQAARRSML 15		
RESULT 3				
ID	Q9S8A2 HELAN	PRELIMINARY;	PRT;	15 AA.
AC	Q9S8A2:			
DT	01-MAY-2000 (TReMBLrel. 13,	Created)		
DT	01-MAY-2000 (TReMBLrel. 13,	Last sequence update)		
DT	01-JUN-2000 (TReMBLrel. 14,	Last annotation update)		
DE	Oleosin (fragment) .			
OC	Helianthus annuus (Common sunflower).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; asterids;			
OC	campnuliids; Asterales; Asteraceae; Asteroideae; Heliantheae;			
CC	Helianthus.			
CX	NCBI_TaxID=4232;			
RN	[1]			
RP	PROTEIN SEQUENCE.			
RX	MEDLINE=96195148; PubMed=8660304;			
RA	Milliclip M., Tatham A.S., Jackson F., Griffiths G., Shewry P.R.,			
RA	Strobat A.K.;			
RT	"Purification and characterization of oil-bodies (oleosomes) and oil-			
RT	-body boundary proteins (Oleosins) from the developing cotyledons of			
RL	sunflower (Helianthus annuus L.).";			
RL	Biochem. J. 314:333-337(1996).			
SQ	SEQUENCE	15 AA; 1619 MW; CDC28A062F7F8704 CRC64;		
Query Match	24.2%;	Score 30;	DB 2; Length 15;	
Best Local Similarity	54.5%;	Pred. No. 1.2e+03;		
Matches	6; Conservative	1; Mismatches	4; Indels	0; Gaps
				0;

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RESULT 4
PUF_K_RHOSH STANDARD; PRT; 20 AA.
ID PUF_K_RHOSH
AC Q5121; 008033;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Transcriptional regulatory protein pufK.
GN Name=pufK;
OS Rhodospirillum rubrum (Rhodospirillum rubrum)
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales
OC Rhodospirillaceae; Rhodospirillum.
OX NCBI_TaxID=1063;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 17023 / 2.4.1 / NCBI 8253 / DSM 158;
RX MEDLINE=9634911; PubMed=8760918;
RA Gong L., Kaplan S.;
RT "Translational control of puf operon expression in Rhodospirillum rubrum"
RT sphaeroides 2.4.1.";
RL Microbiology 142:2057-2069(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 17023 / 2.4.1 / NCBI 8253 / DSM 158;
RX McGlynn P.;
RT "R. rubrum genes bchC, bchX, bchY, bchZ and pufK";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 17023 / 2.4.1 / NCBI 8253 / DSM 158;
RX MEDLINE=2011511; PubMed=10648776; DOI=10.1093/nar/28.4.862;
RA Choudhary M., Kaplan S.;
RT "DNA sequence analysis of the photosynthesis region of Rhodobacter
  sphaeroides 2.4.1.";
RL Nucleic Acids Res. 28:862-867(2000).
CC -!- FUNCTION: Involved in the transcriptional regulation of putB.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as the content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AB2643; AAB46798.1; -, Genomic_DNA.
DR EMBL; AJ010302; CAB38751.1; -, Genomic_DNA.
DR EMBL; AF195122; AAF24301.1; -, Genomic_DNA.
DR PIR; T50757; T50757.
KW Transcription; transcription regulation.
SQ SEQUENCE 20 AA; 2262 MW; 764DBD64B9DD990C CRC64;

Query Match 24.2%; Score 30; DB 1; Length 20;
Best Local Similarity 40.0%; Pred. No. 1.7e+03;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 9 RQGFQISVLNNGATQ 20
DB 8 RHQHVAVSLRSG 19
| | : | | : |
| | : | | : |

RESULT 5
O4YUES_PLABE PRELIMINARY; PRT; 20 AA.
O4YUES;
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB105963.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
CX NCBI_TaxID=5821;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
RA Berriman M., Florens L., Jansen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford D., Hargis B., Harris D., Churcher C.,
RA Quail M.A., Omond D., Duggett J., Trueman H.E., Mendoza J.,
RA Bitwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Jansz C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.,
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
  transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; CAAT01002380; CAH98362.1; -, Genomic_DNA.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 20 AA; 2265 MW; 1322E950F0B057BF CRC64;

Query Match 23.4%; Score 29; DB 2; Length 20;
Best Local Similarity 44.4%; Pred. No. 2.5e+03;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 7 KYRQGFQISVLNNGATQ 24
DB 2 KHMOCIIYSNLNGLATNE 19
| | : | | : |
| | : | | : |

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ID	Q7RBF8_PLAYO PRELIMINARY;	PRT;	21 AA.
AC	Q7RBF8		
DT	01-MAR-2004 (TREMBLrel. 26, Created)		
DT	01-MAR-2004 (TREMBLrel. 26, Last sequence update)		
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)		
DE	Hypothetical protein (Fragment).		
GN	Name=PY06186;		
OS	Plasmodium yoelii yoelii.		
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.		
OX	NCBI_TaxID=73239;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=17XNL;		
RC	MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;		
RA	Carlton J.M., Angiolini S.V., Suh B.B., Kooij T.W., Pertea M.,		
RA	Salva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,		
RA	Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,		
RA	Shallow S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,		
RA	Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,		
RA	Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,		
RA	Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,		
RA	van Lin L.H., Jense C.J., Waters A.P., Smith H.O., White O.R.,		
RA	Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,		
RA	Carucci D.J.		
RT	"Genome sequence and comparative analysis of the model rodent malaria		
RT	parasite Plasmodium yoelii yoelii."		
RL	Nature 419:512-519(2002).		
CC	-!- CAUTION: The sequence shown here is derived from an		
CC	EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is		
CC	preliminary data.		
DR	EMBL; AABJ01002064; EAA18352.1; -; Genomic_DNA.		
DR	Hypothetical protein.		
KW	NON TER		
FT	SEQUENCE 21 AA; 2763 MW; BD4713F274E82473 CRC64;		
SQ			
Query Match	23.4%;	Score 29;	DB 2;
Best Local Similarity	35.7%;	Pred. NO. 2.6e+03;	Length 21;
Matches 5;	Conservative 2;	Mismatches 7;	Indels 0;
Gaps 0;			
5	NYKRYQOQFIOGVN	18	
4	NYMTRHIMHIVN	17	
RESULT 7			
Q7RKZ7_PLAYO PRELIMINARY;	PRT;	21 AA.	
ID	Q7RKZ7		
AC	Q7RKZ7		
DT	01-MAR-2004 (TREMBLrel. 26, Created)		
DT	01-MAR-2004 (TREMBLrel. 26, Last sequence update)		
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)		
DE	Hypothetical protein (Fragment).		
GN	Name=PY02751.		
OS	Plasmodium yoelii yoelii.		
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.		
OX	NCBI_TaxID=73239;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=17XNL;		
RC	MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;		
RA	Carlton J.M., Angiolini S.V., Suh B.B., Kooij T.W., Pertea M.,		
RA	Salva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,		
RA	Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,		
RA	Shallow S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,		
RA	Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,		
RA	Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,		
RA	Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,		
RA	van Lin L.H., Jense C.J., Waters A.P., Smith H.O., White O.R.,		
RA	Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,		
RA	Carucci D.J.		
RT	"Genome sequence and comparative analysis of the model rodent malaria		
RT	parasite Plasmodium yoelii yoelii."		
RL	Nature 419:512-519(2002).		

-1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; AABU01000761; EAA22236.1; -; Genomic_DNA.
DR Hypothetical protein.
KW NON_TER
SQ SEQUENCE 21 AA; 2533 MW; C7BB3387484628C1 CRC64;

Query March 23.4%; Score 29; DB 2; Length 21;
Best Local Similarity 55.6%; Pred. No. 2.6e+03;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 11 QFIQSVLNN 19
Db 10 KFIISIINN 18

RESULT 8
Q38371_BPMS2 PRELIMINARY; PRT; 19 AA.
AC Q38371
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Coat protein; NCBI gi: 553004 (Fragment).
OS Bacteriophage MS2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Levivirus; Levivirus subgroup I.
NCBI_TaxID=12022;
RX NUCLEOTIDE SEQUENCE.
RP MEDLINE=73163785; PubMed=4512458;
RA Contreras R.R., Ysebaert M., Jou W.M., Fiers W.;
RT "Bacteriophage MS2 RNA: nucleotide sequence of the end of the a
RL Nature New Biol. 241:99-101(1973).
DR EMBL; M25187; AAA32258.1; -; Genomic_RNA.
DR HSSP; P03612; IMSC.
KW Capsid protein.
FT NON_TER 19
SQ SEQUENCE 19 AA; 1972 MW; 71CB7F78026D26C8 CRC64;
Query Match 23.0%; Score 28.5; DB 2; Length 19;
Best Local Similarity 38.1%; Pred. No. 2.8e+03;
Matches 8; Conservative 5; Mismatches 3; Indels 5; Gaps 2;

QY 2 MAONKYRQFIQSVLNNCAT 22
Db 1 MASNF--TFV--LVNDGGT 16
RESULT 9
Q7BVD5_BORBU PRELIMINARY; PRT; 17 AA.
AC Q7BVD5;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Borrelia burgdorferi plasmid cp32-7, possible partition proteins,
DS complete cds. (Fragment).
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Plasmid cp32-7.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;
OC Borrelia burgdorferi group.
NCBI_TaxID=139;
RX NUCLEOTIDE SEQUENCE.
RP STRAIN=B31;
RA MEDLINE=98361033; PubMed=9695920;
RT "Evidence of past recombination events among the genes encoding the
RL Microbiology 144:1869-1879(1998).

DR EMBL; AF022483; AAC35457.1; -; Genomic_DNA.
KW Plasmid.
FT NON_TER 17
SQ SEQUENCE 17 AA; 2060 MW; 6B5830E468E030E2 CRC64;

Query Match 22.6%; Score 28; DB 2; Length 17;
Best Local Similarity 42.9%; Pred. No. 3e+03;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 NYKXROQFIQSVLN 18
Db 3 NLAYRYNIESTKN 16

RESULT 10
Q9RSKO_STRPY PRELIMINARY; PRT; 21 AA.
AC Q9RSKO;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Mitogenic factor (Fragment).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
NCBI_TaxID=1314;
RX NUCLEOTIDE SEQUENCE.
RP MEDLINE=92354761; PubMed=1644200; DOI=10.1016/0014-5793(92)81043-L;
RA Yutsudo T., Mural H., Gonzalez J., Takao T., Shimonishi Y., Takeda Y.,
RA Igataashi H., Hinuma Y.;
RT "A new type of mitogenic factor produced by Streptococcus pyogenes.";
RL FEBS Lett. 308:30-34(1992).
FT NON_TER 1
SQ SEQUENCE 21 AA; 2265 MW; 3ADD561319EF8FB5 CRC64;

Query Match 22.6%; Score 28; DB 2; Length 21;
Best Local Similarity 62.5%; Pred. No. 3.8e+03;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 16 VLNNGATR 23
Db 9 VLNDGASK 16

RESULT 11
Q9RSE1_AERHY PRELIMINARY; PRT; 20 AA.
AC Q9RSE1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE Outer-membrane channel-forming protein IV (Fragment).
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
NCBI_TaxID=644;
RX NUCLEOTIDE SEQUENCE.
RP MEDLINE=9113115; PubMed=1283000;
RA Jeanneur D., Gletsu N., Patrus F., Buckley J.T.;
RT "Purification of Aeromonas hydrophila major outer-membrane proteins:
RT N-terminal sequence analysis and channel-forming properties.";
RL Mol. Microbiol. 6:3355-3363(1992).
SQ SEQUENCE 20 AA; 2458 MW; EEDFCB4EEDC66D00 CRC64;

Query Match 22.2%; Score 27.5; DB 2; Length 20;
Best Local Similarity 53.8%; Pred. No. 4.4e+03;
Matches 7; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 1 DMAQN-YKXROQF 12
Db 1 DMAQN-YKXROQF 12

Db 6 DIHKNDYKRRMQF 18

RESULT 12

HTPE_ACICA STANDARD; PRT; 16 AA.

AC P81876;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Chaperone protein htpg (Heat shock protein htpg) (High temperature protein G) (Fragment).

DE Name=htpg;

GN Acinetobacter calcoaceticus.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Moraxellaceae; Acinetobacter.

OX NCBI_TaxID=471;

RN [1]

RP PROTEIN SEQUENCE.

RC STRAIN=69-V;

RX DOI=10.1002/(STRT)1522-2663(19990101)20:4/5<781::AID-ELPS781>3.0.CO;2-A;

RA Beandorf D., Lofthagen N., Babel W.;

RT "Induction of heat shock proteins in response to primary alcohols in Acinetobacter calcoaceticus."

RL Electrophoresis 20:781-789(1999).

CC -1- FUNCTION: Molecular chaperone. Has ATPase activity (By similarity).

CC -1- SUBUNIT: Homodimer (By similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -1- INDUCTION: By heat shock and primary alcohols.

CC -1- SIMILARITY: Belongs to the heat shock protein 90 family.

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CC -----

DR HAMAP: MF_00505; -; 1.

DR Interpro: IPR001404; Hsp90.

DR PROSITE: PS00298; HSP90; PARTIAL.

KW ATP-binding; Chaperone; Direct protein sequencing; Heat shock;

KW Nucleotide-binding.

FT NON_TER 16

FT SEQUENCE 16 AA; 1770 MW; 316C70D8928CB482 CRC64;

SQ

Query Match 21.8%; Score 27; DB 1; Length 16;

Best Local Similarity 33.3%; Pred. No. 4.1e+03;

Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 3 AQNYKYRQFIQ 14

Db 5 SQNYSFQAEVAQ 16

RESULT 13

Q4Z714_PLABE PRELIMINARY; PRT; 18 AA.

AC Q4Z714;

DT 13-SEP-2005 (TEMBLrel. 31, Created)

DT 13-SEP-2005 (TEMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TEMBLrel. 31, Last annotation update)

DE Hypothetical protein (Fragment).

GN ORFNames=PB100192.00.0;

OS Plasmodium berghel.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OX NCBI_TaxID=5821;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Hall N., Karrae M., Raine J.D., Carlton J.M., Kooij T.W.A.,

RA Bertrman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,

RA James K., Rutherford K., Harris B., Harris D., Churcher C.,

RA Qneil M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,

RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,

RA Janse C.J., Barrell B., Turner C.M.R., Waters A.F., Sinden R.S.;

RT "A comprehensive survey of the Plasmodium life cycle by genomic, transcriptomic, and proteomic analyses."

RL Science 307:82-86(2005).

CC -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.

CC EMBL; CAI0100075; CAH93662.1; -; Genomic_DNA.

DR EMBL; CAI0100075; CAH93662.1; -; Genomic_DNA.

KW Hypothetical protein.

FT NON_TER 1

FT SEQUENCE 18 AA; 2291 MW; 3C53320CDAF8CE29 CRC64;

Query Match 21.8%; Score 27; DB 2; Length 18;

Best Local Similarity 33.3%; Pred. No. 4.7e+03;

Matches 6; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

OY 6 YKRRQFIQSVLNNGATR 23

Db 3 YKRR--FFLSIFKNVWK 18

RESULT 14

Q9TWY2_LEIME PRELIMINARY; PRT; 19 AA.

AC Q9TWY2;

DT 01-MAY-2000 (TEMBLrel. 13, Created)

DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)

DE Membrane-bound acid phosphatase (Fragment).

OS Leishmania mexicana.

OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.

OX NCBI_TaxID=5665;

RN [1]

RP PROTEIN SEQUENCE.

RX MEDLINE=91312388; PubMed=1857378; DOI=10.1016/0166-6851(91)90152-V;

RA Menz B., Winter G., Iig T., Lottspeich F., Overath P.;

RT "Purification and characterization of a membrane-bound acid phosphatase of Leishmania mexicana."

RL Mol. Biochem. Parasitol. 47:101-108(1991).

DR Interpro: IPR000560; HisAc phosphatase.

DR Pfam: PF00328; Acid_phosphat_A; 1.

FT NON_TER 1

FT NON_TER 19

FT SEQUENCE 19 AA; 2178 MW; EC44360F28A7D71B CRC64;

SQ

Query Match 21.8%; Score 27; DB 2; Length 19;

Best Local Similarity 35.7%; Pred. No. 5e+03;

Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 8 YRQFIQSVLNNGA 21

Db 4 YKVELVQVVRHGA 17

RESULT 15

Q4X617_PLACH PRELIMINARY; PRT; 19 AA.

AC Q4X617;

DT 13-SEP-2005 (TEMBLrel. 31, Created)

DT 13-SEP-2005 (TEMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TEMBLrel. 31, Last annotation update)

DE Hypothetical protein (Fragment).

GN ORFNames=PC405777.00.0;

OS Plasmodium chabaudi.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OX NCBI_TaxID=5825;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Hall N., Karrae M., Raine J.D., Carlton J.M., Kooij T.W.A.,

RA Bertrman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,

RA James K., Rutherford K., Harris B., Harris D., Churcher C.,

RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carnucci D.J., Yates J.R., Kafatos F.C.,
 RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses.";
 RL Science 307:82-86(2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; CA01009496; CA87489.1; -; Genomic_DNA.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 19 AA; 2278 MW; FA6AC117648F8A9 CRC64;
 Query Match 21.8%; Score 27; DB 2; Length 19;
 Best Local Similarity 30.8%; Pred. No. 5e+03;
 Matches 4; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 QY 2 MAQNYKRYQCFIQ 14
 Db 5 ITQNYQIKQDMAE 17

RESULT 16
 Q4YBES_PLABE PRELIMINARY; PRT; 21 AA.
 ID Q4YBES_PLABE PRELIMINARY;
 AC Q4YBES_PLABE PRELIMINARY;
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN ORFNames=PB106774.00.0;
 OS Plasmodium berghei;
 CC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 CC NCBI_TaxID=5821;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
 RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carnucci D.J., Yates J.R., Kafatos F.C.,
 RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses.";
 RL Science 307:82-86(2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; CA01006816; CA104804.1; -; Genomic_DNA.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 21 AA; 2501 MW; F4140B6CCFA1E386 CRC64;
 Query Match 21.8%; Score 27; DB 2; Length 21;
 Best Local Similarity 55.6%; Pred. No. 5.6e+03;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 MAQNYKRYQ 10
 Db 6 LVQNYKCSQ 14

RESULT 17
 Q7M2E3_SOLTU PRELIMINARY; PRT; 17 AA.
 ID Q7M2E3_SOLTU PRELIMINARY;
 AC Q7M2E3;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Hypothetical 2.1K protein.
 OS Solanum tuberosum (Potato).
 CG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Limids; Solanales; Solanaceae; Solanum.
 CC NCBI_TaxID=4113;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Kwaage Y., Kikuta Y.,
 RT "Chloroplast DNA evolution in potato (Solanum tuberosum L.).";
 RL Theor. Appl. Genet. 81:13-20(1991).
 DR PIR; JQ2320; JQ2320.
 SQ SEQUENCE 17 AA; 2089 MW; 02326E0F9569C176 CRC64;
 Query Match 21.0%; Score 26; DB 2; Length 17;
 Best Local Similarity 50.0%; Pred. No. 6.4e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 MAQNYKRY 9
 Db 1 MKSNYSYK 8

RESULT 18
 Q9TRD8_RABIT PRELIMINARY; PRT; 18 AA.
 ID Q9TRD8_RABIT PRELIMINARY;
 AC Q9TRD8;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Chaperonin (Fragment).
 OS Oryctolagus cuniculus (Rabbit).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
 CC Oryctolagus.
 CC NCBI_TaxID=9986;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=94089752; PubMed=7903455;
 RA Rommelaere H., Van Troys M., Gao Y., Melki R., Cowan N.J.,
 RA Vandekerckhove J., Ampe C.;
 RT "Eukaryotic cytosolic chaperonin contains t-complex polypeptide 1 and
 RT seven related subunits.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:11975-11979(1993).
 SQ SEQUENCE 18 AA; 1884 MW; B608F6EB5A8A2A6 CRC64;
 Query Match 21.0%; Score 26; DB 2; Length 18;
 Best Local Similarity 62.5%; Pred. No. 6.8e+03;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 15 SVLNGAT 22
 Db 10 TVTNDGAT 17

RESULT 19
 Q4Y571_PLACH PRELIMINARY; PRT; 21 AA.
 ID Q4Y571_PLACH PRELIMINARY;
 AC Q4Y571;
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN ORFNames=PC101630.00.0;
 OS Plasmodium chabaudi.
 CC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 CC NCBI_TaxID=5825;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
 RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carnucci D.J., Yates J.R., Kafatos F.C.,
 RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,

RT "A comprehensive survey of the Plasmodium life cycle by genomic, transcriptomic, and proteomic analyses.";
 RL Science 307:82-86 (2005).
 CC -1- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
 DR EMBL; CAJ01000943; CAH75689.1; -; Genomic_DNA.
 KW Hypothetical protein.
 FT NON TER
 SQ SEQUENCE 21 AA; 2792 MW; 56BBD6970F8923FE CRC64;

Query Match 21.0%; Score 26; DB 2; Length 21;
 Best Local Similarity 57.1%; Pred. No. 8.1e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 MAONYKY 8
 DB 6 ICNNYKY 12

RESULT 20

09BYF9_HUMAN
 ID 09BYF9_HUMAN PRELIMINARY; PRT; 9 AA.
 AC 09BYF9;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c19 (Fragment).
 GN Name=C19;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21539745; PubMed=11682035; DOI=10.1016/S0168-8278(01)00167-2;
 RA Kagawa M., Kaneo S., Ohno H., Inamura K., Kobayashi K.;
 RT "Cloning and characterization of the 5'-flanking region of human
 RT cytochrome c19 gene in human cholangiocarcinoma cell line.";
 RL J. Hepatol. 35:504-511(2001).
 DR EMBL; AB045973; BAB40770.1; -; Genomic_DNA.
 DR GO; GO:0005882; C:Intermediate filament; IEA.
 KM Keratin.
 FT NON TER
 SQ SEQUENCE 9 AA; 1122 MW; 9E9FC41B45AB45A1 CRC64;

Query Match 20.2%; Score 25; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.2e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 NYKXKQ 10
 DB 3 SYSYKQ 8

RESULT 21

05G554_BALMU
 ID 05G554_BALMU PRELIMINARY; PRT; 16 AA.
 AC 05G554;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE DNA polymerase beta (Fragment).
 GN Name=POLB;
 OS Balneoptera musculus (Blue whale).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
 OC Mysticeti; Balneopteridae; Balneoptera.
 OX NCBI_TaxID=9771;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Conway C.A., May B.P.;

RT "Global Population Structure of Blue Whales Balneoptera musculus ssp
 RT Based on Nuclear Genetic Variation.";
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY851160; AAM65802.1; -; Genomic_DNA.
 FT NON TER
 FT NON TER
 SQ SEQUENCE 16 AA; 1732 MW; 06E7C60F1ACBE4B0 CRC64;

Query Match 20.2%; Score 25; DB 2; Length 16;
 Best Local Similarity 55.6%; Pred. No. 8.6e+03;
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 14 QSVANGAT 22
 DB 2 QETLNGAT 10

RESULT 22

09UM85_HUMAN
 ID 09UM85_HUMAN PRELIMINARY; PRT; 17 AA.
 AC 09UM85;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Beta-globin protein (Fragment).
 GN Name=beta-globin;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=96352914; PubMed=8718696;
 RA Rahbar S., Nozari G., Forrest G., Gelbart T., Forman S.J., Beutler E.;
 RT "A novel intrachromosomal rearrangement in the beta-globin gene found
 RT in an African-American family.";
 RL Hemoglobin 19:375-388(1995).
 DR EMBL; S82767; AAD14420.1; -; Genomic_DNA.
 DR HSSP; P02023; IC7C.
 FT NON TER
 SQ SEQUENCE 17 AA; 2104 MW; 4197E5BE5260504 CRC64;

Query Match 20.2%; Score 25; DB 2; Length 17;
 Best Local Similarity 40.0%; Pred. No. 9.2e+03;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 6 YKXROQPIQS 15
 DB 5 YPWTOQRPFS 14

RESULT 23

07M2E9_LYCES
 ID 07M2E9_LYCES PRELIMINARY; PRT; 17 AA.
 AC 07M2E9;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical 2.1K protein.
 OS Lycopersicon esculentum (Tomato).
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
 OX NCBI_TaxID=4081;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Kawagoe Y., Kikuta Y.;
 RT "Chloroplast DNA evolution in potato (Solanum tuberosum L.).";
 RL Theor. Appl. Genet. 81:13-20(1991).
 DR PIR; J02310; J02310.
 SQ SEQUENCE 17 AA; 2099 MW; 02326E0F9569C2B9 CRC64;

Query Match 20.2% Score 25; DB 2; Length 17;
 Best Local Similarity 50.0%; Pred. No. 9.2e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 MAQNYKYR 9
 | | | |
 Db 1 MKPNYSYK 8

RESULT 24

09S8Y3 LUPAR PRELIMINARY; PRT; 17 AA.
 ID 09S8Y3 LUPAR
 AC 09S8Y3
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE L-asparaginase isoform A (EC 3.5.1.1) (Fragment).
 OS Lupinus arboreus (Tree lupin).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids 1; Fabales; Fabaceae; Papilionoideae; Genisteae; Lupinus.
 OX NCBI_TaxID=3872;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=92344803; PubMed=1368361; DOI=10.1016/0031-9422(92)83098-J;
 RA Lough T.J., Chang K.S., Carne A., Monk B.C., Reynolds P.H.,
 RA Farnden K.J.;
 RL Phytochemistry 31:1519-1527(1992).
 DR GO; GO:0004067; F:asparaginase activity; IEA.
 SQ SEQUENCE 17 AA; 1703 MW; 9AEDD9691F7F0807 CRC64;

Query Match 20.2% Score 25; DB 2; Length 17;
 Best Local Similarity 60.0%; Pred. No. 9.2e+03;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 13 IOSVLNNGAT 22
 | | | | |
 Db 6 IGSVLNNGT 15

RESULT 25

09TWV6 APLCA PRELIMINARY; PRT; 18 AA.
 ID 09TWV6 APLCA
 AC 09TWV6
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE APLYSIA gonad lectin (Fragment).
 OS Aplysia californica (California sea hare).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspiidea;
 OC Aplysioidea; Aplysiidae; Aplysia.
 OX NCBI_TaxID=6500;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=93057436; PubMed=1431843;
 RA Wilson M.P., Carrow G.W., Levitan I.B.;
 RT "Modulation of growth of Aplysia neurons by an endogenous lectin."
 RL J. Neurobiol. 23:739-750(1992).
 SQ SEQUENCE 18 AA; 2105 MW; 5652840B573057D8 CRC64;

Query Match 20.2% Score 25; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 NYXY 8
 | | | |
 Db 15 NYXY 18

Search completed: January 26, 2006, 08:03:54
 Job time : 74.3793 secs

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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:47:09 : Search time 78.1207 Seconds
(without alignments)
129.360 Million cell updates/sec

Title: US-09-662-293-9

Perfect score: 118
Sequence: 1 DEXNVKXVLYTMHYLNNGATR 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378761 residues

Total number of hits satisfying chosen parameters: 897420

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

1: A_Geneseq_21:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44.5	37.7	20	2	AAR15535 Immunop
2	35	29.7	16	5	ABP46205 Human Bly
3	35	29.7	16	7	ADG97032 scFV VHCD
4	34	28.8	12	6	AAE30892 Human Bly
5	34	28.8	16	5	ABP46248 Human Bly
6	34	28.8	16	7	ADG97075 scFV VHCD
7	34	28.8	20	2	AAR15580 Immunop
8	33.5	28.4	14	8	ADR88216 Human hep
9	33.5	28.4	14	8	ADR78183 Functiona
10	33.5	28.4	15	9	AEA42432 Human hep
11	33.5	28.4	15	9	ADU70841 Human hep
12	33.5	28.4	15	9	ADU71059 Human hep
13	33.5	28.4	15	9	ADU71060 Human hep
14	33.5	28.4	15	9	ADU71272 Human hep
15	33.5	28.4	15	9	ADU70927 Human hep
16	33.5	28.4	15	9	ADY27047 Heparinas
17	33	28.0	15	9	ADU70969 Human hep
18	33	28.0	15	9	ADU71114 Human hep
19	33	28.0	17	3	AAB06372 Randomise
20	33	28.0	18	3	AAB06381 Randomise
21	33	28.0	18	3	AAB06379 Randomise
22	33	28.0	18	3	AAB05890 Randomise
23	33	28.0	18	3	AAB06385 Randomise
24	32	27.1	9	5	ABB94872 CTL epit

25	32	27.1	9	9	ADU70797 Human hep
26	32	27.1	9	9	ADU70700 Human hep
27	32	27.1	9	9	ADU70638 Human hep
28	32	27.1	9	9	ADU70662 Human hep
29	32	27.1	9	9	ADU70639 Human hep
30	32	27.1	10	8	ABY00912 SARS coro
31	32	27.1	13	7	ADM75353 Potential
32	32	27.1	13	7	ADM75618 Potential
33	32	27.1	12	7	ADM74824 Potential
34	32	27.1	15	5	ABP46898 Human Bly
35	32	27.1	15	7	ADG97725 scFV VHCD
36	32	27.1	15	7	ADM75913 Human MHC
37	32	27.1	15	7	ADM75938 Human MHC
38	32	27.1	15	7	ADM75962 Human MHC
39	32	27.1	15	7	ADM75981 Human MHC
40	32	27.1	15	8	ADG06417 Human B-d
41	32	27.1	15	9	ADU71058 Human hep
42	32	27.1	15	9	ADU70968 Human hep
43	32	27.1	15	9	ADU71210 Human hep
44	32	27.1	15	9	AEA00411 Laesra vir
45	32	27.1	16	9	AEA15030 pTRG Lox
46	32	27.1	17	3	AAB06393 Randomise
47	32	27.1	17	3	AAB05887 Randomise
48	32	27.1	18	3	AAB06363 Randomise
49	32	27.1	20	5	ABP46885 Human Bly
50	32	27.1	20	5	ABP46147 Human Bly
51	32	27.1	20	5	ABP46892 Human Bly
52	32	27.1	20	7	ADG97712 scFV VHCD
53	32	27.1	20	7	ADG96974 scFV VHCD
54	32	27.1	20	7	ADG97719 scFV VHCD
55	32	27.1	20	9	ADM52290 Human PL
56	31	26.3	12	7	ADCI4017 Rheumatoid
57	31	26.3	13	1	AAP60378 Antigenic
58	31	26.3	14	9	ADV57777 G protein
59	31	26.3	15	2	AAW49219 Human leu
60	31	26.3	15	7	ADCI7629 Type IV c
61	31	26.3	15	8	ADR19151 Type IV c
62	31	26.3	16	5	ABP46206 Human Bly
63	31	26.3	16	5	ABP46305 Human Bly
64	31	26.3	16	5	ABP46204 Human Bly
65	31	26.3	16	5	ABP46203 Human Bly
66	31	26.3	16	5	ABP46287 Human Bly
67	31	26.3	16	5	ABP46208 Human Bly
68	31	26.3	16	7	ADG97035 scFV VHCD
69	31	26.3	16	7	ADG97031 scFV VHCD
70	31	26.3	16	7	ADG97132 scFV VHCD
71	31	26.3	16	7	ADG97030 scFV VHCD
72	31	26.3	16	7	ADG97114 scFV VHCD
73	31	26.3	16	7	ADG97033 scFV VHCD
74	31	26.3	17	9	AEA44861 Apolipop
75	31	26.3	18	6	ABJ38660 VH-CDR3 p
76	31	26.3	18	6	ADA89069 Human c10
77	31	26.3	18	7	ADG74321 Human VH-
78	31	26.3	18	9	ADW38809 T-cell me
79	31	26.3	20	3	AAI87760 Potato TH
80	31	26.3	20	3	AAI87761 Potato TH
81	31	26.3	20	3	AAI87765 Potato TH
82	31	26.3	20	9	ADU87764 Potato TH
83	31	26.3	20	9	ADU87714 Lung tumo
84	31	26.3	20	9	AEH10519 Mouse mon
85	30	25.4	9	8	ADM12519 MHC class
86	30	25.4	9	8	ADM12519 MHC class
87	30	25.4	10	2	AAV7636 Human tyr
88	30	25.4	11	4	AAW9163 Vaccine r
89	30	25.4	11	8	ADN17001 GI-alpha
90	30	25.4	11	8	ADM12490 Ii-key/hu
91	30	25.4	13	8	ADM12542 Ii-key/hu
92	30	25.4	13	8	ADO38713 Tyrosinase
93	30	25.4	13	8	ADO38773 Human tyr
94	30	25.4	15	2	AAW45823 Peptide r
95	30	25.4	15	2	AAW45818 Peptide r
96	30	25.4	16	6	ABO04914 Human col
97	30	25.4	16	7	ADK40554 KDR & VEG

KM multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
 KM carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
 KM antiinflammatory; antiaesthetic; antiallergic; cytostatic.
 XX unidentified.
 OS
 XX WO2003055979-A2.
 PN
 XX 10-JUL-2003.
 PD
 XX 14-NOV-2002; 2002WO-US036496.
 PF
 XX 16-NOV-2001; 2001US-0311469P.
 PR 19-DEC-2001; 2001US-0340817P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
 XX WPI; 2003-505530/47.
 DR
 XX
 PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
 PT (Blys), useful for detecting and treating diseases or disorders e.g.
 PT rheumatoid arthritis, asthma and leukemia.
 XX
 PS Example 1; SEQ ID NO 2216; 394pp; English.
 XX
 CC This invention relates to novel antibodies that immunospecifically bind
 CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
 CC chromosome 13q34 and encodes a protein that is a member of the tumour
 CC necrosis factor superfamily and induces both in vivo and in vitro B cell
 CC proliferation and differentiation. Specifically, it refers to single
 CC chain antibody molecules (scFvs) derived, preferably, from the variable
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
 CC fragment thereof, of either human, murine, rat or monkey Blys. The
 CC present invention refers to the use of such antibodies in various methods
 CC for the detection, diagnosis and prognosis of diseases related to the
 CC aberrant expression or inappropriate function of Blys or its receptor. As
 CC such, these compositions are useful for identifying immune disorders
 CC including myasthenia gravis and multiple sclerosis, inflammatory
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
 CC as AIDS and proliferative disorders including leukaemia, carcinoma and
 CC lymphoma. Accordingly, they can be described as exhibiting various
 CC activities such as antirheumatic, antiarthritic, neuroprotective,
 CC antiinflammatory, antiaesthetic, antiallergic and cytostatic. This
 CC peptide sequence is a single chain antibody variable heavy CDR3 peptide
 CC that immunospecifically binds Blys of the invention.
 CC
 XX
 SO Sequence 16 AA;
 Query Match 29.7%; Score 35; DB 7; Length 16;
 Best Local Similarity 71.4%; Pred. No. 84;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 11 YTMHYVL 17
 | : |||||
 Db 9 YVLMHYL 15
 RESULT 4
 AAE30892
 ID AAE30892 standard; peptide; 12 AA.
 XX
 AC AAE30892;
 XX
 DT 24-FEB-2003 (first entry)
 XX
 DE MDM2-binding motif #7, identified by phage-peptide display.
 XX
 KM p53 polypeptide; p300 polypeptide; cell cycle; cell death; gene therapy;
 KM cancer; ischaemia; cytostatic; vasotropic.
 XX
 OS Unidentified.

XX
 PN WO200265134-A2.
 XX
 PD 22-AUG-2002.
 XX
 PF 13-FEB-2002; 2002WO-GB000640.
 XX
 PR 13-FEB-2001; 2001GB-00003508.
 XX
 PA (UYDU-) UNIV DUNDEE.
 PI Hupp TR, Dornan D;
 XX WPI; 2003-018623/01.
 DR
 XX
 PT New peptide for modulating the binding of p53 polypeptide to p300
 PT polypeptide, useful for regulating the mammalian cell cycle for the
 PT treatment of cancer or ischemia.
 XX
 PS Example 2; Fig 7B; 87pp; English.
 XX
 CC The invention relates to a peptide for use in modulating the binding of a
 CC p53 polypeptide to a p300 polypeptide. The new peptide is useful in
 CC modulating the binding of a p53 polypeptide to a p300 polypeptide. The
 CC peptide may be used to regulate the mammalian cell cycle or to induce or
 CC prevent cell death, for the treatment of cancer or ischemia. The
 CC invention is useful in gene therapy. The present sequence is MDM2-
 CC binding motif, identified by phage-peptide display
 CC
 XX
 SO Sequence 12 AA;
 Query Match 28.8%; Score 34; DB 6; Length 12;
 Best Local Similarity 50.0%; Pred. No. 88;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 OY 11 YTMHYVINGAT 22
 : ||| : |||
 Db 1 FPFHYMDNINT 12
 RESULT 5
 ABP46248
 ID ABP46248 standard; peptide; 16 AA.
 XX
 AC ABP46248;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human Blys binding scFv VH CDR3 SEQ ID 2259.
 XX
 KM Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KM tumour necrosis factor; B cell proliferation; B cell differentiation;
 KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KM antiAIDS; vaccine; immune; autoimmune disorder; immunodeficiency;
 KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KM common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 PN WO200202641-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 15-JUN-2001; 2001WO-US019110.
 XX
 PR 16-JUN-2000; 2000US-0212210P.
 PR 17-OCT-2000; 2000US-0240816P.
 PR 16-MAR-2001; 2001US-0276248P.
 PR 21-MAR-2001; 2001US-0277379P.
 PR 25-MAY-2001; 2001US-0293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX	Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
PI	WPI; 2002-114799/15.
DR	
XX	
PT	Antibodies against B lymphocyte stimulating polypeptides, useful for the
PT	diagnosis and treatment of cancers and immune disorders.
PS	Claim 2; Page 2960; 3148pp; English.
XX	
CC	This invention describes novel antibodies that immunospecifically bind to
CC	B lymphocyte stimulator (BLyS) polypeptides. BLyS is a member of the
CC	tumour necrosis factor (TNF) super family and induces B cell
CC	proliferation and differentiation. The antibodies of the invention have
CC	cytostatic, immunosuppressive, immunomodulatory, immunoinhibitory,
CC	antirheumatic and antiAIDS activity and can be used in vaccines to
CC	inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC	and so may be used to detect and quantitate the presence of BLyS in
CC	biological samples and may be used in this way to diagnose disease
CC	associated with aberrant expression of BLyS. They may also be
CC	administered to treat diseases associated with aberrant BLyS expression
CC	and activity such as cancer, immune, and autoimmune disorders and
CC	diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC	immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC	acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent
CC	the antibodies and fragments of the antibodies described in the method of
CC	the invention
SQ	Sequence 16 AA:
	Query Match 28.8%; Score 34; DB 5; Length 16;
	Best Local Similarity 83.3%; Pred. No. 1.2e+02;
	Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0
OY	11 YTMHYT 16 9 YMAMYT 14
Db	
	RESULT 6
	ADG97075
ID	ADG97075 standard; peptide; 16 AA.
XX	
AC	ADG97075;
XX	
DT	11-MAR-2004 (first entry)
XX	
DE	scFv VHCDR3 peptide that immunospecifically binds BLyS SeqID 2259.
XX	
KM	antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor;
KM	B cell proliferation; differentiation; scFv; myasthenia gravis;
KM	multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KM	carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
KM	antiinflammatory; antiaesthetic; antiallergic; cytostatic.
XX	
OS	Unidentified.
XX	
PN	WO2003055979-A2.
PD	
XX	10-JUL-2003.
PF	
XX	14-NOV-2002; 2002WO-US036496.
PR	
XX	16-NOV-2001; 2001US-0331469P.
PR	
XX	19-DEC-2001; 2001US-0340817P.
PA	(HUMAN-) HUMAN GENOME SCI INC.
XX	
PI	Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX	
DR	WPI; 2003-505530/47.
XX	
PT	Novel antibody that immunospecifically binds to a B lymphocyte stimulator

(Blys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.

Example 1; SEQ ID NO 2259; 394dp; English.

This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (Blys). The Blys gene has been mapped to chromosome 19q34 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scFvs) derived, preferably, from the variable heavy CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey Blys. The present invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of Blys or its receptor. As such, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various activities such as antitumour, antiarthritic, neuroprotective, antiinflammatory, antisthmatic, antiallergic and cytostatic. This peptide sequence is a single chain antibody variable heavy CDR3 peptide that immunospecifically binds Blys of the invention.

Sequence 16 AA;

Query Match 28.8%; Score 34; DB 7; Length 16;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

11 YTMHY 16
| | | | |
Db 9 YTMHY 14

RESULT 7
AAR15580
ID AAR15580 standard; protein; 20 AA.
XX
AC AAR15580;
XX
DT 02-MAR-1992 (first entry)
XX
DE Immunopeptide derived from HPV18 E2 peptide.
XX
KM cervical cancer; cervical intraepithelial neoplasia; CIN; wart;
XX squamous cell carcinoma; EUSA; HPV 18.
XX
OS Synthetic.
XX
PN WO9118294-A.
XX
PD 28-NOV-1991.
XX
PF 11-MAY-1990; 90SE-00001705.
XX
PR 11-MAY-1990; 90SE-00001705.
XX
PA (MEDS-) MEDSCAND AB.
XX
PI Dillner J, Dillner L, Cheng HM;
XX
XX WPI, 1991-369390/50.
XX
PT Diagnosis of human papilloma virus infection and PV-carrying tumours -
XX using synthetic peptide(s) to detect virus specific antigen-antibody
XX complexes by immunoassay.
XX
PS Disclosure; Page 39; 72pp; English.
XX
CC This is one of a large number of peptides which have been synthesised on

CC the basis of the amino acid sequences for the E2, E4, E7, I1 or I2
CC proteins of HPV 1, 5, 6, 8, 11, 16, 18, 31 and 33. The selection of
CC peptide sequences was based on the assumption that an immunoreactive
CC region might be situated in the same relative region of a protein from
CC different HPV types. The peptides were used in diagnostic immunoassays to
CC detect HPV-infection. See AAR15523-R15601
XX
SO Sequence 20 AA;
Query Match 28.8%; Score 34; DB 2; Length 20;
Best Local Similarity 35.3%; Pred. No. 1.6e+02;
Matches 6; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
OY 1 DEXNVMXYVLYTMHYL 17
DB 4 NKDNCMYTVAMDVYTM 20
RESULT 8
ADR88216
ID ADR88216 standard; peptide; 14 AA.
XX
AC ADR88216;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human heparanase epitope pep10.
XX
KM Targeted drug delivery; inflammatory disorder; wound; scar; vasculopathy;
KM autoimmune disorder; cancer; angiogenesis; metastatic disease;
KM atherosclerosis; restenosis; aneurysm; solid cancer; non-solid cancer;
KM hemangioma; lymphocytic leukaemia; myelogenous leukaemia;
KM Hodgkin's disease; multiple myeloma; haemangiosarcoma; Kaposi's sarcoma;
KM human; heparanase; enzyme; epitope.
XX
OS Homo sapiens.
XX
PN US2004170631-A1.
XX
PD 02-SEP-2004.
XX
PF 28-NOV-2003; 2003US-00722502.
XX
PR 02-SEP-1997; 97US-00922170.
PR 01-MAY-1998; 98US-00071739.
PR 04-NOV-1998; 98US-00186200.
PR 19-FEB-2003; 2003US-00368044.
PR 22-AUG-2003; 2003US-00645659.
XX
PA (YACO/) YACOBY-ZEEVI O.
PA (PERE/) PERETZ T.
PA (MIRO/) MIRON D.
PA (SHLO/) SHLOMI Y.
PA (PECK/) PECKER I.
PA (AYAL/) AYAL-HERSHKOVITZ M.
PA (FEIN/) FEINSTEIN E.
PA (VGEI/) VAN GELDER J M.
PA (VLOD/) VLODAVSKY I.
PA (FRIE/) FRIEDMANN Y.
XX
PI Yacoby-Zeevi O, Peretz T, Miron D, Shlomi Y, Pecker I;
PI Ayal-Hershkovitz M, Feinsein E, Van Gelder JM, Vlodavsky I;
PI Friedmann Y;
XX
XX WPI; 2004-625084/60.
XX
XX
XX Targeted drug delivery to a heparanase-expressing tissue of a patient,
PT useful for treating heparanase-associated conditions such as inflammation
PT or cancer; comprises administering a drug and an anti-heparanase antibody
PT complex.
XX
PS Claim 7; SEQ ID NO 10; 58pp; English.
XX

CC The invention relates to a method of targeted drug delivery to a tissue
CC of a patient, the tissue expressing heparanase. The method comprises
CC providing a complex of a drug directly or indirectly linked to an anti-
CC heparanase antibody, and administering the complex to the patient. In the
CC targeted drug delivery, the antibody comprises an antibody or its portion
CC capable of specifically binding to at least one epitope of a heparanase
CC protein. The composition and methods of the invention are useful for
CC diagnosing, preventing or treating conditions associated with heparanase
CC catalytic activity (e.g. an inflammatory disorder, wound, scar,
CC vasculopathy, an autoimmune disorder, cancer, angiogenesis, cell
CC proliferation, invasion of circulating tumour cells and metastatic
CC disease), for purifying heparanase, or for developing drugs for those
CC heparanase-associated conditions. The vasculopathy is atherosclerosis,
CC restenosis or aneurysm. The cancerous condition is a solid cancer or a
CC non-solid cancer. The non-solid cancer is a hematopoietic malignancy
CC selected from acute lymphocytic leukaemia (ALL), acute myelogenous
CC leukaemia, chronic lymphocytic leukaemia (CLL), chronic myelogenous
CC leukaemia (CMML), myelodysplastic syndrome (MDS), mast cell leukaemia,
CC Hodgkin's disease, non-Hodgkin's lymphomas, Burkitt's lymphoma and
CC multiple myeloma. The solid cancer is selected from tumours in lip and
CC oral cavity, pharynx, larynx, paranasal sinuses, major salivary glands,
CC thyroid gland, oesophagus, stomach, small intestine, colon, colorectum,
CC anal canal, liver, gallbladder, extrahepatic bile ducts, ampulla of
CC Vater, exocrine pancreas, lung, pleural mesothelioma, soft tissue
CC sarcoma, carcinoma and malignant melanoma of the skin, breast, vulva,
CC vagina, cervix uteri, ovary, fallopian tube, gestational trophoblastic
CC tumours, penis, prostate, testis, kidney, renal pelvis, ureter, urinary
CC bladder, urethra, carcinoma of the eyelid, carcinoma of the conjunctiva,
CC retinoblastoma, carcinoma of the conjunctiva, malignant melanoma of the uvea,
CC lacrimal gland, carcinoma of the lacrimal gland, sarcoma of the orbit,
CC brain, spinal cord, vascular system, haemangiosarcoma and Kaposi's
CC sarcoma. The present sequence is human heparanase epitope.
XX
SQ Sequence 14 AA;
Query Match 28.4%; Score 33.5; DB 8; Length 14;
Best Local Similarity 72.7%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
OY 14 HYYLN-NGATR 23
DB 4 HYYLNGRTATR 14
RESULT 9
ADR78183
ID ADR78183 standard; peptide; 14 AA.
XX
AC ADR78183;
XX
DT 13-JAN-2005 (first entry)
XX
DE Functional peptide epitope of human heparanase, pep10.
XX
KM Antibody; epitope; heparanase; pathological condition; angiogenesis;
KM cell proliferation; cancerous condition; tumour cell invasion;
KM metastatic disease; heparanase-related disorder; inflammatory disorder;
KM wound; scar; vasculopathy; autoimmune condition; renal disease;
KM cytoskeletal; antiinflammatory; vulnery; antiarteriosclerotic;
KM vasotropic; immunosuppressive; nephrotropic; antidiabetic; human.
XX
OS Homo sapiens.
XX
PN US2004213789-A1.
XX
PD 28-OCT-2004.
XX
PF 22-AUG-2003; 2003US-00645659.
XX
PR 02-SEP-1997; 97US-00922170.
PR 01-MAY-1998; 98US-00071739.
PR 04-NOV-1998; 98US-00186200.
PR 19-FEB-2003; 2003US-00368044.

XX PA (VACO/) YACOBV-ZEEVI O.
 PA (PERE/) PERETZ T.
 PA (MIRO/) MIRON D.
 PA (SHLO/) SHLOMI Y.
 PA (PECK/) PECKER I.
 PA (AYAL/) AYAL-HERSHKOVITZ M.
 PA (FEIN/) FEINSTEIN E.
 PA (GELD/) GELDER J M V.
 PA (VLAD/) VLADAVSKY I.
 PA (FRIE/) FRIEDMANN Y.
 XX PI Yacoby-Zeevi O, Peretz T, Miron D, Shlomi Y, Pecker I;
 PI Ayal-Hershkovitz M, Feinstein E, Gelder JMV, Vladavsky I;
 PI Friedmann Y;
 XX DR WPI: 2004-774790/76.
 XX DR
 PT New neutralizing monoclonal anti-heparanase antibodies, useful for
 PT detecting, treating or preventing cancer, inflammatory or autoimmune
 PT disorder, wound, atherosclerosis, restenosis, or diabetic nephropathy.
 XX
 PS Claim 67; SEQ ID NO 10; 68bp; English.
 XX
 CC The invention relates to an isolated antibody or antibody portion capable
 CC of specifically binding to or elicited by at least one epitope of a
 CC heparanase protein, where the heparanase protein is at least 60%
 CC homologous to any of the 6 sequences given as SEQ ID NOS:1-5 or 11, and
 CC where at least one epitope comprises a sequence at least 70% homologous
 CC to any of the sequences given as SEQ ID NOS: 6-10. Also disclosed are (a)
 CC a hybridoma cell line comprising a cell line for producing the monoclonal
 CC antibody, (b) a method for detecting, treating or preventing a
 CC pathological condition or a heparanase-related disorder or condition in a
 CC subject, (c) a method for monitoring the state of a heparanase-related
 CC disorder or condition in a subject, and (d) a pharmaceutical composition
 CC comprising the isolated anti-heparanase antibody or antibody portion and
 CC a pharmaceutical carrier. The antibody, method, and composition are
 CC useful for detecting, treating, preventing or monitoring a pathological
 CC condition, e.g. angiogenesis, cell proliferation, a cancerous condition
 CC (blood, breast, bladder, rectum, stomach, cervix, ovarian, colon, renal,
 CC or prostate cancer), tumor cell proliferation, invasion of circulating
 CC tumor cells, or a metastatic disease, or a heparanase-related disorder
 CC or condition, e.g. an inflammatory disorder, wound, scar, vasculopathy
 CC (atherosclerosis, restenosis, or aneurysm), autoimmune condition, or
 CC renal disease or disorder (diabetic nephropathy, glomerulosclerosis,
 CC nephrotic syndrome, minimal change nephrotic syndrome, or a renal cell
 CC carcinoma) in a mammal. This sequence represents a functional peptide
 CC epitope of human heparanase.
 CC
 XX
 SQ Sequence 14 AA;
 Query Match 28.4%; Score 33.5; DB 8; Length 14;
 Best Local Similarity 72.7%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 Oy 14 HYYLN-NGATR 23
 Db 4 HYYLNGRTATR 14
 RESULT 10
 AEA42432
 ID AEA42432 standard; peptide; 14 AA.
 XX
 AC AEA42432;
 XX
 DT 28-JUL-2005 (first entry)
 XX
 DE Human heparanase epitope peptide SEQ ID NO:10.
 XX
 KW antibody; heparanase; antiinflammatory; vulnery; immunosuppressive;
 KW antiangiogenic; cytostatic; antiarteriosclerotic; vasotropic;
 KW inflammation; wound healing; scarring; vasculopathy; autoimmune disease;

KW angiogenesis disorder; cancer; tumor; metastasis; epitope.
 XX
 OS Homo sapiens.
 XX
 FN AU2004201462-A1.
 XX
 PD 06-MAY-2004.
 XX
 PE 08-APR-2004; 2004AU-00201462.
 XX
 PR 08-APR-2004; 2004AU-00201462.
 XX
 PA (INSI-) INSIGHT BIOPHARMACEUTICALS LTD.
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
 XX
 PI Vladavsky I, Pecker I, Mimon M, Gilboa A, Miron D, Moskowitz H;
 PI Shlomi Y, Peleg Y, Yacoby-Zeevi O, Ayal-Hershkovitz M, Ben-Artzi H;
 PI Feinstein E;
 XX
 DR WPI: 2005-173343/19.
 XX
 PT Novel isolated antibody capable of specifically binding to epitope of
 PT heparanase protein, useful for preventing and creating heparanase-related
 PT disorder such as inflammatory disorder, scars, autoimmune conditions or
 PT angiogenesis.
 XX
 PS Claim 7; SEQ ID NO 10; 260bp; English.
 XX
 CC The invention relates to an isolated antibody or its portion (i) capable
 CC of specifically binding to an epitope of a heparanase protein. Also
 CC described: (1) a cell line (ii) for producing a monoclonal antibody or
 CC its portion, comprising a cell line for producing (1); (2) a
 CC pharmaceutical composition comprising (1) and a carrier; and (3) an
 CC affinity medium (iii) for binding human heparanase polypeptides,
 CC comprising (1) immobilized to a chemically inert, insoluble carrier. (1)
 CC useful for treating a subject suffering from a pathological condition,
 CC which involves administering (1) to the subject. (1) is useful for
 CC preventing and treating heparanase-related disorder or condition chosen
 CC from inflammatory disorder, wound, scar, vasculopathy, autoimmune
 CC condition, angiogenesis, cell proliferation, cancerous condition, tumor
 CC cell proliferation, invasion of circulating tumor cells and metastatic
 CC disease. (1) is useful for detecting the presence of heparanase
 CC polypeptide in a sample. (1) is useful for detecting heparanase-related
 CC disease or condition in a subject such as vertebrate, preferably mammal
 CC e.g., human. The heparanase-related disorder or condition further
 CC includes renal disease or disorder chosen from diabetic nephropathy,
 CC glomerulosclerosis, nephrotic syndrome, minimal change nephrotic syndrome
 CC and renal cell carcinoma. The present sequence represents a human
 CC heparanase epitope peptide, which is used in the exemplification of the
 CC present invention.
 CC
 XX
 SQ Sequence 14 AA;
 Query Match 28.4%; Score 33.5; DB 9; Length 14;
 Best Local Similarity 72.7%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 Oy 14 HYYLN-NGATR 23
 Db 4 HYYLNGRTATR 14
 RESULT 11
 ADU70841
 ID ADU70841 standard; peptide; 15 AA.
 XX
 AC ADU70841;
 XX
 DT 10-FEB-2005 (first entry)
 XX
 DE Human heparanase peptide SEQ ID NO:526.
 XX
 KW enzyme; heparinase; vaccine; human leukocyte antigen; HLA;

KM immunostimulant; cytostatic; immune disorder; metastasis.
 XX Homo sapiens.
 XX EPI479764-A1.
 XX
 XX 24-NOV-2004.
 XX
 XX 19-MAY-2003; 2003EP-00011038.
 XX
 XX 19-MAY-2003; 2003EP-00011038.
 XX
 XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 XX (UYHE-) UNIV HEIDELBERG RUPRECHT-KARLS.
 XX
 XX Schirmacher V, Beckhove P, Sommerfeldt N;
 XX WPI; 2005-014847/02.
 XX
 XX New heparanase nonapeptide that binds to a human leukocyte antigen (HLA)
 PT molecule or its functional derivative, useful for preparing a medicament
 PT for inducing an immune response or for treating metastatic tumors.
 PT
 XX
 XX Disclosure; SEQ ID NO 526; 269pp; English.
 XX
 CC The invention relates to a novel heparanase peptide that binds to a human
 CC leukocyte antigen (HLA) molecule, where the peptide is a nonapeptide, or
 CC its functional derivative. A peptide of the invention has immunostimulant
 CC and cytostatic activity, and is used in a vaccine. The heparinase peptide
 CC is useful for preparing a medicament which induces an immune response or
 CC for treating metastatic tumors. The present sequence represents a
 CC heparinase peptide of the invention.
 CC
 XX
 XX Sequence 15 AA;
 SQ
 Query Match 28.4%; Score 33.5; DB 9; Length 15;
 Best Local Similarity 72.7%; Pred. No. 1.4e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 OY 14 HYYLN-NGATR 23
 DB 3 HYYLNGRTATR 13
 RESULT 12
 ADU71059
 ID ADU71059 standard; peptide; 15 AA.
 XX
 XX ADU71059;
 AC
 XX 10-FEB-2005 (first entry)
 DT
 XX
 DE Human heparanase peptide SEQ ID NO:744.
 XX
 XX enzyme; heparinase; vaccine; human leukocyte antigen; HLA;
 KM immunostimulant; cytostatic; immune disorder; metastasis.
 XX
 XX Homo sapiens.
 OS
 XX EPI479764-A1.
 XX
 XX 24-NOV-2004.
 XX
 XX 19-MAY-2003; 2003EP-00011038.
 XX
 XX 19-MAY-2003; 2003EP-00011038.
 XX
 XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 XX (UYHE-) UNIV HEIDELBERG RUPRECHT-KARLS.
 XX
 XX Schirmacher V, Beckhove P, Sommerfeldt N;
 XX WPI; 2005-014847/02.
 XX

XX
 XX New heparanase nonapeptide that binds to a human leukocyte antigen (HLA)
 PT molecule or its functional derivative, useful for preparing a medicament
 PT for inducing an immune response or for treating metastatic tumors.
 PT
 XX
 XX Disclosure; SEQ ID NO 744; 269pp; English.
 XX
 CC The invention relates to a novel heparanase peptide that binds to a human
 CC leukocyte antigen (HLA) molecule, where the peptide is a nonapeptide, or
 CC its functional derivative. A peptide of the invention has immunostimulant
 CC and cytostatic activity, and is used in a vaccine. The heparinase peptide
 CC is useful for preparing a medicament which induces an immune response or
 CC for treating metastatic tumors. The present sequence represents a
 CC heparinase peptide of the invention.
 CC
 XX
 XX Sequence 15 AA;
 SQ
 Query Match 28.4%; Score 33.5; DB 9; Length 15;
 Best Local Similarity 72.7%; Pred. No. 1.4e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 OY 14 HYYLN-NGATR 23
 DB 5 HYYLNGRTATR 15
 RESULT 13
 ADU71060
 ID ADU71060 standard; peptide; 15 AA.
 XX
 XX ADU71060;
 AC
 XX 10-FEB-2005 (first entry)
 DT
 XX
 DE Human heparanase peptide SEQ ID NO:745.
 XX
 XX enzyme; heparinase; vaccine; human leukocyte antigen; HLA;
 KM immunostimulant; cytostatic; immune disorder; metastasis.
 XX
 XX Homo sapiens.
 OS
 XX EPI479764-A1.
 XX
 XX 24-NOV-2004.
 XX
 XX 19-MAY-2003; 2003EP-00011038.
 XX
 XX 19-MAY-2003; 2003EP-00011038.
 XX
 XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 XX (UYHE-) UNIV HEIDELBERG RUPRECHT-KARLS.
 XX
 XX Schirmacher V, Beckhove P, Sommerfeldt N;
 XX WPI; 2005-014847/02.
 XX
 XX New heparanase nonapeptide that binds to a human leukocyte antigen (HLA)
 PT molecule or its functional derivative, useful for preparing a medicament
 PT for inducing an immune response or for treating metastatic tumors.
 PT
 XX
 XX Disclosure; SEQ ID NO 745; 269pp; English.
 XX
 CC The invention relates to a novel heparanase peptide that binds to a human
 CC leukocyte antigen (HLA) molecule, where the peptide is a nonapeptide, or
 CC its functional derivative. A peptide of the invention has immunostimulant
 CC and cytostatic activity, and is used in a vaccine. The heparinase peptide
 CC is useful for preparing a medicament which induces an immune response or
 CC for treating metastatic tumors. The present sequence represents a
 CC heparinase peptide of the invention.
 CC
 XX
 XX Sequence 15 AA;
 SQ
 Query Match 28.4%; Score 33.5; DB 9; Length 15;

Best Local Similarity 72.7%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 14 HYYLN-NGATR 23
DB 4 HYYLNGRTATR 14

RESULT 14

ADU71272
ID ADU71272 standard; peptide; 15 AA.

XX ADU71272;

DT 10-FEB-2005 (first entry)

XX Human heparanase peptide SEQ ID NO:957.

XX enzyme; heparinase; vaccine; human leukocyte antigen; HLA;

KW immunostimulant; cytostatic; immune disorder; metastasis.

XX Homo sapiens.

PN EPI479764-A1.

PD 24-NOV-2004.

PF 19-MAY-2003; 2003EP-00011038.

PR 19-MAY-2003; 2003EP-00011038.

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

PA (UYHE-) UNIV HEIDELBERG RUPRECHT-KARLS.

XX Schirmacher V, Beckhove P, Sommerfeldt N;

DR WPI; 2005-014847/02.

XX New heparanase nonapeptide that binds to a human leukocyte antigen (HLA)

PT molecule or its functional derivative, useful for preparing a medicament

PS for inducing an immune response or for treating metastatic tumors.

XX Disclosure; SEQ ID NO 957; 269pp; English.

XX The invention relates to a novel heparanase peptide that binds to a human

CC leukocyte antigen (HLA) molecule, where the peptide is a nonapeptide, or

CC its functional derivative. A peptide of the invention has immunostimulant

CC and cytostatic activity, and is used in a vaccine. The heparinase peptide

CC is useful for preparing a medicament which induces an immune response or

CC for treating metastatic tumors. The present sequence represents a

CC heparinase peptide of the invention.

XX Sequence 15 AA:

QY Query Match 28.4%; Score 33.5; DB 9; Length 15;

DB Best Local Similarity 72.7%; Pred. No. 1.4e+02;

XX Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 14 HYYLN-NGATR 23

DB 1 HYYLNGRTATR 11

RESULT 15

ADU70927
ID ADU70927 standard; peptide; 15 AA.

XX ADU70927;

DT 10-FEB-2005 (first entry)

XX Human heparanase peptide SEQ ID NO:612.

KW enzyme; heparinase; vaccine; human leukocyte antigen; HLA;

XX immunostimulant; cytostatic; immune disorder; metastasis.

XX Homo sapiens.

PN EPI479764-A1.

PD 24-NOV-2004.

PF 19-MAY-2003; 2003EP-00011038.

PR 19-MAY-2003; 2003EP-00011038.

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

PA (UYHE-) UNIV HEIDELBERG RUPRECHT-KARLS.

XX Schirmacher V, Beckhove P, Sommerfeldt N;

DR WPI; 2005-014847/02.

XX New heparanase nonapeptide that binds to a human leukocyte antigen (HLA)

PT molecule or its functional derivative, useful for preparing a medicament

PS for inducing an immune response or for treating metastatic tumors.

XX Disclosure; SEQ ID NO 612; 269pp; English.

XX The invention relates to a novel heparanase peptide that binds to a human

CC leukocyte antigen (HLA) molecule, where the peptide is a nonapeptide, or

CC its functional derivative. A peptide of the invention has immunostimulant

CC and cytostatic activity, and is used in a vaccine. The heparinase peptide

CC is useful for preparing a medicament which induces an immune response or

CC for treating metastatic tumors. The present sequence represents a

CC heparinase peptide of the invention.

XX Sequence 15 AA:

QY Query Match 28.4%; Score 33.5; DB 9; Length 15;

DB Best Local Similarity 72.7%; Pred. No. 1.4e+02;

XX Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 14 HYYLN-NGATR 23

DB 2 HYYLNGRTATR 12

RESULT 16

ADY27047
ID ADY27047 standard; peptide; 15 AA.

XX ADY27047;

DT 05-MAY-2005 (first entry)

XX Heparanase inhibitor peptide #6.

XX Heparanase; cancer; neoplasm; inflammation; cardiovascular disease;

XX neurological disease; viral infection; infection; cytostatic;

XX antiinflammatory; cardiovascular-gen.; neuroprotective; virucide;

XX heparanase modulator; enzyme purification.

XX Synthetic.

XX WO2005016227-A2.

XX 24-FEB-2005.

XX 12-AUG-2004; 2004WO-IL000744.

XX 14-AUG-2003; 2003US-049480P.

XX 12-JAN-2004; 2004US-0535492P.

XX (INSI-) INSIGHT BIOPHARMACEUTICALS LTD.

PI Van-Gelder JW, Miron D;
 XX WPI; 2005-182203/19.
 XX
 PT Regulating heparanase activity, useful for treating heparanase-associated
 PT diseases (e.g. cancer, inflammation, cardiovascular diseases,
 PT neurological diseases or viral diseases) comprises modulating heparanase
 PT activation.
 XX
 PS Claim 56; SEQ ID NO 21; 211pp; English.
 XX
 CC The invention relates to a method of regulating heparanase activity in a
 CC tissue or regulating a biological process depending at least in part on
 CC heparanase activity comprising modulating heparanase activation. The
 CC heparanase also relates to methods of treating a heparanase- or heparin
 CC binding protein-associated disease or disorder in a subject, a
 CC pharmaceutical composition for use in the treatment of a heparanase-
 CC associated disease or disorder comprising a therapeutic amount of an
 CC agent capable of modulating heparanase activation and a pharmaceutical
 CC carrier or diluent, a method of identifying a protease activator of
 CC heparanase, a protease substrate mimetic comprising a peptide
 CC representing a subset or all substrate residues or cleavage sites of
 CC human heparanase or an equivalent non-human heparanase, a method of
 CC producing active heparanase and a method of modulating an adhesion
 CC activity of heparanase. The composition and methods are useful for
 CC modulating heparanase activation and for treating heparanase-associated
 CC diseases or disorders such as cancer, inflammation, cardiovascular
 CC diseases, neurological diseases or viral infections. This sequence
 CC represents a heparanase inhibitor peptide used in the scope of the
 CC invention.
 CC
 XX
 SO Sequence 15 AA;

Query Match 28.4%; Score 33.5; DB 9; Length 15;
 Best Local Similarity 72.7%; Pred. No. 1.4e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 14 HYYLN-NGATR 23
 |||||
 Db 5 HYYLNGRTATR 15

RESULT 17
 ADU70969
 ID ADU70969 standard; peptide; 15 AA.
 XX
 AC ADU70969;
 XX
 DT 10-FEB-2005 (first entry)
 XX
 DE Human heparanase peptide SEQ ID NO:654.
 XX
 KM enzyme; heparinase; vaccine; human leukocyte antigen; HLA;
 KM immunostimulant; cytostatic; immune disorder; metastasis.
 XX
 OS Homo sapiens.
 XX
 PN EP1479764-A1.
 XX
 PD 24-NOV-2004.
 XX
 PF 19-MAY-2003; 2003EP-00011038.
 XX
 PR 19-MAY-2003; 2003EP-00011038.
 XX
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 PA (UYHE-) UNIV HEIDELBERG RUPRECHT-KARLS.
 PI Schirmacher V, Beckhove P, Sommerfeldt N;
 PT WPI; 2005-014847/02.
 XX
 XX New heparanase nonapeptide that binds to a human leukocyte antigen (HLA)

PT molecule or its functional derivative, useful for preparing a medicament
 PT for inducing an immune response or for treating metastatic tumors.
 XX
 PS Disclosure; SEQ ID NO 654; 269pp; English.
 XX
 CC The invention relates to a novel heparanase peptide that binds to a human
 CC leukocyte antigen (HLA) molecule, where the peptide is a nonapeptide, or
 CC its functional derivative. A peptide of the invention has immunostimulant
 CC and cytostatic activity, and is used in a vaccine. The heparinase peptide
 CC is useful for preparing a medicament which induces an immune response or
 CC for treating metastatic tumors. The present sequence represents a
 CC heparinase peptide of the invention.
 CC
 XX
 SO Sequence 15 AA;

Query Match 28.0%; Score 33; DB 9; Length 15;
 Best Local Similarity 54.5%; Pred. No. 1.7e+02;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 12 TMHYYLNGAT 22
 ||:|
 Db 5 TMHYYLNGRT 15

RESULT 18
 ADU71114
 ID ADU71114 standard; peptide; 15 AA.
 XX
 AC ADU71114;
 XX
 DT 10-FEB-2005 (first entry)
 XX
 DE Human heparanase peptide SEQ ID NO:799.
 XX
 KM enzyme; heparinase; vaccine; human leukocyte antigen; HLA;
 KM immunostimulant; cytostatic; immune disorder; metastasis.
 XX
 OS Homo sapiens.
 XX
 PN EP1479764-A1.
 XX
 PD 24-NOV-2004.
 XX
 PF 19-MAY-2003; 2003EP-00011038.
 XX
 PR 19-MAY-2003; 2003EP-00011038.
 XX
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 PA (UYHE-) UNIV HEIDELBERG RUPRECHT-KARLS.
 PI Schirmacher V, Beckhove P, Sommerfeldt N;
 PT WPI; 2005-014847/02.
 XX
 XX New heparanase nonapeptide that binds to a human leukocyte antigen (HLA)
 PT molecule or its functional derivative, useful for preparing a medicament
 PT for inducing an immune response or for treating metastatic tumors.
 XX
 PS Disclosure; SEQ ID NO 799; 269pp; English.
 XX
 CC The invention relates to a novel heparanase peptide that binds to a human
 CC leukocyte antigen (HLA) molecule, where the peptide is a nonapeptide, or
 CC its functional derivative. A peptide of the invention has immunostimulant
 CC and cytostatic activity, and is used in a vaccine. The heparinase peptide
 CC is useful for preparing a medicament which induces an immune response or
 CC for treating metastatic tumors. The present sequence represents a
 CC heparinase peptide of the invention.
 CC
 XX
 SO Sequence 15 AA;

Query Match 28.0%; Score 33; DB 9; Length 15;
 Best Local Similarity 54.5%; Pred. No. 1.7e+02;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 12 TMHYLNNGAT 22
| : | | |
DB 3 TMHHYLNNGRT 13

RESULT 19

AAB06372 ID AAB06372 standard; peptide: 17 AA.

AC AAB06372;

DT 17-OCT-2000 (first entry)

XX Randomised V13 sequence of anti-VEGF antibody variant Y0229-9.

XX Humanised; antibody variant; phage display; randomised library;
KM cytosarctic; antiarthritic; antipsoriatic; antidiabetic; antiinflammatory;
KM antiarteriosclerotic; vascular endothelial growth factor; VEGF;
KM breast cancer; lung cancer; retinoblastoma; rheumatoid arthritis;
KM psoriasis; atherosclerosis; diabetic retinopathy;
KM complementarity determining region; CDR.

XX Homo sapiens.
OS Synthetic.

XX WO200029584-A1.

XX 25-MAY-2000.

XX 16-NOV-1999; 99WO-US027153.

XX 18-NOV-1998; 98US-0108945P.

XX (GETH) GENENTECH INC.

XX Chen YM, Lowman HB, Muller Y;

XX WPI: 2000-387797/33.

XX Antibody variants with higher binding affinity than native antibodies
PT useful for diagnosis, prevention and treatment of neoplastic and non-
PT neoplastic diseases comprises amino acid insertion in hypervariable
PT region.

XX Example 1; Page 58; 110pp; English.

XX The present sequence is the randomised V13 region of a variant of anti-
CC vascular endothelial growth factor (VEGF) antibody from phage library YC-
CC 95. A large number of antibody variants containing randomised peptide
CC inserts within the complementarity determining regions (CDRs) were
CC prepared by phage display. Libraries were subjected to eight rounds of
CC selection to isolate variants with an antigen binding affinity at least
CC two-fold stronger than the binding affinity of parent antibody for the
CC target VEGF antibody. The anti-VEGF antibody variants may be useful in
CC diagnostic assays for detecting expression of VEGF in cells, tissue or
CC serum. They may also be used in the prevention and treatment of
CC neoplastic diseases such as breast cancer, lung cancer and
CC retinoblastoma, and non-neoplastic diseases including rheumatoid
CC arthritis, psoriasis, atherosclerosis, and diabetic and other
CC proliferative retinopathies

XX Sequence 17 AA;

QY Query Match 28.0%; Score 33; DB 3; Length 17;
Best Local Similarity 83.3%; Pred. NO. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 HYVLNN 19
| | | | |
DB 3 HYVLND 8

RESULT 20
AAB06381 ID AAB06381 standard; peptide: 18 AA.

AC AAB06381;

DT 17-OCT-2000 (first entry)

XX Randomised V13 sequence of anti-VEGF antibody variant Y0239-8.

XX Humanised; antibody variant; phage display; randomised library;
KM cytosarctic; antiarthritic; antipsoriatic; antidiabetic; antiinflammatory;
KM antiarteriosclerotic; vascular endothelial growth factor; VEGF;
KM breast cancer; lung cancer; retinoblastoma; rheumatoid arthritis;
KM psoriasis; atherosclerosis; diabetic retinopathy;
KM complementarity determining region; CDR.

XX Homo sapiens.
OS Synthetic.

XX WO200029584-A1.

XX 25-MAY-2000.

XX 16-NOV-1999; 99WO-US027153.

XX 18-NOV-1998; 98US-0108945P.

XX (GETH) GENENTECH INC.

XX Chen YM, Lowman HB, Muller Y;

XX WPI: 2000-387797/33.

XX Antibody variants with higher binding affinity than native antibodies
PT useful for diagnosis, prevention and treatment of neoplastic and non-
PT neoplastic diseases comprises amino acid insertion in hypervariable
PT region.

XX Claim 19; Page 59; 110pp; English.

XX The present sequence is the randomised V13 region of a variant of anti-
CC vascular endothelial growth factor (VEGF) antibody from phage library YC-
CC 95. A large number of antibody variants containing randomised peptide
CC inserts within the complementarity determining regions (CDRs) were
CC prepared by phage display. Libraries were subjected to eight rounds of
CC selection to isolate variants with an antigen binding affinity at least
CC two-fold stronger than the binding affinity of parent antibody for the
CC target VEGF antibody. The anti-VEGF antibody variants may be useful in
CC diagnostic assays for detecting expression of VEGF in cells, tissue or
CC serum. They may also be used in the prevention and treatment of
CC neoplastic diseases such as breast cancer, lung cancer and
CC retinoblastoma, and non-neoplastic diseases including rheumatoid
CC arthritis, psoriasis, atherosclerosis, and diabetic and other
CC proliferative retinopathies

XX Sequence 18 AA;

QY Query Match 28.0%; Score 33; DB 3; Length 18;
Best Local Similarity 71.4%; Pred. NO. 2.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 14 HYVLNG 20
| | | | |
DB 3 HYVLRDG 9

RESULT 21

AAB06379 ID AAB06379 standard; peptide: 18 AA.

AC AAB06379;

XX

DT 17-OCT-2000 (first entry)
XX Randomised VH3 sequence of anti-VEGF antibody variant Y0239-6.
DE
XX
KM Humanised; antibody variant; phage display; randomised library;
KM cytostatic; antiarthritic; antipsoriatic; antidiabetic; antiinflammatory;
KM antiarteriosclerotic; vascular endothelial growth factor; VEGF;
KM breast cancer; lung cancer; retinoblastoma; rheumatoid arthritis;
KM psoriasis; atherosclerosis; diabetic retinopathy;
KM complementarity determining region; CDR.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200029584-A1.
XX
PD 25-MAY-2000.
XX
PF 16-NOV-1999; 99WO-US027153.
XX
PR 18-NOV-1998; 98US-0108945P.
XX
PA (GETH) GENENTECH INC.
XX
PI Chen YM, Lowman HB, Muller Y;
XX
DR WPI; 2000-387797/33.
XX
PT Antibody variants with higher binding affinity than native antibodies
PT useful for diagnosis, prevention and treatment of neoplastic and non-
PT neoplastic diseases comprises amino acid insertion in hypervariable
PT region.
XX
PS Example 1; Page 59; 110pp; English.
XX
CC The present sequence is the randomised VH3 region of a variant of anti-
CC vascular endothelial growth factor (VEGF) antibody from phage library YC-
CC 95. A large number of antibody variants containing randomised peptide
CC inserts within the complementarity determining regions (CDRs) were
CC prepared by phage display. Libraries were subjected to eight rounds of
CC selection to isolate variants with an antigen binding affinity at least
CC two-fold stronger than the binding affinity of parent antibody for the
CC target VEGF antibody. The anti-VEGF antibody variants may be useful in
CC diagnostic assays for detecting expression of VEGF in cells, tissue or
CC serum. They may also be used in the prevention and treatment of
CC neoplastic diseases such as breast cancer, lung cancer and
CC retinoblastoma, and non-neoplastic diseases including rheumatoid
CC arthritis, psoriasis, atherosclerosis, and diabetic and other
CC proliferative retinopathies
XX
SQ Sequence 18 AA;
XX
Query Match 28.0%; Score 33; DB 3; Length 18;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 14 HYLLNG 20
DB 3 HYLLKDG 9
XX
RESULT 22
AAB05890
ID AAB05890 standard; peptide; 18 AA.
XX
AC AAB05890;
XX
DT 17-OCT-2000 (first entry)
XX
DE Randomised VH3 sequence of anti-VEGF antibody variant Y0261-4.
XX
KM Humanised; antibody variant; phage display; randomised library;
KM cytostatic; antiarthritic; antipsoriatic; antidiabetic; antiinflammatory;
KM

KM antiarteriosclerotic; vascular endothelial growth factor; VEGF;
KM breast cancer; lung cancer; retinoblastoma; rheumatoid arthritis;
KM psoriasis; atherosclerosis; diabetic retinopathy;
KM complementarity determining region; CDR.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200029584-A1.
XX
PD 25-MAY-2000.
XX
PF 16-NOV-1999; 99WO-US027153.
XX
PR 18-NOV-1998; 98US-0108945P.
XX
PA (GETH) GENENTECH INC.
XX
PI Chen YM, Lowman HB, Muller Y;
XX
DR WPI; 2000-387797/33.
XX
PT Antibody variants with higher binding affinity than native antibodies
PT useful for diagnosis, prevention and treatment of neoplastic and non-
PT neoplastic diseases comprises amino acid insertion in hypervariable
PT region.
XX
PS Example 1; Page 60; 110pp; English.
XX
CC The present sequence is the randomised VH3 region of a variant of anti-
CC vascular endothelial growth factor (VEGF) antibody from phage library YC-
CC 98. A large number of antibody variants containing randomised peptide
CC inserts within the complementarity determining regions (CDRs) were
CC prepared by phage display. Libraries were subjected to eight rounds of
CC selection to isolate variants with an antigen binding affinity at least
CC two-fold stronger than the binding affinity of parent antibody for the
CC target VEGF antibody. The anti-VEGF antibody variants may be useful in
CC diagnostic assays for detecting expression of VEGF in cells, tissue or
CC serum. They may also be used in the prevention and treatment of
CC neoplastic diseases such as breast cancer, lung cancer and
CC retinoblastoma, and non-neoplastic diseases including rheumatoid
CC arthritis, psoriasis, atherosclerosis, and diabetic and other
CC proliferative retinopathies
XX
SQ Sequence 18 AA;
XX
Query Match 28.0%; Score 33; DB 3; Length 18;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 14 HYLLNG 20
DB 3 HYLLKDG 9
XX
RESULT 23
AAB06385
ID AAB06385 standard; peptide; 18 AA.
XX
AC AAB06385;
XX
DT 17-OCT-2000 (first entry)
XX
DE Randomised VH3 sequence of anti-VEGF antibody variant Y0261-2.
XX
KM Humanised; antibody variant; phage display; randomised library;
KM cytostatic; antiarthritic; antipsoriatic; antidiabetic; antiinflammatory;
KM antiarteriosclerotic; vascular endothelial growth factor; VEGF;
KM breast cancer; lung cancer; retinoblastoma; rheumatoid arthritis;
KM psoriasis; atherosclerosis; diabetic retinopathy;
KM complementarity determining region; CDR.
XX
OS Homo sapiens.
XX

OS Synthetic.
XX WO200029584-A1.
XX 25-MAY-2000.
XX 16-NOV-1999; 99WO-US027153.
XX 18-NOV-1998; 98US-0108945P.
XX (GETH) GENENTECH INC.
XX Chen YM, Lowman HB, Muller Y;
XX WPI: 2000-387797/33.
XX
XX Antibody variants with higher binding affinity than native antibodies
XX useful for diagnosis, prevention and treatment of neoplastic and non-
XX neoplastic diseases comprises amino acid insertion in hypervariable
XX region.
XX
XX Example 1; Page 59; 110pp; English.
XX
XX The present sequence is the randomised VH3 region of a variant of anti-
XX vascular endothelial growth factor (VEGF) antibody from phage library YC-
XX 95. A large number of antibody variants containing randomised peptide
XX inserts within the complementarity determining regions (CDRs) were
XX prepared by phage display. Libraries were subjected to eight rounds of
XX selection to isolate variants with an antigen binding affinity at least
XX two-fold stronger than the binding affinity of parent antibody for the
XX target VEGF antibody. The anti-VEGF antibody variants may be useful in
XX diagnostic assays for detecting expression of VEGF in cells, tissue or
XX serum. They may also be used in the prevention and treatment of
XX neoplastic diseases such as breast cancer, lung cancer and
XX retinoblastoma, and non-neoplastic diseases including rheumatoid
XX arthritis, psoriasis, atherosclerosis, and diabetic and other
XX proliferative retinopathies
XX
XX Sequence 18 AA:
SQ
Query Match 28.0%; Score 33; DB 3; Length 18;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 14 HYYLNG 20
DB 3 HYLKDG 9
RESULT 24
ABB94872
ID ABB94872 standard; peptide; 9 AA.
XX ABB94872;
XX
DT 17-JUN-2002 (first entry)
XX
XX CTL epitope HLA peptide SEQ ID NO:401.
XX
XX Human; 158P1H4; chromosome 8q22-q23, 158P1F4; chromosome 8q23; cancer;
XX bladder cancer; immune response; cytotoxic T lymphocyte; CTL; HLA;
XX human leukocyte antigen; helper T lymphocyte; HTL.
XX
XX Homo sapiens.
XX Synthetic.
XX WO200216598-A2.
XX
XX 28-FEB-2002.
XX
XX 22-AUG-2001; 2001WO-US026411.
XX
XX 22-AUG-2000; 2000US-0227098P.
XX

PR 10-APR-2001; 2001US-0282739P.
XX (AGEN-) AGENSYS INC.
XX
XX Chailita-Eid PM, Hubert RS, Raitano AB, Afar DEH, Levin E;
XX Faris M, Ge W, Jakobovits A;
XX WPI: 2002-269357/31.
XX
XX Monitoring 158P1H4 gene products in biological sample from patient who
XX has or is suspected of having cancer, useful for treating cancer,
XX comprises identifying presence of aberrant 158P1H4 gene products in
XX biological sample.
XX
XX Claim 64; Page 155; 209pp; English.
XX
XX The present invention describes a method for monitoring 158P1H4 gene
XX products in a biological sample from a patient who has or is suspected of
XX having cancer. The method comprises determining the status of 158P1H4
XX gene products in a tissue sample from an individual, comparing the status
XX to the status of 158P1H4 gene products in a normal sample, and
XX identifying the presence of aberrant 158P1H4 gene products in the sample.
XX 158P1H4 sequences have cytostatic activity and can be used in vaccine
XX production. 158P1H4 polynucleotides may be used in monitoring genetic
XX abnormalities. The 158P1H4 proteins may be used in assessing the status
XX of 158P1H4 gene products in normal versus cancerous tissues and so
XX elucidating the malignant phenotype, in generating and characterizing
XX domain-specific antibodies, for identifying agents or cellular factors
XX that bind to 158P1H4 or its particular domain, and for generating cancer
XX vaccines. Antibodies against 158P1H4 are useful in diagnostic and
XX prognostic assays, in treating patients with cancer, in generating
XX cytotoxic T lymphocyte (CTL) or helper T lymphocyte (HTL) responses, and
XX as immunological reagents for detecting 158P1H4-expressing cells. The
XX antibodies are particularly useful in bladder cancer diagnostic and
XX prognostic assays, and imaging methodologies. The 158P1H4 gene has been
XX located to chromosome 8q22-q23, and the 158P1H4 gene also described in
XX the present invention has been located to chromosome 8q23. ABL50400 to
XX ABL50429 and ABB94468 to ABB95188 represent sequences used in the
XX exemplification of the present invention
XX
XX Sequence 9 AA:
SQ
Query Match 27.1%; Score 32; DB 5; Length 9;
Best Local Similarity 71.4%; Pred. No. 2e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 8 YVLYTMH 14
DB 2 YVLYSVH 8
RESULT 25
ADU70797
ID ADU70797 standard; peptide; 9 AA.
XX ADU70797;
XX
DT 10-FEB-2005 (first entry)
XX
XX Human heparanase peptide SEQ ID NO:482.
XX
XX enzyme; heparinase; vaccine; human leukocyte antigen; HLA;
XX immunostimulant; cytostatic; immune disorder; metastasis.
XX
XX Homo sapiens.
XX
XX EPI479764-A1.
XX
XX 24-NOV-2004.
XX
XX 19-MAY-2003; 2003EP-00011038.
XX
XX 19-MAY-2003; 2003EP-00011038.
XX

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 PA (UYHE-) UNIV HEIDELBERG RUPRECHT-KARLS.
 XX
 XX Schirmacher V, Beckhove P, Sommerfeldt N;
 XX WPI; 2005-014847/02.
 DR
 XX
 PT New heparanase nonapeptide that binds to a human leukocyte antigen (HLA)
 PT molecule or its functional derivative, useful for preparing a medicament
 PT for inducing an immune response or for treating metastatic tumors.
 XX
 PS Claim 3; SEQ ID NO 482; 269pp; English.
 XX
 CC The invention relates to a novel heparanase peptide that binds to a human
 CC leukocyte antigen (HLA) molecule, where the peptide is a nonapeptide, or
 CC its functional derivative. A peptide of the invention has immunostimulant
 CC and cytostatic activity, and is used in a vaccine. The heparinase peptide
 CC is useful for preparing a medicament which induces an immune response or
 CC for treating metastatic tumors. The present sequence represents a
 CC heparinase peptide of the invention.
 XX
 SQ Sequence 9 AA;

Query March 27.1k; Score 32; DB 9; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 HYYLN 18
 |||||
 Db 4 HYYLN 8

Search completed: January 26, 2006, 07:58:01
 Job time : 81.1207 secs

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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:50:06 : Search time 21.6121 Seconds
(without alignments)
87.985 Million cell updates/sec

Title: US-09-662-293-9

Perfect score: 118
Sequence: 1 DEXNMKYYLYTMHYILNNGATR 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 229350

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5_COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/6_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/PTCUS_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44.5	37.7	20	1	US-08-934-915-13 Sequence 13, Appl
2	34	28.8	20	1	US-08-934-915-58 Sequence 58, Appl
3	33	28.0	17	2	US-09-440-781-44 Sequence 44, Appl
4	33	28.0	18	2	US-09-440-781-51 Sequence 51, Appl
5	33	28.0	18	2	US-09-440-781-53 Sequence 53, Appl
6	33	28.0	18	2	US-09-440-781-57 Sequence 57, Appl
7	33	28.0	18	2	US-09-440-781-87 Sequence 87, Appl
8	32	27.1	17	2	US-09-440-781-65 Sequence 65, Appl
9	32	27.1	17	2	US-09-440-781-84 Sequence 84, Appl
10	32	27.1	18	2	US-09-440-781-35 Sequence 35, Appl
11	31	26.3	12	2	US-10-395-434A-2 Sequence 2, Appl
12	30	25.4	17	2	US-09-440-781-73 Sequence 73, Appl
13	30	25.4	20	1	US-08-934-915-7 Sequence 7, Appl
14	29.5	25.0	20	2	US-09-287-070-9 Sequence 9, Appl
15	29	24.6	9	1	US-08-370-909-10 Sequence 10, Appl
16	29	24.6	9	2	US-09-774-639-201 Sequence 201, Appl
17	29	24.6	12	2	US-09-419-381-14 Sequence 14, Appl
18	29	24.6	15	2	US-08-793-331-13 Sequence 13, Appl
19	29	24.6	17	2	US-09-440-781-19 Sequence 19, Appl
20	29	24.6	17	2	US-09-440-781-85 Sequence 85, Appl
21	29	24.6	17	2	US-09-440-781-92 Sequence 92, Appl
22	29	24.6	18	2	US-09-461-325-279 Sequence 279, Appl
23	29	24.6	18	2	US-10-012-542-579 Sequence 279, Appl
24	29	24.6	18	2	US-10-115-123-279 Sequence 279, Appl
25	29	24.6	21	2	US-09-178-093B-19 Sequence 19, Appl
26	28.5	24.2	19	2	US-09-828-645-6 Sequence 6, Appl
27	28	23.7	6	2	US-09-563-222C-56 Sequence 56, Appl

28	28	23.7	10	1	US-08-077-797A-12 Sequence 12, Appl
29	28	23.7	10	2	US-09-042-428-8 Sequence 8, Appl
30	28	23.7	10	2	US-09-546-013-41 Sequence 41, Appl
31	28	23.7	10	2	US-09-910-706A-8 Sequence 8, Appl
32	28	23.7	11	4	PCT-US94-01238-12 Sequence 12, Appl
33	28	23.7	10	2	US-09-809-517A-21 Sequence 21, Appl
34	28	23.7	16	1	US-08-372-887-15 Sequence 15, Appl
35	28	23.7	17	1	US-08-116-778E-7 Sequence 7, Appl
36	28	23.7	17	1	US-08-438-562-7 Sequence 7, Appl
37	28	23.7	17	1	US-08-483-528B-95 Sequence 95, Appl
38	28	23.7	17	2	US-09-393-385B-106 Sequence 106, Appl
39	28	23.7	17	2	US-09-440-781-66 Sequence 66, Appl
40	28	23.7	17	2	US-09-440-781-90 Sequence 90, Appl
41	28	23.7	17	2	US-09-440-781-91 Sequence 91, Appl
42	28	23.7	17	2	US-10-195-752-106 Sequence 106, Appl
43	27.5	23.3	11	2	US-09-341-982-56 Sequence 56, Appl
44	27.5	23.3	19	2	US-09-828-645-1 Sequence 1, Appl
45	27.5	23.3	20	1	US-08-934-915-28 Sequence 28, Appl
46	27.5	23.3	20	1	US-08-934-915-11 Sequence 31, Appl
47	27	22.9	7	2	US-09-268-992-78 Sequence 78, Appl
48	27	22.9	7	2	US-09-657-474-78 Sequence 78, Appl
49	27	22.9	8	2	US-08-818-655-41 Sequence 41, Appl
50	27	22.9	9	2	US-09-341-982-26 Sequence 26, Appl
51	27	22.9	16	2	US-09-440-781-54 Sequence 54, Appl
52	27	22.9	17	2	US-09-440-781-38 Sequence 38, Appl
53	27	22.9	17	2	US-09-440-781-47 Sequence 47, Appl
54	27	22.9	17	2	US-09-440-781-50 Sequence 50, Appl
55	27	22.9	17	2	US-09-440-781-62 Sequence 62, Appl
56	27	22.9	17	2	US-09-440-781-79 Sequence 79, Appl
57	27	22.9	17	2	US-09-440-781-82 Sequence 82, Appl
58	27	22.9	17	2	US-09-440-781-86 Sequence 86, Appl
59	27	22.9	17	2	US-09-440-781-89 Sequence 89, Appl
60	27	22.9	18	2	US-09-440-781-56 Sequence 56, Appl
61	27	22.9	18	2	US-09-440-781-72 Sequence 72, Appl
62	27	22.9	18	2	US-09-563-222C-55 Sequence 55, Appl
63	27	22.9	19	2	US-09-177-249-142 Sequence 142, Appl
64	27	22.9	19	2	US-09-812-283-142 Sequence 142, Appl
65	26.5	22.5	20	1	US-08-934-915-136 Sequence 136, Appl
66	26.5	22.5	21	2	US-08-652-877-61 Sequence 61, Appl
67	26.5	22.5	21	2	US-08-476-515A-61 Sequence 61, Appl
68	26	22.0	5	2	US-08-981-122-68 Sequence 68, Appl
69	26	22.0	9	2	US-09-935-430-114 Sequence 114, Appl
70	26	22.0	9	2	US-09-935-430-132 Sequence 132, Appl
71	26	22.0	9	2	US-09-935-430-492 Sequence 492, Appl
72	26	22.0	10	2	US-09-462-645C-29 Sequence 29, Appl
73	26	22.0	10	2	US-09-755-330B-119 Sequence 119, Appl
74	26	22.0	10	2	US-09-935-430-157 Sequence 157, Appl
75	26	22.0	10	2	US-09-935-430-621 Sequence 621, Appl
76	26	22.0	10	2	US-10-658-180-119 Sequence 119, Appl
77	26	22.0	17	1	US-08-480-190-168 Sequence 168, Appl
78	26	22.0	17	1	US-08-488-579-168 Sequence 168, Appl
79	26	22.0	17	1	US-08-475-399A-168 Sequence 31, Appl
80	26	22.0	17	2	US-09-440-781-31 Sequence 31, Appl
81	26	22.0	17	2	US-09-440-781-46 Sequence 46, Appl
82	26	22.0	17	2	US-09-440-781-48 Sequence 48, Appl
83	26	22.0	17	2	US-09-440-781-55 Sequence 55, Appl
84	26	22.0	17	2	US-09-440-781-67 Sequence 67, Appl
85	26	22.0	17	2	US-08-077-255A-168 Sequence 168, Appl
86	26	22.0	17	4	PCT-US93-07545-167 Sequence 167, Appl
87	26	22.0	18	1	US-08-480-190-167 Sequence 167, Appl
88	26	22.0	18	1	US-08-488-579-167 Sequence 167, Appl
89	26	22.0	18	2	US-08-475-399A-167 Sequence 167, Appl
90	26	22.0	18	2	US-09-440-781-30 Sequence 30, Appl
91	26	22.0	18	2	US-09-440-781-43 Sequence 43, Appl
92	26	22.0	18	2	US-09-440-781-52 Sequence 52, Appl
93	26	22.0	18	2	US-08-077-255A-167 Sequence 167, Appl
94	26	22.0	18	4	PCT-US93-07545-167 Sequence 167, Appl
95	26	22.0	20	2	US-08-825-852-59 Sequence 59, Appl
96	26	22.0	20	2	US-09-052-888-60 Sequence 60, Appl
97	26	22.0	20	2	US-09-643-997-250 Sequence 250, Appl
98	26	22.0	20	2	US-09-480-884A-250 Sequence 250, Appl
99	26	22.0	20	2	US-09-542-115A-250 Sequence 250, Appl
100	26	22.0	20	2	US-09-606-421B-250 Sequence 250, Appl

ALIGNMENTS

RESULT 1
US-08-934-915-13
Sequence 13, Application US/08934915
Patent No. 5932412
GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEI-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. FOUCH
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-13

Query Match 37.7%; Score 44.5; DB 1; Length 20;
Best Local Similarity 62.5%; Pred. No. 0.91;
Matches 10; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 2 EXNVMKXYLYTMHYL 17
| | | | | | | | | | | | | | | | | | | | | |
Db 5 EDNVMYVYVWT-HIYL 19

RESULT 2
US-08-934-915-58
Sequence 58, Application US/08934915
Patent No. 5932412
GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEI-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,

TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. FOUCH
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-58

Query Match 28.8%; Score 34; DB 1; Length 20;
Best Local Similarity 35.3%; Pred. No. 48;
Matches 6; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 DEXNVMKXYLYTMHYL 17
: | | | | | : | | | | |
Db 4 KDNQMTYVWDSVYVM 20

RESULT 3
US-09-440-781-44
Sequence 44, Application US/09440781
Patent No. 6632926
GENERAL INFORMATION:
APPLICANT: Yvonne Man-yea Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 44
LENGTH: 17
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: artificial
LOCATION: 1-17
OTHER INFORMATION: variant CDR sequence
US-09-440-781-44

Query Match 28.0%; Score 33; DB 2; Length 17;
Best Local Similarity 83.3%; Pred. No. 58;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 HYYLNN 19
| | | | |

Db 3 HYLND 8

RESULT 4

US-09-440-781-51
; Sequence 51, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-ye Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 51
; LENGTH: 18
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-18
; OTHER INFORMATION: variant CDR sequence
US-09-440-781-51

Query Match 28.0%; Score 33; DB 2; Length 18;
Best Local Similarity 71.4%; Pred. No. 62;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 14 HYLNDG 20
|||:|
Db 3 HYLKDG 9

RESULT 5

US-09-440-781-53
; Sequence 53, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-ye Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 53
; LENGTH: 18
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-18
; OTHER INFORMATION: variant CDR sequence
US-09-440-781-53

Query Match 28.0%; Score 33; DB 2; Length 18;
Best Local Similarity 71.4%; Pred. No. 62;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 14 HYLNDG 20
|||:|
Db 3 HYLKDG 9

RESULT 6

US-09-440-781-57
; Sequence 57, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-ye Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16

NUMBER OF SEQ ID NOS: 99

SEQ ID NO 57
; LENGTH: 18
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-18
; OTHER INFORMATION: variant CDR sequence
US-09-440-781-57

Query Match 28.0%; Score 33; DB 2; Length 18;
Best Local Similarity 71.4%; Pred. No. 62;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 14 HYLNDG 20
|||:|
Db 3 HYLKDG 9

RESULT 7

US-09-440-781-87
; Sequence 87, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-ye Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 87
; LENGTH: 18
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-18
; OTHER INFORMATION: variant CDR sequence
US-09-440-781-87

Query Match 28.0%; Score 33; DB 2; Length 18;
Best Local Similarity 71.4%; Pred. No. 62;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 14 HYLNDG 20
|||:|
Db 3 HYLKDG 9

RESULT 8

US-09-440-781-65
; Sequence 65, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-ye Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 65
; LENGTH: 17
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-17
; OTHER INFORMATION: variant CDR sequence
US-09-440-781-65

Query Match 27.1%; Score 32; DB 2; Length 17;
Best Local Similarity 71.4%; Pred. No. 85;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 14 HYYLNG 20
Db 3 HYYORNG 9

RESULT 9

US-09-440-781-84
; Sequence 84, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-yea Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 84
; LENGTH: 17
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-17
; OTHER INFORMATION: variant CDR sequence
US-09-440-781-84

Query Match 27.1%; Score 32; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 HYYLN 18
Db 3 HYYLN 7

RESULT 10

US-09-440-781-35
; Sequence 35, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-yea Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 35
; LENGTH: 18
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-18
; OTHER INFORMATION: variant CDR sequence
US-09-440-781-35

Query Match 27.1%; Score 32; DB 2; Length 18;
Best Local Similarity 71.4%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 14 HYYLNG 20
Db 3 HYYORNG 9

RESULT 11

US-10-395-434A-2
; Sequence 2, Application US/10395434A
; Patent No. 6939948
; GENERAL INFORMATION:
; APPLICANT: Ferrone, Soldano

; TITLE OF INVENTION: GD2 Peptide Mimics
; FILE REFERENCE: 03551.0092
; CURRENT APPLICATION NUMBER: US/10/395,434A
; CURRENT FILING DATE: 2003-03-24
; PRIORITY APPLICATION NUMBER: US 60/366,558
; PRIORITY FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 2
; LENGTH: 12
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: J8C peptide mimic for GD2
US-10-395-434A-2

Query Match 26.3%; Score 31; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 83;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 11 YTMHY 16
Db 5 YTLHY 10

RESULT 12

US-09-440-781-73
; Sequence 73, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-yea Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 73
; LENGTH: 17
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-17
; OTHER INFORMATION: variant CDR sequence
US-09-440-781-73

Query Match 25.4%; Score 30; DB 2; Length 17;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 14 HYYLN 19
Db 3 HYYND 8

RESULT 13

US-08-934-915-7
; Sequence 7, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILNER, JOAKIM
; APPLICANT: DILNER, LENA
; APPLICANT: CHENG, HWEI-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA

COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foulch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-7

Query Match 25.4%; Score 30; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 NWKXYVLYTMHY 15
| | | | |
| | | | |
Db 7 NTMDYVWTVDY 18

RESULT 14
US-09-287-070-9
Sequence 9, Application US/09287070A
Patent No. 6495139
GENERAL INFORMATION:
APPLICANT: Tuomanen, Elaine
APPLICANT: Gosink, Knoosneh
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF NOVEL
TITLE OF INVENTION: PNEUMOCOCCAL CHOLINE BINDING PROTERINS CPGC, AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USES THEREOF
FILE REFERENCE: 1340-1-024cid
CURRENT APPLICATION NUMBER: US/09/287,070A
CURRENT FILING DATE: 1999-04-06
EARLIER APPLICATION NUMBER: 09/196,389
EARLIER FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 20
TYPE: PRT
ORGANISM: Pneumococcus
US-09-287-070-9

Query Match 25.0%; Score 29.5; DB 2; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 15 YVLN-NGA 21
| | | | |
| | | | |
Db 10 YVLNANGA 17

RESULT 15
US-08-370-909-10

Sequence 10, Application US/08370909
Patent No. 5843648
GENERAL INFORMATION:
APPLICANT: ROBBINS, PAUL F.; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: D15 AND TYROSINASE
TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC
TITLE OF INVENTION: AND THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCIT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,909
FILING DATE: 10-JAN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPT
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
MOLECULE TYPE: PEPTIDE
US-08-370-909-10

Query Match 24.6%; Score 29; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 MHYLN 18
| | | | |
| | | | |
Db 3 MHYVS 8

RESULT 16
US-09-774-639-201
Sequence 201, Application US/09774639
Patent No. 6806351
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 90 Human Secreted Proteins
FILE REFERENCE: P2013P1
CURRENT APPLICATION NUMBER: US/09/774,639
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 371
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 201
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (9)
OTHER INFORMATION: Xaa equals stop translation

US-09-774-639-201

Query Match 24.6%; Score 29; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 MHYYLN 18
Db 1 MHYYLN 6

RESULT 17
US-09-419-381-14
; Sequence 14, Application US/09419381
; Patent No. 6747135
; GENERAL INFORMATION:
; APPLICANT: No. 6747135a1, Garry P.
; APPLICANT: Rozinov, Michael N.
; TITLE OF INVENTION: Fluorescent Dye Binding Peptides
; FILE REFERENCE: A65681-1/DUS/RMS/DSS
; CURRENT APPLICATION NUMBER: US/09/419,381
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: 60/104,465
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-419-381-14

Query Match 24.6%; Score 29; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 YTMHY 16
Db 4 YSMHY 9

RESULT 18
US-08-793-331-13
; Sequence 13, Application US/08793331
; Patent No. 6071877
; GENERAL INFORMATION:
; APPLICANT: DELCLOUSE, ARMELLE
; APPLICANT: THIERY, ISABELLE
; TITLE OF INVENTION: NEW POLYPEPTIDES HAVING A TOXIC ACTIVITY AGAINST
; TITLE OF INVENTION: INSECTS OF THE DIPTERA FAMILY
; FILE REFERENCE: 0660-0116-0 PCT
; CURRENT APPLICATION NUMBER: US/08/793,331
; CURRENT FILING DATE: 1997-05-13
; EARLIER APPLICATION NUMBER: PCT/FR95/01116
; EARLIER FILING DATE: 1995-08-24
; EARLIER APPLICATION NUMBER: FR 94/10299
; EARLIER FILING DATE: 1994-08-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: JEG66
US-08-793-331-13

Query Match 24.6%; Score 29; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 MHYYLN 18
Db 1 MHYYGN 6

RESULT 19
US-09-440-781-49
; Sequence 49, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-yea Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 49
; LENGTH: 17
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-17
; OTHER INFORMATION: variant CDR sequence
US-09-440-781-49

Query Match 24.6%; Score 29; DB 2; Length 17;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 HYYLN 18
Db 3 HYYVN 7

RESULT 20
US-09-440-781-85
; Sequence 85, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-yea Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 85
; LENGTH: 17
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-17
; OTHER INFORMATION: variant CDR sequence
US-09-440-781-85

Query Match 24.6%; Score 29; DB 2; Length 17;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 HYYLN 18
Db 3 HYYVN 7

RESULT 21
US-09-440-781-92
; Sequence 92, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-yea Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1

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; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 92
; LENGTH: 17
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-17
; OTHER INFORMATION: variant CDR sequence
US-09-440-781-92

Query Match      24.6%; Score 29; DB 2; Length 17;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      14 HYYLN 18
       |||:|
       3 HYYVN 7

Db
RESULT 22
US-09-461-325-279
; Sequence 279, Application US/09461325A
; Patent No. 6475753
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/09/461,325A
; EARLIER FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: PCT/US99/13418
; EARLIER FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,507
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,508
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,509
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,510
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/090,112
; EARLIER FILING DATE: 1998-06-22
; EARLIER APPLICATION NUMBER: 60/090,113
; EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 279
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-461-325-279

Query Match      24.6%; Score 29; DB 2; Length 18;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      12 TMHYLYNN 19
       |||:|
       1 TVLFYLYNN 8

Db
RESULT 23
US-10-012-542-279
; Sequence 279, Application US/10012542
; Patent No. 6627741
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/10/012,542
; CURRENT FILING DATE: 2001-12-12
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; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 279
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-123-279

Query Match      24.6%; Score 29; DB 2; Length 18;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      12 TMHYLYNN 19
       |||:|
       1 TVLFYLYNN 8

Db
RESULT 24
US-10-115-123-279
; Sequence 279, Application US/10115123
; Patent No. 6774216
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029G30APID2
; CURRENT APPLICATION NUMBER: US/10/115,123
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: PCT/US99/13418
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090,113
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 279
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-123-279

Query Match      24.6%; Score 29; DB 2; Length 18;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      12 TMHYLYNN 19
       |||:|
       1 TVLFYLYNN 8

Db
RESULT 25
```

```

US-09-178-093B-19
; Sequence 19, Application US/09178093B
; Patent No. 6660846
; GENERAL INFORMATION:
; APPLICANT: Robert H. Edwards
; APPLICANT: Richard J. Reimer
; APPLICANT: Steve L. McIntire
; APPLICANT: Erik M. Jorgenson
; APPLICANT: Kim Schuke
; TITLE OF INVENTION: Vesicular Amino Acid Transported
; FILE REFERENCE: 2002-0005.30
; CURRENT APPLICATION NUMBER: US/09/178, 093B
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/063, 012
; PRIOR FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO: 19
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-178-093B-19

```

```

Query Match      24.6%; Score 29; DB 2; Length 21;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      11 YTMHYVYLN 19
         |||:|
Db       12 YTSHIFLPN 20

```

Search completed: January 26, 2006, 08:07:01
Job time : 22.7787 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 08:04:12 ; Search time 74.75 Seconds
(without alignments)
128.563 Million cell updates/sec

Title: US-09-662-293-9

Perfect score: 118
Sequence: 1 DEKVMKKYVLYTMHYLNNGATR 23

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 369445

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA Main:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	30.5	20	4	US-10-346-198-43
2	35	29.7	16	3	US-09-880-748-2216
3	35	29.7	16	4	US-10-293-418-2216
4	34	28.8	12	4	US-10-467-758-35
5	34	28.8	16	3	US-09-880-748-2259
6	34	28.8	16	4	US-10-293-418-2259
7	34	28.8	21	4	US-10-086-814-30
8	34	28.8	21	4	US-10-086-814-36
9	34	28.8	21	4	US-10-424-599-147622
10	33.5	28.4	14	4	US-10-723-502-10
11	33.5	28.4	14	4	US-10-645-659-10
12	33.5	28.4	15	5	US-10-916-598-21
13	33	28.0	17	4	US-10-624-153-41
14	33	28.0	18	4	US-10-624-153-51
15	33	28.0	18	4	US-10-624-153-53
16	33	28.0	18	4	US-10-624-153-57
17	33	28.0	18	4	US-10-624-153-87
18	33	28.0	18	4	US-10-624-153-87
19	32	27.1	9	3	US-09-935-384-901
20	32	27.1	15	3	US-09-880-748-2909
21	32	27.1	15	6	US-10-293-418-2909
22	32	27.1	15	6	US-11-009-460-104
23	32	27.1	17	4	US-10-624-153-65
24	32	27.1	17	4	US-10-624-153-84
25	32	27.1	18	4	US-10-624-153-85
26	32	27.1	20	3	US-09-880-748-2158
27	32	27.1	20	3	US-09-880-748-2896
			20	3	US-09-880-748-2903

28	32	27.1	20	4	US-10-293-418-2158	Sequence 2158, Ap
29	32	27.1	20	4	US-10-293-418-2896	Sequence 2896, Ap
30	32	27.1	20	4	US-10-293-418-2903	Sequence 2903, Ap
31	31	26.3	15	4	US-10-206-639-234	Sequence 234, App
32	31	26.3	16	3	US-09-880-748-2214	Sequence 2214, Ap
33	31	26.3	16	3	US-09-880-748-2215	Sequence 2215, Ap
34	31	26.3	16	3	US-09-880-748-2217	Sequence 2217, Ap
35	31	26.3	16	3	US-09-880-748-2219	Sequence 2219, Ap
36	31	26.3	16	3	US-09-880-748-2298	Sequence 2298, Ap
37	31	26.3	16	3	US-09-880-748-2316	Sequence 2316, Ap
38	31	26.3	16	4	US-10-293-418-2214	Sequence 2214, Ap
39	31	26.3	16	4	US-10-293-418-2215	Sequence 2215, Ap
40	31	26.3	16	4	US-10-293-418-2217	Sequence 2217, Ap
41	31	26.3	16	4	US-10-293-418-2219	Sequence 2219, Ap
42	31	26.3	16	4	US-10-293-418-2298	Sequence 2298, Ap
43	31	26.3	16	4	US-10-293-418-2316	Sequence 2316, Ap
44	31	26.3	18	5	US-10-734-661A-20	Sequence 20, App
45	31	26.3	20	5	US-10-775-972-562	Sequence 562, App
46	31	26.3	20	5	US-10-922-124-562	Sequence 562, App
47	30.5	25.8	19	3	US-09-748-875-23	Sequence 23, App
48	30.5	25.8	19	3	US-09-298-523B-23	Sequence 23, App
49	30.5	25.8	19	5	US-10-341-201-23	Sequence 23, App
50	30	25.4	9	4	US-10-245-871-489	Sequence 23, App
51	30	25.4	11	4	US-10-253-286-489	Sequence 489, App
52	30	25.4	11	4	US-10-239-313A-266	Sequence 266, App
53	30	25.4	14	4	US-10-245-871-512	Sequence 512, App
54	30	25.4	14	4	US-10-253-286-512	Sequence 512, App
55	30	25.4	14	5	US-10-342-896-1	Sequence 1, App
56	30	25.4	16	4	US-10-001-883-128	Sequence 128, App
57	30	25.4	16	5	US-10-661-156-11	Sequence 11, App
58	30	25.4	17	4	US-10-661-156-205	Sequence 205, App
59	30	25.4	17	4	US-10-245-871-513	Sequence 513, App
60	30	25.4	17	4	US-10-253-286-513	Sequence 513, App
61	30	25.4	17	4	US-10-624-153-73	Sequence 73, App
62	30	25.4	19	3	US-09-880-748-2811	Sequence 2811, Ap
63	30	25.4	19	4	US-10-293-418-2811	Sequence 2811, Ap
64	30	25.4	19	4	US-10-413-943-13	Sequence 53, App
65	30	25.4	20	4	US-10-396-073-22	Sequence 22, App
66	29.5	25.0	20	3	US-09-748-875-18	Sequence 18, App
67	29.5	25.0	20	3	US-09-748-875-20	Sequence 20, App
68	29.5	25.0	20	3	US-09-748-875-27	Sequence 27, App
69	29.5	25.0	20	3	US-09-748-875-28	Sequence 28, App
70	29.5	25.0	20	3	US-09-748-875-31	Sequence 31, App
71	29.5	25.0	20	3	US-09-748-875-32	Sequence 32, App
72	29.5	25.0	20	3	US-09-748-875-33	Sequence 33, App
73	29.5	25.0	20	3	US-09-287-070-9	Sequence 9, App
74	29.5	25.0	20	3	US-09-298-523B-18	Sequence 18, App
75	29.5	25.0	20	3	US-09-298-523B-20	Sequence 20, App
76	29.5	25.0	20	3	US-09-298-523B-27	Sequence 27, App
77	29.5	25.0	20	3	US-09-298-523B-28	Sequence 28, App
78	29.5	25.0	20	3	US-09-298-523B-32	Sequence 32, App
79	29.5	25.0	20	3	US-09-298-523B-33	Sequence 33, App
80	29.5	25.0	20	4	US-10-243-977-9	Sequence 9, App
81	29.5	25.0	20	5	US-10-341-201-18	Sequence 18, App
82	29.5	25.0	20	5	US-10-341-201-27	Sequence 27, App
83	29.5	25.0	20	5	US-10-341-201-28	Sequence 28, App
84	29.5	25.0	20	5	US-10-341-201-32	Sequence 32, App
85	29.5	25.0	20	5	US-10-341-201-33	Sequence 33, App
86	29.5	25.0	20	5	US-10-341-201-33	Sequence 33, App
87	29.5	25.0	20	5	US-10-341-201-33	Sequence 33, App
88	29.5	25.0	20	5	US-10-341-201-33	Sequence 33, App
89	29.5	25.0	20	5	US-10-341-201-33	Sequence 33, App
90	29.5	25.0	20	5	US-10-341-201-33	Sequence 33, App
91	29.5	25.0	20	5	US-10-341-201-33	Sequence 33, App
92	29.5	25.0	20	5	US-10-341-201-33	Sequence 33, App
93	29.5	25.0	20	5	US-10-341-201-33	Sequence 33, App
94	29.5	25.0	20	5	US-10-341-201-33	Sequence 33, App
95	29.5	25.0	20	5	US-10-341-201-33	Sequence 33, App
96	29.5	25.0	20	5	US-10-341-201-33	Sequence 33, App
97	29.5	25.0	20	5	US-10-341-201-33	Sequence 33, App
98	29.5	25.0	20	5	US-10-341-201-33	Sequence 33, App
99	29.5	25.0	20	5	US-10-341-201-33	Sequence 33, App
100	29.5	25.0	20	5	US-10-341-201-33	Sequence 33, App

ALIGNMENTS

RESULT 1

US-10-346-198-43
; Sequence 43, Application US/10346198
; Publication No. US20040043485A1
; GENERAL INFORMATION:
; APPLICANT: WESSLER, SUSAN R.
; APPLICANT: JIANG, NING
; APPLICANT: BAO, ZHIRONG
; APPLICANT: ZHANG, XIAOYU
; APPLICANT: EDY, SEAN R.
; TITLE OF INVENTION: TRANSPOSABLE ELEMENTS IN RICE AND METHODS OF USE
; FILE REFERENCE: 18465-0018
; CURRENT APPLICATION NUMBER: US/10/346,198
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: 60/337,409
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-346-198-43

Query Match 30.5% Score 36; DB 4; Length 20;
Best Local Similarity 63.6% Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 10 YTMHYLYLNG 20
|||
Db 7 LYNTGYLYLNG 17

RESULT 2

US-09-880-748-2216
; Sequence 2216, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2216
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2216

Query Match 29.7% Score 35; DB 3; Length 16;
Best Local Similarity 71.4% Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 11 YTMHYLYL 17
|:|
Db 9 YVLHYLYL 15

RESULT 3

US-10-293-418-2216
; Sequence 2216, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2216
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2216

Query Match 29.7% Score 35; DB 4; Length 16;
Best Local Similarity 71.4% Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 11 YTMHYLYL 17
|:|
Db 9 YVLHYLYL 15

RESULT 4

US-10-467-758-35
; Sequence 35, Application US/10467758
; Publication No. US20040132108A1
; GENERAL INFORMATION:
; APPLICANT: Hupp, Theodore
; APPLICANT: Dornan, David
; TITLE OF INVENTION: Screening Method and Agents
; FILE REFERENCE: 9013.54
; CURRENT APPLICATION NUMBER: US/10/467,758
; CURRENT FILING DATE: 2003-08-13
; PRIOR APPLICATION NUMBER: PCT/GB02/00640
; PRIOR FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: GB 0103508.8
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-467-758-35

Query Match 28.8% Score 34; DB 4; Length 12;
Best Local Similarity 50.0% Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 11 YTMHYLYLNGAT 22
|:|:|
Db 9 YVLHYLYLNGAT 15

Db 1 FPFHYWMDIAT 12

RESULT 5

US-09-880-748-2259
; Sequence 2259, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2259
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2259

Query Match 28.8%; Score 34; DB 3; Length 16;

Best Local Similarity 83.3%; Pred. No. 2.1e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 YTMHY 16
| | | | |
Db 9 YVWHY 14

RESULT 6

US-10-293-418-2259
; Sequence 2259, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2259
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2259

Query Match

28.8%; Score 34; DB 4; Length 16;

Best Local Similarity 83.3%; Pred. No. 2.1e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 YTMHY 16
| | | | |
Db 9 YVWHY 14

RESULT 7

US-10-086-814-30
; Sequence 30, Application US/10086814
; Publication No. US20030092632A1
; GENERAL INFORMATION:; APPLICANT: Dragic, Tatjana
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 61010-AB-1
; CURRENT APPLICATION NUMBER: US/10/086,814
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (9)..(9)
; OTHER INFORMATION: SULFATATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (13)..(13)
; OTHER INFORMATION: SULFATATION
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (21)..(21)
; OTHER INFORMATION: BIOTIN
US-10-086-814-30

Query Match

28.8%; Score 34; DB 4; Length 21;

Best Local Similarity 41.7%; Pred. No. 2.8e+02;

Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 10 LYTMHYLLNNGA 21
.:.:.:.:
Db 8 IYDINYTSEGA 19

RESULT 8

US-10-086-814-36
; Sequence 36, Application US/10086814
; Publication No. US20030092632A1
; GENERAL INFORMATION:; APPLICANT: Dragic, Tatjana
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 61010-AB-1
; CURRENT APPLICATION NUMBER: US/10/086,814
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (9)..(9)
; OTHER INFORMATION: PHOSPHORYLATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (13)..(13)

```

; OTHER INFORMATION: PHOSPHORYLATION
;
; FEATURE:
;
; NAME/KEY: BINDING
;
; LOCATION: (21)..(21)
;
; OTHER INFORMATION: BIOTIN
;
US-10-086-814-36

```

Query Match	28.8%	Score 34	DB 4	Length 21
Best Local Similarity	41.7%	Pred. No. 2.8e+02		
Matches	5	Conservative	4	Mismatches 3
				Indels 0
				Gaps 0

```
QY      10 LYTMHYLLNGA 21
          :|::||: ||
Db       8 IYDINYTSEGA 19
```

```

RESULT 9
US-10-424-599-147622
Sequence 147622, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 147622
LENGTH: 21
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_104320C.1 pep
US-10-424-599-147622

```

Query Match	28.8%;	Score 34;	DB 4;	Length 21;
Best Local Similarity	35.3%;	Pred. No. 2.8e+02;		
Matches	6;	Conservative	5;	Mismatches 4;
				Indels 2;
				Gaps 1

QY	4	NVMMXYVLVTMHY--YLIN	18
	: : : :		
Db	2	NLNRYFINFTLHYISYFN	18

```

1      RESULT 10
2      US-10-722-502-10
3      Sequence 10, Application US/10722502
4      Publication No. US20040170631A1
5      GENERAL INFORMATION:
6      APPLICANT: Yacoby-Zeevi, Oron
7      APPLICANT: Pereetz, Tuvia
8      APPLICANT: Miron, Daphna
9      APPLICANT: Shlomi, Yinon
10     APPLICANT: Pecker, Itis
11     APPLICANT: Ayal-Hershkovitz, Maly
12     APPLICANT: Feinstein, Elena
13     APPLICANT: Van Gelder, Joel M.
14     APPLICANT: Vlodavsky, Israel
15     APPLICANT: Friedmann, Yael
16     TITLE OF INVENTION: HEPARANASE ACTIVITY NEUTRALIZING ANTI- HEPARANASE MONOCLONAL
17     ANTIBODIES
18     TITLE OF INVENTION: ANTIBODY AND OTHER ANTI-HEPARANASE ANTIBODIES
19     FILE REFERENCE: 26872
20     CURRENT APPLICATION NUMBER: US/10/722,502
21     CURRENT FILING DATE: 2003-11-28
22     NUMBER OF SEQ ID NOS: 11
23     SOFTWARE: PatentIn version 3.2
24     SEQ ID NO 10
25     LENGTH: 14
26     TYPE: PRT
27

```

```

; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Functional peptide epitope of heparanases
US-10-722-502-10

```

Query Match	28.4%	Score 33.5;	DB 4;	Length 14;
Best Local Similarity	72.7%	Pred. No. 2.2e+02;		
Matches	8;	Conservative	0;	Mismatches 2;
				Indels 1;
				Gaps 1

QY	14	HYLLN-NGATR	23
Db	4	HYLLNGRTATR	14

```

; RESULT 11
; US-10-645-659-10
; Sequence 10, Application US/10645659
; Publication No. US20040213789A1
; GENERAL INFORMATION:
; APPLICANT: Yacoby-Zeevi, Oron
; APPLICANT: Peretz, Tuvia
; APPLICANT: Miron, Daphna
; APPLICANT: Shloml, Yimon
; APPLICANT: Pecker, Itis
; APPLICANT: Ayal-Hershkovitz, Macy
; APPLICANT: Vlodavsky, Israel
; APPLICANT: Friedmann, Yael
; TITLE OF INVENTION: HEPARANASE ACTIVITY NEUTRALIZING ANTI- HEPARANASE MONOCLONAL ANTIBODY AND OTHER ANTI-HEPARANASE ANTIBODIES
; FILE REFERENCE: 26128
; CURRENT APPLICATION NUMBER: US/10/645,659
; CURRENT FILING DATE: 2003-08-22
; NUMBER OF SEQ. ID NOS.: 11
; SOFTWARE: PatentIn version 3.2
; SEQ. ID NO 10
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Functional peptide epitope of heparanase
; US-10-645-659-10

```

Query Match	28.4%	Score 33.5;	DB 4;	Length 14;
Best Local Similarity	72.7%	Pred. No. 2.2e+02;		
Matches	8;	Conservative	0;	Mismatches 2;
				Indels 1;
				Gaps 1

QY	14	HYLLN-NGATR	23
Db	4	HYLLNGRTATR	14

```

RESULT 12
US-10-916-598-21
Sequence 21, Application US/10916598
Publication No. US2005004213A1
GENERAL INFORMATION:
APPLICANT: Van Gelder, Joel M.
APPLICANT: Miron, Daphna
TITLE OF INVENTION: 27413
FILE REFERENCE: METHODS AND PHARMACEUTICAL COMPOSITIONS FOR MODULATING HEPARANASE
ACTIVATION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/916,598
CURRENT FILING DATE: 2004-08-12
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.2
SEQ ID NO 21
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-10-916-598-21

```


Query Match 28.4%; Score 33.5; DB 5; Length 15;
Best Local Similarity 72.7%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 14 HYYLNN-NGATR 23
Db 5 HYYLNGRTATR 15

RESULT 13

US-10-624-153-44
; Sequence 44, Application US/10624153
; Publication No. US20040086502A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, YVONNE M.
; APPLICANT: LOWMAN, HENRY B.
; APPLICANT: MULLER, YVES
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1C1
; CURRENT APPLICATION NUMBER: US/10/624,153
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: US 09/440,781
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: US 60/108,945
; PRIOR FILING DATE: 1998-11-18
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 44
; LENGTH: 17
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
; NAME/KEY: artificial
; LOCATION: 1-17
; OTHER INFORMATION: variant CDR sequence
US-10-624-153-44

Query Match 28.0%; Score 33; DB 4; Length 17;
Best Local Similarity 83.3%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 HYYLNN 19
Db 3 HYYLND 8

RESULT 14

US-10-624-153-51
; Sequence 51, Application US/10624153
; Publication No. US20040086502A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, YVONNE M.
; APPLICANT: LOWMAN, HENRY B.
; APPLICANT: MULLER, YVES
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1C1
; CURRENT APPLICATION NUMBER: US/10/624,153
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: US 09/440,781
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: US 60/108,945
; PRIOR FILING DATE: 1998-11-18
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 51
; LENGTH: 18
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
; NAME/KEY: artificial
; LOCATION: 1-18

OTHER INFORMATION: variant CDR sequence
US-10-624-153-51

Query Match 28.0%; Score 33; DB 4; Length 18;
Best Local Similarity 71.4%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 14 HYYLNG 20
Db 3 HYYLKDQ 9

RESULT 15

US-10-624-153-53
; Sequence 53, Application US/10624153
; Publication No. US20040086502A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, YVONNE M.
; APPLICANT: LOWMAN, HENRY B.
; APPLICANT: MULLER, YVES
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1C1
; CURRENT APPLICATION NUMBER: US/10/624,153
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: US 09/440,781
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: US 60/108,945
; PRIOR FILING DATE: 1998-11-18
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 53
; LENGTH: 18
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
; NAME/KEY: artificial
; LOCATION: 1-18
; OTHER INFORMATION: variant CDR sequence
US-10-624-153-53

Query Match 28.0%; Score 33; DB 4; Length 18;
Best Local Similarity 71.4%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 14 HYYLNG 20
Db 3 HYYLKDQ 9

RESULT 16

US-10-624-153-57
; Sequence 57, Application US/10624153
; Publication No. US20040086502A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, YVONNE M.
; APPLICANT: LOWMAN, HENRY B.
; APPLICANT: MULLER, YVES
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1C1
; CURRENT APPLICATION NUMBER: US/10/624,153
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: US 09/440,781
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: US 60/108,945
; PRIOR FILING DATE: 1998-11-18
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 57
; LENGTH: 18
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized

FEATURE:
NAME/KEY: artificial
LOCATION: 1-18
OTHER INFORMATION: variant CDR sequence
US-10-624-153-57

Query March 28.0%; Score 33; DB 4; Length 18;
Best Local Similarity 71.4%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 14 HYYLNG 20
|||:|
Db 3 HYYLKD 9

RESULT 17
US-10-624-153-87
Sequence 87, Application US/10624153
Publication No. US20040086502A1
GENERAL INFORMATION:
APPLICANT: CHEN, YVONNE M.
APPLICANT: LOWMAN, HENRY B.
APPLICANT: MULLER, YVES
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1C1
CURRENT APPLICATION NUMBER: US/10/624,153
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: US 09/440,781
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: US 60/108,945
PRIOR FILING DATE: 1998-11-18
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 87
LENGTH: 18
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
FEATURE:
NAME/KEY: artificial
LOCATION: 1-18
OTHER INFORMATION: variant CDR sequence
US-10-624-153-87

Query Match 28.0%; Score 33; DB 4; Length 18;
Best Local Similarity 71.4%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 14 HYYLNG 20
|||:|
Db 3 HYYLKD 9

RESULT 18
US-09-935-384-401
Sequence 401, Application US/09935384
Publication No. US20030166526A1
GENERAL INFORMATION:
APPLICANT: CHALLITA-ETD, PIA
APPLICANT: HUBERT, RENE
APPLICANT: RAITANO, ARTHUR
APPLICANT: APAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: PARIS, MARY
APPLICANT: GE, WANGMAO
APPLICANT: JAKOBOVITZ, AYA
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
TITLE OF INVENTION: OTHER CANCERS
FILE REFERENCE: 51158-20033.00
CURRENT APPLICATION NUMBER: US/09/935,384
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227,098

PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 783
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 401
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-935-384-401

Query March 27.1%; Score 32; DB 3; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 YVLYTMH 14
|||:|
Db 2 YVLYSVH 8

RESULT 19
US-09-880-748-2909
Sequence 2909, Application US/09880748
Publication No. US20030058937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2909
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-2909

Query Match 27.1%; Score 32; DB 3; Length 15;
Best Local Similarity 33.3%; Pred. No. 4e+02;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 8 YVLYTMHYYLNN 19
||:|:|:|
Db 4 YIMTAHYYDS 15

RESULT 20
US-10-293-418-2909
Sequence 2909, Application US/10293418
Publication No. US20030229396A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 2909
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-2909

Query Match 27.1% Score 32; DB 4; Length 15;
Best Local Similarity 33.3% Pred. No. 4e+02;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 8 VVLYTMHYLYNN 19
DB 4 YIMTAHYIDS 15

RESULT 21
US-11-009-460-104
Sequence 104, Application US/11009460
Publication No. US20050181459A1
GENERAL INFORMATION:
APPLICANT: BAKER, Matthew
APPLICANT: CARTER, Francis J.
APPLICANT: GRAHAM
TITLE OF INVENTION: METHOD FOR MAPPING AND ELIMINATING
TITLE OF INVENTION: T-CELL EPTOPES
FILE REFERENCE: MER-135
CURRENT APPLICATION NUMBER: US/11/009,460
CURRENT FILING DATE: 2004-12-10
PRIOR APPLICATION NUMBER: PCT/EP03/06110
PRIOR FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: EP02012919.3
PRIOR FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 127
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 104
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Potential T-cell Epitopes
US-11-009-460-104

Query Match 27.1% Score 32; DB 6; Length 15;
Best Local Similarity 75.0% Pred. No. 4e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 16 YLNGATR 23
DB 6 YLNGPQR 13

RESULT 22
US-10-624-153-65
Sequence 65, Application US/10624153
Publication No. US20040086502A1
GENERAL INFORMATION:
APPLICANT: CHEN, YVONNE M.
APPLICANT: LOWMAN, HENRY B.
APPLICANT: MULLER, YVES
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1C1
CURRENT APPLICATION NUMBER: US/10/624,153
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: US 09/440,781

PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: US 60/108,945
PRIOR FILING DATE: 1998-11-18
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 65
LENGTH: 17
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
FEATURE:
NAME/KEY: artificial
LOCATION: 1-17
OTHER INFORMATION: variant CDR sequence
US-10-624-153-65

Query Match 27.1% Score 32; DB 4; Length 17;
Best Local Similarity 71.4% Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 14 HYLYNG 20
DB 3 HYQYNG 9

RESULT 23
US-10-624-153-84
Sequence 84, Application US/10624153
Publication No. US20040086502A1
GENERAL INFORMATION:
APPLICANT: CHEN, YVONNE M.
APPLICANT: LOWMAN, HENRY B.
APPLICANT: MULLER, YVES
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1C1
CURRENT APPLICATION NUMBER: US/10/624,153
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: US 09/440,781
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: US 60/108,945
PRIOR FILING DATE: 1998-11-18
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 84
LENGTH: 17
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
FEATURE:
NAME/KEY: artificial
LOCATION: 1-17
OTHER INFORMATION: variant CDR sequence
US-10-624-153-84

Query Match 27.1% Score 32; DB 4; Length 17;
Best Local Similarity 100.0% Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 HYLYN 18
DB 3 HYLYN 7

RESULT 24
US-10-624-153-35
Sequence 35, Application US/10624153
Publication No. US20040086502A1
GENERAL INFORMATION:
APPLICANT: CHEN, YVONNE M.
APPLICANT: LOWMAN, HENRY B.
APPLICANT: MULLER, YVES
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1C1

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: CURRENT APPLICATION NUMBER: US/10/624,153
: CURRENT FILING DATE: 2003-07-21
: PRIOR APPLICATION NUMBER: US 09/440,781
: PRIOR FILING DATE: 1999-11-16
: PRIOR APPLICATION NUMBER: US 60/108,945
: PRIOR FILING DATE: 1998-11-18
: NUMBER OF SEQ ID NOS: 99
: SEQ ID NO 35
: LENGTH: 18
: TYPE: PRT
: ORGANISM: artificial sequence
: FEATURE:
: OTHER INFORMATION: sequence is synthesized
: FEATURE:
: NAME/KEY: artificial
: LOCATION: 1-18
: OTHER INFORMATION: variant CDR sequence
US-10-624-153-35

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```

Query Match 27.1%; Score 32; DB 4; Length 18;
Best Local Similarity 71.4%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 14 HYUNLNG 20
|||
Db 3 HYQNEG 9

```

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RESULT 25
US-09-880-748-2158
: Sequence 2158, Application US/09880748
: Publication No. US2003005937A1
: GENERAL INFORMATION:
: APPLICANT: Ruben et al.
: TITLE OF INVENTION: Antibodies that Immunospecifically Bind Bvys
: FILE REFERENCE: PF523
: CURRENT APPLICATION NUMBER: US/09/880,748
: CURRENT FILING DATE: 2001-06-15
: PRIOR APPLICATION NUMBER: 60/212,210
: PRIOR FILING DATE: 2000-06-15
: PRIOR APPLICATION NUMBER: 60/240,816
: PRIOR FILING DATE: 2000-10-17
: PRIOR APPLICATION NUMBER: 60/276,248
: PRIOR FILING DATE: 2001-03-16
: PRIOR APPLICATION NUMBER: 60/277,379
: PRIOR FILING DATE: 2001-03-21
: PRIOR APPLICATION NUMBER: 60/293,499
: PRIOR FILING DATE: 2001-05-25
: NUMBER OF SEQ ID NOS: 3239
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 2158
: LENGTH: 20
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-880-748-2158

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Query Match 27.1%; Score 32; DB 3; Length 20;
Best Local Similarity 71.4%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 15 YYLNNGA 21
|||
Db 11 YYIGNGA 17

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Search completed: January 26, 2006, 08:38:36
Job time : 75.75 secs

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OM protein - protein search, using sw model1

Run on: January 26, 2006, 08:05:12 : Search time 4.36207 Seconds
(without alignments)
57.099 Million cell updates/sec

Title: US-09-662-293-9
Perfect score: 118
Sequence: 1 DEXNMVKKVLYTMHYLNNGATR 23

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 37628

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA New:*
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3: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubppa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	29.7	16	7	US-11-054-515-2216 Sequence 2216, Ap
2	34	28.8	16	7	US-11-054-515-2259 Sequence 2259, Ap
3	32	27.1	13	6	US-10-511-559-255 Sequence 255, App
4	32	27.1	13	6	US-10-511-559-256 Sequence 256, App
5	32	27.1	13	6	US-10-511-559-257 Sequence 257, App
6	32	27.1	15	6	US-10-511-559-75 Sequence 75, Appl
7	32	27.1	15	7	US-11-054-515-2309 Sequence 2309, Ap
8	32	27.1	20	7	US-11-054-515-2158 Sequence 2158, Ap
9	32	27.1	20	7	US-11-054-515-2896 Sequence 2896, Ap
10	32	27.1	20	7	US-11-054-515-2903 Sequence 2903, Ap
11	31	26.3	16	7	US-11-054-515-2214 Sequence 2214, Ap
12	31	26.3	16	7	US-11-054-515-2215 Sequence 2215, Ap
13	31	26.3	16	7	US-11-054-515-2217 Sequence 2217, Ap
14	31	26.3	16	7	US-11-054-515-2219 Sequence 2219, Ap
15	31	26.3	16	7	US-11-054-515-2298 Sequence 2298, Ap
16	31	26.3	16	7	US-11-054-515-2316 Sequence 2316, Ap
17	30	25.4	9	7	US-11-033-039-489 Sequence 489, App
18	30	25.4	14	7	US-11-033-039-512 Sequence 512, App
19	30	25.4	16	6	US-10-939-890-205 Sequence 205, App
20	30	25.4	17	7	US-11-033-039-513 Sequence 513, App
21	30	25.4	17	7	US-11-033-039-513 Sequence 513, App
22	30	25.4	19	7	US-11-054-515-2811 Sequence 2811, Ap
23	29	24.6	8	6	US-10-986-501-203 Sequence 203, App
24	29	24.6	13	6	US-10-511-559-254 Sequence 254, App
25	29	24.6	16	7	US-11-054-515-2258 Sequence 2258, Ap

26	29	24.6	16	7	US-11-054-515-2260 Sequence 2260, Ap
27	28	24.6	19	7	US-11-054-515-3087 Sequence 3087, Ap
28	28	23.7	16	7	US-11-054-515-2832 Sequence 2832, Ap
29	28	23.7	18	6	US-10-939-890-117 Sequence 117, App
30	28	23.7	20	7	US-11-054-515-2743 Sequence 2743, Ap
31	27	22.9	16	7	US-11-054-515-2257 Sequence 2257, Ap
32	27	22.9	16	7	US-11-054-515-2302 Sequence 2302, Ap
33	27	22.9	16	7	US-11-054-515-2333 Sequence 2333, Ap
34	27	22.9	19	7	US-11-054-515-2928 Sequence 2928, Ap
35	27	22.9	19	7	US-11-148-108-42 Sequence 42, Appl
36	27	22.9	20	6	US-10-485-788A-539 Sequence 539, Appl
37	26	22.0	9	7	US-11-010-748A-78 Sequence 78, Appl
38	26	22.0	9	7	US-11-010-748A-84 Sequence 84, Appl
39	26	22.0	9	7	US-11-010-748A-85 Sequence 85, Appl
40	26	22.0	9	7	US-11-010-748A-127 Sequence 127, App
41	26	22.0	9	7	US-11-010-748A-133 Sequence 133, App
42	26	22.0	9	7	US-11-010-748A-134 Sequence 134, App
43	26	22.0	9	7	US-11-010-748A-193 Sequence 193, App
44	26	22.0	9	7	US-11-010-748A-199 Sequence 199, App
45	26	22.0	9	7	US-11-010-748A-200 Sequence 200, App
46	26	22.0	9	7	US-11-033-039-443 Sequence 443, App
47	26	22.0	14	6	US-10-501-411A-149 Sequence 149, App
48	26	22.0	14	6	US-11-128-440-65 Sequence 65, Appl
49	26	22.0	14	7	US-11-033-039-453 Sequence 453, App
50	26	22.0	15	6	US-10-866-120-4 Sequence 4, Appl
51	26	22.0	16	7	US-11-010-748A-77 Sequence 77, Appl
52	26	22.0	16	7	US-11-010-748A-126 Sequence 126, App
53	26	22.0	16	7	US-11-054-515-2145 Sequence 2145, App
54	26	22.0	16	7	US-11-054-515-2293 Sequence 2293, Ap
55	26	22.0	16	7	US-11-054-515-2336 Sequence 2336, Ap
56	26	22.0	17	7	US-11-010-748A-192 Sequence 192, App
57	26	22.0	20	6	US-10-623-155-250 Sequence 250, App
58	25.5	21.6	17	7	US-11-054-515-2862 Sequence 2862, App
59	25	21.2	5	7	US-11-093-274-3 Sequence 3, Appl1
60	25	21.2	5	7	US-11-223-834-1 Sequence 1, Appl1
61	25	21.2	9	7	US-11-010-748A-90 Sequence 90, Appl
62	25	21.2	9	7	US-11-010-748A-95 Sequence 95, Appl
63	25	21.2	9	7	US-11-010-748A-97 Sequence 97, Appl
64	25	21.2	9	7	US-11-010-748A-139 Sequence 139, App
65	25	21.2	9	7	US-11-010-748A-144 Sequence 144, App
66	25	21.2	9	7	US-11-010-748A-146 Sequence 146, App
67	25	21.2	9	7	US-11-010-748A-205 Sequence 205, App
68	25	21.2	9	7	US-11-010-748A-210 Sequence 210, App
69	25	21.2	9	7	US-11-010-748A-212 Sequence 212, App
70	25	21.2	10	6	US-10-507-662-2 Sequence 2, Appl1
71	25	21.2	14	7	US-11-033-039-336 Sequence 336, App
72	25	21.2	15	6	US-10-501-411A-329 Sequence 329, App
73	25	21.2	15	7	US-10-501-411A-329 Sequence 329, App
74	25	21.2	15	7	US-11-054-515-2734 Sequence 2734, App
75	25	21.2	15	7	US-11-106-332-144 Sequence 144, App
76	25	21.2	16	7	US-11-010-748A-89 Sequence 89, Appl
77	25	21.2	16	7	US-11-010-748A-138 Sequence 138, App
78	25	21.2	16	7	US-11-054-515-2218 Sequence 2218, App
79	25	21.2	16	7	US-11-054-515-2251 Sequence 2251, App
80	25	21.2	16	7	US-11-054-515-2255 Sequence 2255, App
81	25	21.2	17	7	US-11-010-748A-204 Sequence 204, App
82	25	21.2	17	7	US-11-054-515-2871 Sequence 2871, App
83	25	21.2	18	7	US-11-054-515-2748 Sequence 2748, App
84	25	21.2	20	7	US-11-058-735-5 Sequence 5, Appl1
85	25	21.2	21	7	US-11-054-515-2172 Sequence 2172, Ap
86	25	21.2	21	7	US-11-054-515-2972 Sequence 2972, Ap
87	25	21.2	21	7	US-11-058-735-6 Sequence 6, Appl1
88	24	20.3	8	7	US-11-045-024-380 Sequence 380, App
89	24	20.3	8	7	US-11-045-024-4925 Sequence 4925, App
90	24	20.3	8	7	US-11-045-024-8046 Sequence 8046, App
91	24	20.3	8	7	US-11-045-024-10543 Sequence 10543, A
92	24	20.3	9	7	US-11-045-024-8039 Sequence 8039, App
93	24	20.3	9	7	US-11-033-039-465 Sequence 465, App
94	24	20.3	9	7	US-11-033-039-492 Sequence 492, App
95	24	20.3	9	7	US-11-136-079-76 Sequence 76, Appl
96	24	20.3	10	7	US-11-105-268-11 Sequence 11, Appl
97	24	20.3	10	7	US-11-045-024-396 Sequence 396, App
98	24	20.3	10	7	US-11-045-024-4977 Sequence 4977, Ap

99 24 20.3 10 7 US-11-045-024-8057 Sequence 8057, Ap
100 24 20.3 10 7 US-11-045-024-10532 Sequence 10532, A

ALIGNMENTS

RESULT 1

US-11-054-515-2216
; Sequence 2216, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:

APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: PFS23P3
CURRENT APPLICATION NUMBER: US/11/054,515

PRIOR FILING DATE: 2005-02-10

PRIOR APPLICATION NUMBER: 60/543,296

PRIOR FILING DATE: 2004-02-11

PRIOR APPLICATION NUMBER: 60/580,347

PRIOR FILING DATE: 2004-06-18

PRIOR APPLICATION NUMBER: 10/293,418

PRIOR FILING DATE: 2002-11-14

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 09/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 3247

SEQ ID NO 2216

LENGTH: 16

TYPE: PRT

ORGANISM: Homo sapiens

US-11-054-515-2216

Query Match 29.7%; Score 35; DB 7; Length 16;

Best Local Similarity 71.4%; Pred. No. 5.3;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 YTMHYL 17

Db 9 YVLHYL 15

RESULT 2

US-11-054-515-2259

; Sequence 2259, Application US/11054515

; Publication No. US20050255532A1

; GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: PFS23P3

CURRENT APPLICATION NUMBER: US/11/054,515

PRIOR FILING DATE: 2005-02-10

PRIOR APPLICATION NUMBER: 60/543,296

PRIOR FILING DATE: 2004-02-11

PRIOR APPLICATION NUMBER: 60/580,347

PRIOR FILING DATE: 2004-06-18

PRIOR APPLICATION NUMBER: 10/293,418

PRIOR FILING DATE: 2002-11-14

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2259
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2259

Query Match 28.8%; Score 34; DB 7; Length 16;

Best Local Similarity 83.3%; Pred. No. 7.6;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 YTMHY 16

Db 9 YVMHY 14

RESULT 3

US-10-511-559-255

; Sequence 255, Application US/10511559

; Publication No. US20050256304A1

; GENERAL INFORMATION:

APPLICANT: BAKER, Matthew

TITLE OF INVENTION: MODIFIED FACTOR VIII

FILE REFERENCE: MER-133

CURRENT APPLICATION NUMBER: US/10/511,559

PRIOR FILING DATE: 2004-10-15

PRIOR APPLICATION NUMBER: PCT/EP03/04063

PRIOR FILING DATE: 2003-04-17

PRIOR APPLICATION NUMBER: EP 02008712.8

PRIOR FILING DATE: 2002-04-18

PRIOR APPLICATION NUMBER: EP 03006554.4

PRIOR FILING DATE: 2003-03-24

NUMBER OF SEQ ID NOS: 1147

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 255

LENGTH: 13

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Potential Epitope of human Factor VIII

US-10-511-559-255

Query Match 27.1%; Score 32; DB 6; Length 13;

Best Local Similarity 75.0%; Pred. No. 13;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 16 YLNNGATR 23

Db 5 YLNNGPOR 12

RESULT 4

US-10-511-559-256

; Sequence 256, Application US/10511559

; Publication No. US20050256304A1

; GENERAL INFORMATION:

APPLICANT: JONES, Tim

TITLE OF INVENTION: BAKER, Matthew

APPLICANT: BAKER, Matthew

APPLICANT: JONES, J.

```

; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 256
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-256

```

```

Query Match      27.1%; Score 32; DB 6; Length 13;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Oy      16 YLNGGATR 23
        |||||
Db      3 YLNGGPR 10

```

```

RESULT 5
US-10-511-559-257
; Sequence 257, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 257
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-257

```

```

Query Match      27.1%; Score 32; DB 6; Length 13;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Oy      16 YLNGGATR 23
        |||||
Db      2 YLNGGPR 9

```

```

RESULT 6
US-10-511-559-75
; Sequence 75, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew

```

```

; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Epitope of human Factor VIII
US-10-511-559-75

```

```

Query Match      27.1%; Score 32; DB 6; Length 15;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Oy      16 YLNGGATR 23
        |||||
Db      6 YLNGGPR 13

```

```

RESULT 7
US-11-054-515-2909
; Sequence 2909, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2909
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2909

```

```

Query Match      27.1%; Score 32; DB 7; Length 15;
Best Local Similarity 33.3%; Pred. No. 15;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

```

```

Oy      8 YVLYTMHYIYLN 19

```

Db 4 YIMTAHHYIDS 15

RESULT 8
US-11-054-515-2158

Sequence 2158, Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:

APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: PFS23P3

CURRENT APPLICATION NUMBER: US/11/054,515

CURRENT FILING DATE: 2005-02-10

PRIOR APPLICATION NUMBER: 60/543,296

PRIOR FILING DATE: 2004-02-11

PRIOR APPLICATION NUMBER: 60/580,347

PRIOR FILING DATE: 2004-06-18

PRIOR APPLICATION NUMBER: 10/293,418

PRIOR FILING DATE: 2002-11-14

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 09/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 3247

SEQ ID NO 2158

LENGTH: 20

TYPE: PRT

ORGANISM: Homo sapiens

US-11-054-515-2158

Query Match 27.1%; Score 32; DB 7; Length 20;

Best Local Similarity 71.4%; Pred. No. 20;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 15 YLNLNGA 21

Db 11 YLNGGA 17

RESULT 9

US-11-054-515-2896

Sequence 2896, Application US/11054515

Publication No. US20050255532A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: PFS23P3

CURRENT APPLICATION NUMBER: US/11/054,515

CURRENT FILING DATE: 2005-02-10

PRIOR APPLICATION NUMBER: 60/543,296

PRIOR FILING DATE: 2004-02-11

PRIOR APPLICATION NUMBER: 60/580,347

PRIOR FILING DATE: 2004-06-18

PRIOR APPLICATION NUMBER: 10/293,418

PRIOR FILING DATE: 2002-11-14

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 09/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 3247

SEQ ID NO 2896

LENGTH: 20

TYPE: PRT

ORGANISM: Homo sapiens

US-11-054-515-2896

Query Match 27.1%; Score 32; DB 7; Length 20;

Best Local Similarity 71.4%; Pred. No. 20;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 15 YLNLNGA 21

Db 11 YLNGGA 17

RESULT 10

US-11-054-515-2903

Sequence 2903, Application US/11054515

Publication No. US20050255532A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: PFS23P3

CURRENT APPLICATION NUMBER: US/11/054,515

CURRENT FILING DATE: 2005-02-10

PRIOR APPLICATION NUMBER: 60/543,296

PRIOR FILING DATE: 2004-02-11

PRIOR APPLICATION NUMBER: 60/580,347

PRIOR FILING DATE: 2004-06-18

PRIOR APPLICATION NUMBER: 10/293,418

PRIOR FILING DATE: 2002-11-14

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 09/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 3247

SEQ ID NO 2903

LENGTH: 20

TYPE: PRT

ORGANISM: Homo sapiens

US-11-054-515-2903

Query Match 27.1%; Score 32; DB 7; Length 20;

Best Local Similarity 71.4%; Pred. No. 20;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 15 YLNLNGA 21

Db 11 YLNGGA 17

RESULT 11


```
US-11-054-515-2214
; Sequence 2214, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2214
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2214

Query Match      26.3%; Score 31; DB 7; Length 16;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      11 YTMHY 16
      | : |||
Db      9 YVLHY 14

RESULT 12
US-11-054-515-2215
; Sequence 2215, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
```

```
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2215
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2215

Query Match      26.3%; Score 31; DB 7; Length 16;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      11 YTMHY 16
      | : |||
Db      9 YVLHY 14

RESULT 13
US-11-054-515-2217
; Sequence 2217, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2217
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2217

Query Match      26.3%; Score 31; DB 7; Length 16;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      11 YTMHY 16
      | : |||
Db      9 YVLHY 14

RESULT 14
US-11-054-515-2219
; Sequence 2219, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
```

```
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2219
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2219
```

```
Query Match      26.3%; Score 31; DB 7; Length 16;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      11 YTMHY 16
      | : |||
Db      9 YVLHY 14
```

```
RESULT 15
; Sequence 2298, Application US/11/054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
```

```
; SEQ ID NO 2298
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2298
```

```
Query Match      26.3%; Score 31; DB 7; Length 16;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      11 YTMHY 16
      | : |||
Db      9 YVLHY 14
```

```
RESULT 16
US-11-054-515-2316
; Sequence 2316, Application US/11/054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2316
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2316
```

```
Query Match      26.3%; Score 31; DB 7; Length 16;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      11 YTMHY 16
      | : |||
Db      9 YVLHY 14
```

```
RESULT 17
US-11-033-039-489
; Sequence 489, Application US/11/033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPTOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
```

```

; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 489
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-039-489

```

```

Query Match      25.4%; Score 30; DB 7; Length 9;
Best Local Similarity 55.6%; Pred. No. 5.8e+04;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

OY      13 MHYLLNNGA 21
DB      1 MHYVSMDB 9

```

```

RESULT 18
US-11-033-039-512
; Sequence 512, Application US/11033039
; Publication No. US2006002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REF-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; PRIOR FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 512
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: hybrid peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: Ava
US-11-033-039-512

```

```

Query Match      25.4%; Score 30; DB 7; Length 14;
Best Local Similarity 55.6%; Pred. No. 29;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

OY      13 MHYLLNNGA 21
DB      6 MHYVSMDB 14

```

```

RESULT 19
US-10-939-890-11
; Sequence 11, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.

```

```

; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; PRIOR FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 893
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KDR or VEGF/KDR Binding Polypeptide
US-10-939-890-11

```

```

Query Match      25.4%; Score 30; DB 6; Length 16;
Best Local Similarity 71.4%; Pred. No. 33;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

OY      14 HYLLNNG 20
DB      3 HCYLLNNG 9

```

```

RESULT 20
US-10-939-890-205
; Sequence 205, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES

```

```
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; PRIOR FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 205
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-205
```

```
Query Match      25.4%; Score 30; DB 6; Length 16;
Best Local Similarity 71.4%; Pred. No. 33;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      14 HYYLNG 20
      |||:|
Db      3 HCYLHG 9
```

```
RESULT 21
US-11-033-039-513
; Sequence 513, Application US/11033039
; Publication No. US2006002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; PRIOR FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 513
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: hybrid peptide
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: Ava
US-11-033-039-513
```

```
Query Match      25.4%; Score 30; DB 7; Length 17;
Best Local Similarity 55.6%; Pred. No. 35;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      13 HYYLNGA 21
      |||:|
Db      6 HMYVSMDA 14
```

```
RESULT 22
US-11-054-515-2811
; Sequence 2811, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that immunospecifically bind Blys
; FILE REFERENCE: P5523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2811
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2811
```

```
Query Match      25.4%; Score 30; DB 7; Length 19;
Best Local Similarity 38.5%; Pred. No. 39;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      8 YVLYTHMYLNG 20
      |||:|:|
Db      4 YDLITGYVYHHG 16
```

```
RESULT 23
US-10-986-501-203
; Sequence 203, Application US/10986501
; Publication No. US20050244845A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P2C1
; CURRENT APPLICATION NUMBER: US/10/986,501
; PRIOR FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/10/621,363
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/969,730
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
```

```

; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 203
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-986-501-203

```

```

Query Match      24.6%; Score 29; DB 6; Length 8;
Best Local Similarity 83.3%; Pred. NO. 5.8e+04;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      13 MHVYLN 18
      |||||
Db      1 MHVYLN 6

```

```

RESULT 24
US-10-511-559-254
; Sequence 254, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 254
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-254

```

```

Query Match      24.6%; Score 29; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. NO. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      16 YLNG 20
      |||||
Db      7 YLNG 11

```

```

RESULT 25
US-11-054-515-2258
; Sequence 2258, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: P5523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18

```

```

; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2258
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2258

```

```

Query Match      24.6%; Score 29; DB 7; Length 16;
Best Local Similarity 66.7%; Pred. NO. 47;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      11 YTMHY 16
      |||||
Db      9 YTMHY 14

```

Search completed: January 26, 2006, 08:39:06
 Job time : 4.36207 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 26, 2006, 07:48:50 : Search time 11.5 Seconds
(without alignments)
192.434 Million cell updates/sec

Title: US-09-662-293-9

Perfect score: 118

Sequence: 1 DEKNVMKVVLYTMHYLNQATR 23

Scoring table:

BLOSUM62

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 4071

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

PIR 80:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	26.3	15	2	B41868
2	30	25.4	19	1	LFSAP9
3	30	25.4	19	2	B26930
4	30	25.4	21	2	S08590
5	29	24.6	20	2	B60894
6	27	22.9	14	2	PT0254
7	27	22.9	15	2	S12677
8	26	22.0	12	2	G64003
9	26	22.0	14	2	PH1628
10	26	22.0	17	2	S63503
11	25.5	21.6	20	2	S37684
12	25	21.2	10	2	S42282
13	25	21.2	16	2	PH1604
14	24	20.3	14	2	PH1615
15	24	20.3	14	2	S72217
16	24	20.3	14	2	S59495
17	24	20.3	19	2	PT0332
18	24	20.3	20	2	PQ0544
19	23	19.5	13	2	PT0263
20	23	19.5	14	2	PH1601
21	23	19.5	17	2	PH1607
22	23	19.5	18	2	B24735
23	23	19.5	19	2	PH1307
24	23	19.5	20	2	PQ0751
25	22	18.6	11	2	S68352
26	22	18.6	12	2	PH1587
27	22	18.6	13	2	PT0256
28	22	18.6	13	2	PH1593
29	22	18.6	14	2	S39930

30	22	18.6	15	2	JN0730	hypothetical 1.7K
31	22	18.6	17	2	S57991	hydroxyproline-ric
32	22	18.6	17	2	S60454	38K protein 3129 -
33	22	18.6	18	2	S74195	epoxide hydrolase
34	22	18.6	18	2	I46653	T-cell receptor de
35	22	18.6	18	2	A30541	F7-1 fibribial prot
36	22	18.6	19	2	S43960	Ig mu chain V regi
37	22	18.6	19	2	S43657	hsp90 protein homo
38	22	18.6	20	2	PC2248	lambda 112 protein
39	22	18.6	21	2	S23361	protein-lysine K
40	22	17.8	11	2	S42587	cellf protein - Bsc
41	21	17.8	11	2	PT0301	Ig heavy chain CRD
42	21	17.8	14	2	S39931	S-allele-associate
43	21	17.8	15	2	S47367	T-cell antigen rec
44	21	17.8	15	2	S55312	TSH protein beta c
45	21	17.8	15	2	PH1613	Ig H chain V-D-J r
46	21	17.8	15	2	S36890	ribosomal protein
47	21	17.8	16	2	PH1622	Ig H chain V-D-J r
48	21	17.8	16	2	T14224	NADH2 dehydrogenas
49	21	17.8	17	2	S48655	glutathione dehydr
50	21	17.8	17	2	PH1820	T cell receptor al
51	21	17.8	18	2	PH1323	Ig heavy chain DJ
52	21	17.8	19	2	PH1304	Ig heavy chain DJ
53	21	17.8	19	2	PH1756	T cell receptor al
54	21	17.8	19	2	PH1609	Ig H chain V-D-J r
55	21	17.8	20	2	S17451	flavodoxin B - Azo
56	21	17.8	20	2	S80028	flagellar motor sw
57	21	17.8	20	2	A37968	acid proteinase he
58	20.5	17.4	19	2	S13046	calreticulin - rab
59	20	16.9	9	2	PC7076	spectrin alpha cha
60	20	16.9	10	2	S60589	spem-activating p
61	20	16.9	11	2	S21127	precortin methyltr
62	20	16.9	11	2	PC2330	cyclonucleosidogac
63	20	16.9	12	2	S17869	glutathione transf
64	20	16.9	13	2	H56046	urinary tract ston
65	20	16.9	14	2	PT0232	Ig heavy chain CRD
66	20	16.9	14	2	PT0252	Ig heavy chain CRD
67	20	16.9	14	2	AF0296	phenylalanyl-trna
68	20	16.9	15	2	PH1616	Ig H chain V-D-J r
69	20	16.9	16	2	B44896	heat shock protein
70	20	16.9	17	2	C37520	glutathione transf
71	20	16.9	17	2	S26747	Ig heavy chain J r
72	20	16.9	17	2	S09085	proteasome chain 4
73	20	16.9	19	2	A48354	nonstructural prot
74	20	16.9	20	2	H49034	nuclear antigen EB
75	20	16.9	20	2	A48367	glutaryl-CoA dehyd
76	20	16.9	20	2	A61264	MHC class I histoc
77	20	16.9	21	2	PH1730	Ig heavy chain V r
78	19	16.1	9	2	PT0270	Ig heavy chain CRD
79	19	16.1	11	2	A61575	Timeasaurus seer
80	19	16.1	12	2	I64829	gene HEXA protein
81	19	16.1	12	2	S23168	Z protein - guinea
82	19	16.1	14	2	S39932	S-allele-associate
83	19	16.1	14	2	PH1614	Ig H chain V-D-J r
84	19	16.1	14	2	PH1617	Ig H chain V-D-J r
85	19	16.1	15	2	C37765	hypothetical prote
86	19	16.1	15	2	PA0016	glycine cleavage T
87	19	16.1	15	2	PA0092	protein QP200011 -
88	19	16.1	15	2	C43334	orf33 3' to aadr -
89	19	16.1	15	2	S03955	acidic fibroblast
90	19	16.1	16	2	S17217	ribulose-bisphosph
91	19	16.1	16	2	PH1588	Ig H chain V-D-J r
92	19	16.1	16	2	C90981	his operon leader
93	19	16.1	16	2	S10678	aldehyde dehydroge
94	19	16.1	16	2	A85827	his operon leader
95	19	16.1	16	2	A33171	hypothetical prote
96	19	16.1	17	2	C37396	pollen allergen Fe
97	19	16.1	18	2	PH1368	Ig heavy chain DJ
98	19	16.1	20	2	FX0042	venomabin B (EC 3.4
99	19	16.1	20	2	PT0248	Ig heavy chain CDR
100	19	16.1	20	2	D37396	pollen allergen Fe

ALIGNMENTS

RESULT 1

B41868 hypochemical protein (traE1 3' region) - Enterococcus faecalis plasmid PAD1

C:Species: Enterococcus faecalis

C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: B41868; B37391

R:Pontius, L.T.; Clewell, D.B.

J. Bacteriol. 174, 3152-3160, 1992

A:Title: Conjugative transfer of Enterococcus faecalis plasmid PAD1: nucleotide sequence

A:Reference number: A41868; MUID:92250408; PMID:1315730

A:Contents: plasmid PAD1

A:Accession: B41868

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-15 <PON>

A:Cross-references: UNIPROT:Q52135; UNIPARC:UPI00000B26AA

A:Note: sequence extracted from NCBI backbone (NCBI:99901, NCBI:99906)

R:Clewell, D.B.; Pontius, L.T.; An, F.Y.; Ike, Y.; Suzuki, A.; Nakayama, J.

Plasmid 24, 156-161, 1990

A:Title: Nucleotide sequence of the sex pheromone inhibitor (iAD1) determinant of Enteroc

A:Reference number: A37391; MUID:91261999; PMID:2128961

A:Accession: B37391

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-15 <CLE>

A:Cross-references: UNIPARC:UPI00000B26AA; GB:M62888; NID:g141853; PIDN:AAA98040.1; PID:

C:Genetics:

A:Genome: plasmid

Query Match

Best Local Similarity 26.3%; Score 31; DB 2; Length 15;

Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 10 LYTWHYYL 17

Db 1 MYTVHVIY 8

RESULT 2

ermC leader peptide - Staphylococcus aureus plasmids

C:Species: Staphylococcus aureus

C:Date: 29-Jul-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004

C:Accession: B93717; B93866; A46568; S03586; A03599

R:Gryczan, T.J.; Grandi, G.; Hahn, J.; Grandi, R.; Dubnau, D.

Nucleic Acids Res. 8, 6081-6097, 1980

A:Title: Conformational alteration of mRNA structure and the posttranscriptional regulat

A:Reference number: A93717; MUID:81124320; PMID:6162157

A:Accession: B93717

A:Molecule type: DNA

A:Residues: 1-19 <GRY>

A:Cross-references: UNIPROT:P03063; UNIPARC:UPI00000003A9; GB:V01278; GB:J01755; GB:J017

R:Horinouchi, S.; Weisblum, B.

Proc. Natl. Acad. Sci. U.S.A. 77, 7079-7083, 1980

A:Title: Posttranscriptional modification of mRNA conformation: mechanism that regulated

A:Reference number: A93866; MUID:81175093; PMID:6938954

A:Accession: B93866

A:Molecule type: DNA

A:Residues: 1-19 <HOR>

A:Cross-references: UNIPARC:UPI00000003A9; GB:V01278; GB:J01755; GB:J01756; GB:J01757; G

A:Experimental source: plasmid pE194

R:Catchpole, I.; Thomas, C.; Davies, A.; Dyke, K.G.H.

J. Gen. Microbiol. 134, 697-709, 1988

A:Title: The nucleotide sequence of Staphylococcus aureus plasmid pT48 conferring induc

ve resistance.

A:Reference number: A46568; MUID:89036120; PMID:3141573

A:Accession: A46568

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-19 <CAT>

A:Cross-references: UNIPARC:UPI00000003A9; GB:M19652; NID:g153070; PIDN:AAA20193.1; PID:

A:Experimental source: plasmid pT48

R:Mayford, M.; Weisblum, B.

J. Mol. Biol. 206, 69-79, 1989

A:Title: ermC leader peptide. Amino acid sequence critical for induction by translationa

A:Reference number: S03586; MUID:89199652; PMID:2467989

A:Accession: S03586

A:Molecule type: DNA

A:Residues: 1-19 <CAT>

A:Cross-references: UNIPARC:UPI00000003A9

C:Genetics:

A:Genome: plasmid

C:Superfamily: ermC leader peptide

Query Match

Best Local Similarity 25.4%; Score 30; DB 1; Length 19;

Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 8 YLVYTHYYLN 18

Db 7 FVISTVHYQPN 17

RESULT 3

ermG leader peptide 2 - Bacillus sphaericus

C:Species: Bacillus sphaericus

C:Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 09-Jul-2004

C:Accession: B26930

R:Monod, M.; Mohan, S.; Dubnau, D.

J. Bacteriol. 169, 340-350, 1987

A:Title: Cloning and analysis of ermG, a new macrolide-lincosamide-streptogramin B resist

A:Reference number: A91840; MUID:87083389; PMID:3025178

A:Accession: B26930

A:Molecule type: DNA

A:Residues: 1-19 <MON>

A:Cross-references: UNIPROT:Q45558; UNIPARC:UPI00000B5B8C; GB:M15332; NID:g142881; PIDN:

C:Superfamily: ermC leader peptide

Query Match

Best Local Similarity 25.4%; Score 30; DB 2; Length 19;

Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 8 YLVYTHYYLN 18

Db 7 FVISTVHYQPN 17

RESULT 4

NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - Debney's tobacco chloroplast (fr

C:Species: chloroplast Nicotiana debneyi (Debney's tobacco)

C:Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 03-Jun-2002

C:Accession: S08590

R:Hayashida, N.; Matsubayashi, T.; Shinozaki, K.; Sugitara, M.; Inoue, K.; Hiyaama, T.

Curr. Genet. 12, 247-250, 1987

A:Title: The gene for the 9 kd polypeptide, a possible apoprotein for the iron-sulfur ce

A:Reference number: S07170; MUID:88210537; PMID:3329576

A:Accession: S08590

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-21 <HAV>

A:Cross-references: UNIPARC:UPI0000000AD9; EMBL:X05881; NID:g11790; PIDN:CAA29305.1; PID

C:Genetics:

A:Gene: ndnd

A:Genome: chloroplast

C:Superfamily: NADH dehydrogenase (ubiquinone) chain 4

C:Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match

Best Local Similarity 25.4%; Score 30; DB 2; Length 21;

Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY	5	V	M	X	Y	V	L	T	M	H	Y	16
				:	:		:		:			
Db	2	V	Q	V	L	V	F	T	T	N	Y	13

RESULT 5

crystallin - Pacific cuttlefish (fragment)
C:Species: Sepia esculenta (Pacific cuttlefish)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: E60894
R:Chou, S. H.
J. Protein Chem. 7, 527-534, 1988
A:Title: The protein sequence homology of gamma-crystallins among major vertebrate classes
A:Reference number: A60894; MUID:89351593; PMID:3255376
A:Accession: E60894
A:Molecule type: protein
A:Residues: 1-20 <CH1>
A:Cross-references: UNIPROT:Q7M447; UNIPARC:UPI00001754DB
C:Superfamily: glutathione transferase
C:Keywords: eye lens

Query Match	24.6%	Score 29	DB 2	Length 20
Beet Local Similarity	40.0%	Pred. No. 2.7e+02		
Matches 4	Conservative 3	Mismatches 3	Indels 0	Gaps 0

QY	11	YTMHYYLNNG	20
		:: :	
Db	3	YTLYYFNGRG	12

RESULT 6

IG heavy chain CDR3 region (clone 2-115A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: P70254
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Catton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: P70222; MUID:91108337; PMID:1899102
A:Accession: P70254
A:Molecule type: DNA
A:Residues: 1-14 <YAM>
A:Cross-references: UNIPARC:UPI000017C1EB
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match	22.9%	Score 27	DB 2	Length 14
Best Local Similarity	50.0%	Pred. No.	3.8e+02	
Matches 5	Conservative 2	Mismatches 3	Indels 0	Gaps 0

QY	14	HYLLNGATR	23
		:	
Db	5	HYDSSGYHR	14

RESULT 7

nitrogenase cofactor synthetase protein nifS - *Anabaena variabilis* (fragment)
N:Conting: L-cysteine sulfinyltransferase (EC 2.6.1.-)
C:Species: *Anabaena variabilis*
C:Date: 06-Jan-1995 #sequence__revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S32677
R:Monmeriah, U., Boehme, H.
submitted to the EMBL Data Library, December 1992
A:Description: Cloning and expression in *E. coli* of the *Anabaena*.
A:Reference number: S32675
A:Accession: S32677
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-15 <MON>

A:Cross-references: UNIPROT:Q44507; UNIPARC:UD1000013010C; EMBL:X65898; NID:G296503; PDB:1W33; C:Superfamily: nitrogen fixation protein nifs
C:Keywords: sulfotransferase

Query Match	22.9%	Score 27	DB 2	Length 15
Best Local Similarity	71.4%	Pred. No. 4.1e+02		
Matches	5	Conservative	1	Indels 0; Gaps 0;
		Mismatches	1	

QY	16	YLNGAT	22
		:	
Db	5	YLDNAT	11

RESULT 8

hypocretin-like protein H10195 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_influenzae_revision 18-Aug-1995 #text_change 30-Jun-1998
C:Accession: G64003
R:Flaeschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage,
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman,
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrman, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: G64003
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-12 <TIGR>
C:Cross-references: UNIPARC:UPI0000017AAED; GB:U32704; GB:L42023; NID:g1573143; PID:g157

Query Match	22.0%	Score 26;	DB 2;	Length 12;
Best Local Similarity	57.1%	Pred. No. 4.7e+02;		
Matches	4;	Conservative	1;	Mismatches 2;
			Indels	0;
			Gaps	0;

QY	11	YTMHXYL	1
		:	
Db	3	YQYHYWL	9

RESULT 9

I: Ig H chain V-D-J region (clone B-less 151) - mouse (Frigment)
C: Species: Mus musculus (house mouse)
C: Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C: Accession: P11628
R: Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A: Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A: Reference number: P11580; MUID:93301609; PMID:8315387
A: Accession: P11628
A: Molecule type: DNA
A: Residues: 1-14 <LEV>
A: Cross-references: UNIPARC:UPI000017C694
A: Experimental source: bone marrow pre-B lymphocyte
C: Keywords: Immunoglobulin

Query Match	22.0%	Score 26	DB 2	length 14
Best Local Similarity	80.0%	Pred.	0.55e+02	
Matches	4	Conservative	0	Mismatches 1
				Indels 0
				Gaps 0

QY	14	HY	LN	1
Db	4	HY	SN	8

RESULT 10

83K protein - Eubacterium acidaminophilum (Fragment)
 C|Species: Eubacterium acidaminophilum
 C|Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
 C|Accession: 563503

R:Meyer, M.; Granderath, K.; Andreesen, J.R.

Eur. J. Biochem. 234, 184-191, 1995

A:Title: Purification and characterization of protein P(B) of betaine reductase and its
phylum.

A:Reference number: S63502; MUID:96096737; PMID:8529639

A:Accession: S63503

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-17 <MEY>

A:Cross-references: UNIPARC:UPI000017AD3D

Query Match 22.0%; Score 26; DB 2; Length 17;
Best Local Similarity 44.4%; Pred. No. 6.8e+02;

Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 13 MHYIANGA 21
: : : :
Db 3 LHKFLEDGA 11

RESULT 11

protein IEF SSP 9125 - human (fragments)

C:Species: Homo sapiens (man)

C:Date: 09-Dec-1993 #sequence_revision 17-Nov-1995 #text_change 17-Nov-1995

C:Accession: S37684

R:Jeffers, H.; Madsen, P.; Rasmussen, H.H.; Honore, B.; Andersen, A.H.; Walbum, E.; Vand

J. Mol. Biol. 231, 982-998, 1993

A:Title: Molecular cloning and expression of the transformation sensitive epithelial mar

A:Reference number: S34753; MUID:93294871; PMID:8515476

A:Accession: S37684

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-20 <LEF>

A:Cross-references: UNIPARC:UPI000017C321

Query Match 21.6%; Score 25.5; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 9.7e+02;

Matches 6; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

OY 2 EXNVXXVLYTMHY 16
: : : :
Db 6 ERNLLS-VAYKVIFY 19

RESULT 12

S42282 paraeoral crystal protein cryIIIB - *Bacillus thuringiensis* plasmid (fragment)

N:Alternate names: delta-endotoxin

C:Species: *Bacillus thuringiensis*

C:Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 24-Jul-1998

C:Accession: S42282

R:Crickmore, N.; Wheeler, V.C.; Ellar, D.J.

Mol. Gen. Genet. 242, 365-368, 1994

A:Title: Use of an operon fusion to induce expression and crystallisation of a *Bacillus*

A:Reference number: S42282; MUID:94150472; PMID:7906381

A:Accession: S42282

A:Molecule type: protein

A:Residues: 1-10 <CRI>

A:Cross-references: UNIPARC:UPI000017ACD4

A:Experimental source: subsp. *galleriae* 916

C:Genetics:

A:Gene: cryIIIB

A:Genome: plasmid

C:Keywords: delta-endotoxin

Query Match 21.2%; Score 25; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 5.5e+02;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 13 MHYIANGA 20
: : : :
Db 1 MNTVLNNG 8

RESULT 13

PH1604

Ig H chain V-D-J region (wild-type clone 327) - mouse (fragment)

C:Species: *Mus musculus* (house mouse)

C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C:Accession: PH1604

R:Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice

A:Reference number: PH1580; MUID:9301609; PMID:8315387

A:Accession: PH1604

A:Molecule type: DNA

A:Residues: 1-16 <LEV>

A:Cross-references: UNIPARC:UPI000017C6C0

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

Query Match 21.2%; Score 25; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 9.1e+02;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 11 YTMHY 16
: : : :
Db 7 WLLHY 12

RESULT 14

PH1615

Ig H chain V-D-J region (clone B-less 22) - mouse (fragment)

C:Species: *Mus musculus* (house mouse)

C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C:Accession: PH1615

R:Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice

A:Reference number: PH1580; MUID:9301609; PMID:8315387

A:Accession: PH1615

A:Molecule type: DNA

A:Residues: 1-14 <LEV>

A:Cross-references: UNIPARC:UPI000017C69E

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

Query Match 20.3%; Score 24; DB 2; Length 14;
Best Local Similarity 40.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 DEXVXXVYL 10
: : : :
Db 3 DESNPIRYAM 12

RESULT 15

S72217

D-arabinose 1-dehydrogenase [NAD(P)] (EC 1.1.1.117) - yeast (*Candida albicans*) (fragment)

C:Species: *Candida albicans*

C:Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 03-Jun-2002

C:Accession: S72217

R:Kim, S.T.; Huh, W.K.; Kim, J.Y.; Hwang, S.W.; Kang, S.O.

Biochim. Biophys. Acta 1297, 1-8, 1996

A:Title: D-arabinose dehydrogenase and biosynthesis of erythroascorbic acid in *Candida a*

A:Reference number: S72217; MUID:96439039; PMID:8841374

A:Accession: S72217

A:Molecule type: protein

A:Residues: 1-14 <KIM>

A:Cross-references: UNIPARC:UPI000017CDB9

C:Keywords: oxidoreductase

Query Match 20.3%; Score 24; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 15 YLNG 20
 : |||
 Db 9 FXLNG 14

RESULT 16

SS9495
 Formate dehydrogenase delta chain - Alcaligenes eutrophus (fragment)
 C/Species: Alcaligenes eutrophus
 C/Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C/Accession: S59495
 R/Friedelbojd, J.; Mayer, F.; Bill, E.; Trautwein, A.X.; Bowien, B.
 Biol. Chem. Hoppe-Seyler 376, 561-568, 1995
 A/Title: Structural and immunological studies on the soluble formate dehydrogenase from
 A/Reference number: S59492; MUID:96145736; PMID:8561915
 A/Accession: S59495
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-14 <FRI>
 A/Cross-references: UNIPROT:Q7MON7; UNIPARC:UPI000017AA11

Query Match 20.3%; Score 24; DB 2; Length 14;
 Best Local Similarity 80.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 YLNG 20
 : |||
 Db 9 YANNG 13

RESULT 17

PT0332
 Ig heavy chain CND3 region (clone J2-139) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C/Accession: PT0332
 R/Yamada, M.; Maeserger, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A/Reference number: PT0222; MUID:91108337; PMID:1899102
 A/Accession: PT0332
 A/Molecule type: DNA
 A/Residues: 1-19 <YAM>
 A/Cross-references: UNIPARC:UPI000017C21A
 A/Experimental source: B lymphocyte
 C/Keywords: heterotrimer; immunoglobulin

Query Match 20.3%; Score 24; DB 2; Length 19;
 Best Local Similarity 33.3%; Pred. No. 1.6e+03;
 Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 14 HYLLNGAT 22
 : |||
 Db 6 YYYGSGSS 14

RESULT 18

P00544
 capsid protein VP5 - human herpesvirus 1 (fragments)
 C/Species: human herpesvirus 1
 C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 C/Accession: P00544
 R/Davison, M.D.; Rixon, F.J.; Davison, A.J.
 J. Gen. Virol. 73, 2709-2713, 1992
 A/Title: Identification of genes encoding two capsid proteins (VP24 and VP26) of herpes
 A/Reference number: P00544; MUID:93019027; PMID:1338463
 A/Accession: P00544
 A/Molecule type: protein
 A/Residues: 1-20 <DAV>
 A/Cross-references: UNIPARC:UPI000017A7CA
 A/Experimental source: strain 17
 C/Genetics:

A/Gene: UL19
 C/Keywords: capsid protein

Query Match 20.3%; Score 24; DB 2; Length 20;
 Best Local Similarity 80.0%; Pred. No. 1.7e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 16 YLNG 20
 : |||
 Db 3 YLDNG 7

RESULT 19

PT0263
 Ig heavy chain CND3 region (clone 2-121B) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C/Accession: PT0263
 R/Yamada, M.; Maeserger, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A/Reference number: PT0222; MUID:91108337; PMID:1899102
 A/Accession: PT0263
 A/Molecule type: DNA
 A/Residues: 1-13 <YAM>
 A/Cross-references: UNIPARC:UPI000017C1F0
 A/Experimental source: B lymphocyte
 C/Keywords: heterotrimer; immunoglobulin

Query Match 19.5%; Score 23; DB 2; Length 13;
 Best Local Similarity 80.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 YLNG 20
 : |||
 Db 9 YLNG 13

RESULT 20

PH1601
 Ig H chain V-D-J region (wild-type clone 311) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C/Accession: PH1601
 R/Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic
 A/Reference number: PH1580; MUID:93301609; PMID:8315387
 A/Accession: PH1601
 A/Molecule type: DNA
 A/Residues: 1-14 <LEV>
 A/Cross-references: UNIPARC:UPI000017C6BE
 A/Experimental source: bone marrow pre-B lymphocyte
 C/Keywords: immunoglobulin

Query Match 19.5%; Score 23; DB 2; Length 14;
 Best Local Similarity 50.0%; Pred. No. 1.6e+03;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 YVLYTMHY 15
 : |||
 Db 7 YYYAMDY 14

RESULT 21

PH1607
 Ig H chain V-D-J region (wild-type clone 333) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C/Accession: PH1607
 R/Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic

A:Reference number: PH1580; MUID:93301609; PMID:8315387
A:Accession: PH1607
A:Molecule type: DNA
A:Residues: 1-17 <LEV>
A:Cross-references: UNIPARC:UPI0000176DD3
A:Experimental source: bone marrow pre-B lymphocyte
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 19.5%; Score 23; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 8 YLYTMY 15
| | | |
Db 10 YYYVAMY 17

RESULT 22

B24735
glutathione transferase (EC 2.5.1.18) 1-2 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 18-Jun-1993
C:Accession: B24735
R:Mannervik, B.; Alin, P.; Guttenberg, C.; Jansson, H.; Tahir, M.K.; Warholm, M.; Jorvæ
Proc. Natl. Acad. Sci. U.S.A. 82, 7202-7206, 1985
A:Title: Identification of three classes of cytosolic glutathione transferase common to
A:Reference number: A24735; MUID:86042634; PMID:3864155
A:Accession: B24735
A:Molecule type: protein
A:Residues: 1-18 <MAN>
A:Cross-references: UNIPARC:UPI000017542B
C:Superfamily: glutathione transferase
C:Keywords: transferase

Query Match 19.5%; Score 23; DB 2; Length 18;
Best Local Similarity 37.5%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 13 MHYYLNG 20
| | | |
Db 6 LHYNGRG 13

RESULT 23

PH1307
Ig heavy chain DJ region (clone C96-119) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1307
R:Masserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DH joining in young children with B precursor lymph
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Accession: PH1307
A:Molecule type: DNA
A:Residues: 1-19 <MAS>
A:Cross-references: UNIPARC:UPI0000176935
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 19.5%; Score 23; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 11 YTMHY 16
| | | |
Db 5 YSYYY 10

RESULT 24

PQ0751
self-incompatibility protein S4 - potato (fragment)

C:Species: Solanum tuberosum (potato)
C>Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 31-Dec-2004
C:Accession: PQ0751
R:Kirch, H.H.; Uhrig, H.; Lottepeich, F.; Salami, F.; Thompson, R.D.
Theor. Appl. Genet. 78, 581-588, 1989
A:Title: Characterization of proteins associated with self-incompatibility in Solanum tu
A:Reference number: PQ0749
A:Accession: PQ0751
A:Molecule type: protein
A:Residues: 1-20 <KTR>
A:Cross-references: UNIPARC:UPI0000175A01
A:Experimental source: style
C:Superfamily: RNases
C:Keywords: glycoprotein

Query Match 19.5%; Score 23; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 YLNN 19
| | | |
Db 17 YLNN 20

RESULT 25

S68392
H+-transporting two-sector ATPase (EC 3.6.3.14) chain I - Chlamydomonas reinhardtii chlor
N:Alternate names: ATP synthase chain I
C:Species: Chlamydomonas reinhardtii
C>Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 31-Dec-2004
C:Accession: S68392
R:Fiedler, H.R.; Schmid, R.; Liu, S.; Shavit, N.; Strotmann, H.
FEBS Lett. 377, 163-166, 1995
A:Title: Isolation of CF(0)CF(1) from Chlamydomonas reinhardtii cw15 and the N-terminal e
A:Reference number: S68388; MUID:96128220; PMID:8543042
A:Accession: S68392
A:Molecule type: protein
A:Residues: 1-11 <FIR>
A:Cross-references: UNIPARC:UPI0000175ED3
A:Experimental source: strain CW15
C:Genetics:
A:Genome: Chloroplast
C:Superfamily: H(+)-transporting ATP synthase protein 6
C:Keywords: ATP biosynthesis; chloroplast; hydrolase; membrane-associated complex; chyla

Query Match 18.6%; Score 22; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 HYY 16
| | | |
Db 7 HYY 9

Search completed: January 26, 2006, 08:05:02
Job time : 12.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 26, 2006, 07:47:56 ; Search time 68.4052 Seconds
(without alignments)
237.221 Million cell updates/sec

Title: US-09-662-293-9
Perfect score: 118
Sequence: 1 DEXNMVXYLYTMHYLYNGATR 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 15779

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Uniprot_05.80:*
1: uniprot_sprotc:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	28.0	19	2	OSDU98_STAP
2	33	28.0	19	2	O9EV48_STANU
3	32	27.1	15	2	O9S8A2_HELAN
4	32	27.1	20	2	O4XS28_PLACH
5	32	27.1	20	2	O4YWP2_PLABE
6	31	26.3	15	2	O52135_9ZZZZ
7	31	26.3	21	2	O4YVW6_PLABE
8	30.5	25.8	18	2	O4Z5U3_PLABE
9	30	25.4	15	2	O4XG09_PLACH
10	30	25.4	19	1	LPRM_STANU
11	30	25.4	19	2	O57313_STAP
12	30	25.4	19	2	O799A5_STANU
13	30	25.4	19	2	O799E4_STAP
14	30	25.4	19	2	O7AVR6_STAP
15	30	25.4	19	2	O4S5S8_BACSH
16	30	25.4	19	2	O799W9_STANU
17	30	25.4	19	2	O4JHNS_STANU
18	30	25.4	19	2	O6LBC3_9ZZZZ
19	30	25.4	19	2	O79DTR_9ZZZZ
20	30	25.4	20	2	O7PC06_PLAYO
21	30	25.4	21	2	O4Y2F8_PLACH
22	30	25.4	21	2	O4Y2F8_TOBAC
23	29	24.6	20	2	O7M447_9MOLL
24	29	24.6	21	2	O9ZYB7_9HYME
25	29	24.6	21	2	O4X6E8_PLACH
26	29	24.6	21	2	O4Y144_PLACH
27	28.5	24.2	12	2	O4Y9H1_PLABE
28	28	23.7	18	2	O4X1Q2_PLACH
29	28	23.7	19	2	O4X1Z2_PLACH
30	28	23.7	20	2	O4XA28_PLACH
31	28	23.7	21	2	O4X533_PLACH

32	28	23.7	21	2	O4X6E1_PLACH	O4X6E1_plasmodium
33	27.5	23.3	21	2	O4X877_PLACH	O4X877_plasmodium
34	27	22.9	15	1	NIFSL_ANAVA	O4X507_anabena va
35	27	22.9	16	2	O7RHS8_PLAYO	O7RHS8_plasmodium
36	27	22.9	18	2	O4XAQ4_PLACH	O4XAQ4_plasmodium
37	27	22.9	19	2	O9L434_SALTY	O9L434_salmonella
38	27	22.9	21	2	O7RBS5_PLAYO	O7RBS5_plasmodium
39	27	22.9	21	2	O4X839_PLACH	O4X839_plasmodium
40	27	22.9	21	2	O4YK04_PLABE	O4YK04_plasmodium
41	26	22.0	17	1	GST_ASADI	P83246_aaparis dic
42	26	22.0	15	2	O70Y71_9LAMI	O70Y71_thornicrofti
43	26	22.0	18	2	O4YH66_PLABE	O4YH66_plasmodium
44	26	22.0	19	2	O4XJ65_PLACH	O4XJ65_plasmodium
45	26	22.0	19	2	O9F6J8_YERPE	O9F6J8_yersinia pe
46	26	22.0	20	2	O5C1Y0_SCHTA	O5C1Y0_echinocoma
47	26	22.0	20	2	O4YR09_PLABE	O4YR09_plasmodium
48	26	22.0	21	2	O5XUW8_HUMAN	O5XUW8_homo sapien
49	26	22.0	21	2	O4XX24_PLACH	O4XX24_plasmodium
50	26	22.0	21	2	O4YDB9_PLABE	O4YDB9_plasmodium
51	25.5	21.6	20	2	O4Z007_PLABE	O4Z007_plasmodium
52	25	21.2	15	2	O7RHH2_PLAYO	O7RHH2_plasmodium
53	25	21.2	17	2	O19716_HUMAN	O19716_homo sapien
54	25	21.2	18	2	O4X8U6_PLACH	O4X8U6_plasmodium
55	25	21.2	18	2	O4YGB7_PLABE	O4YGB7_plasmodium
56	25	21.2	18	2	O95MB1_HORSE	O95MB1_eguus cabal
57	25	21.2	19	2	O60F81_CARCR	O60F81_caretta car
58	25	21.2	21	2	O7RUB6_PLAYO	O7RUB6_plasmodium
59	25	21.2	21	2	O4XMC7_PLACH	O4XMC7_plasmodium
60	25	21.2	21	2	O4YPC6_PLABE	O4YPC6_plasmodium
61	24.5	20.8	19	2	O86DB6_HALBO	O86DB6_halocynthia
62	24.5	20.8	19	2	O4YGY2_PLABE	O4YGY2_plasmodium
63	24.5	20.8	21	2	O7R2U5_PLAYO	O7R2U5_plasmodium
64	24	20.3	11	2	O4XCL2_PLACH	O4XCL2_plasmodium
65	24	20.3	12	2	O6ITW2_HUMAN	O6ITW2_homo sapien
66	24	20.3	14	2	O7MON7_ALCEU	O7MON7_alcaligenes
67	24	20.3	15	2	P91578_CFEYV	P91578_choristoneu
68	24	20.3	15	2	O80277_9CAVD	O80277_lactococcus
69	24	20.3	16	2	O4Z674_PLABE	O4Z674_plasmodium
70	24	20.3	16	2	P82444_TOBAC	P82444_nicotiana t
71	24	20.3	16	2	O9KU10_STANA	O9KU10_staphylococ
72	24	20.3	17	2	O4YXY7_PLABE	O4YXY7_plasmodium
73	24	20.3	17	2	O4Z344_PLABE	O4Z344_plasmodium
74	24	20.3	17	2	O9OPC8_TYLCV	O9OPC8_tomato yell
75	24	20.3	18	2	O4Y8A5_PLACH	O4Y8A5_plasmodium
76	24	20.3	18	2	O4YUR7_PLABE	O4YUR7_plasmodium
77	24	20.3	18	2	O4Z6B5_PLABE	O4Z6B5_plasmodium
78	24	20.3	19	2	O7RR06_PLAYO	O7RR06_plasmodium
79	24	20.3	19	2	O4XG21_PLACH	O4XG21_plasmodium
80	24	20.3	19	2	O4YEN3_PLABE	O4YEN3_plasmodium
81	24	20.3	19	2	O4YVW0_PLABE	O4YVW0_plasmodium
82	24	20.3	19	2	O4Z6S8_PLABE	O4Z6S8_plasmodium
83	24	20.3	19	2	O38371_BPMS2	O38371_bacterioph
84	24	20.3	20	1	O9OV31_9MUDI	O9OV31_rattus sp.
85	24	20.3	20	1	HMEC_ARCPR	P84668_archaeoglob
86	24	20.3	20	2	O7RPN2_PLAYO	O7RPN2_plasmodium
87	24	20.3	20	2	O4Y8L0_PLACH	O4Y8L0_plasmodium
88	24	20.3	20	2	O4YH32_PLABE	O4YH32_plasmodium
89	24	20.3	20	2	O9R4G2_9VIBR	O9R4G2_vibrio. bet
90	24	20.3	21	2	O4XKF6_PLACH	O4XKF6_plasmodium
91	24	20.3	21	2	O9RSK0_STRYP	O9RSK0_streptococ
92	23	19.5	11	2	O4X942_PLACH	O4X942_plasmodium
93	23	19.5	11	2	O4L8Q1_STANU	O4L8Q1_staphylococ
94	23	19.5	16	2	O7JN10_DROME	O7JN10_drosophila
95	23	19.5	16	2	O4XVQ2_PLACH	O4XVQ2_plasmodium
96	23	19.5	16	2	O4Y227_PLABE	O4Y227_plasmodium
97	23	19.5	17	2	O4XHV2_PLACH	O4XHV2_plasmodium
98	23	19.5	17	2	O4Y2Z5_PLABE	O4Y2Z5_plasmodium
99	23	19.5	19	2	O4XOC6_PLACH	O4XOC6_plasmodium
100	23	19.5	19	2	O4YER2_PLABE	O4YER2_plasmodium

ALIGNMENTS

RESULT 1
 Q5DU98_9STAP PRELIMINARY; PRT; 19 AA.
 ID Q5DU98_9STAP PRELIMINARY; PRT; 19 AA.
 AC Q5DU98;
 DT 10-MAY-2005 (TREMBlrel. 30, Created)
 DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
 DE Hypothetical protein.
 OS Staphylococcus lentus.
 OC Plasmid PST2.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=42858;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=44;
 RA Hauschild T., Luehje P., Schwarz S.;
 RT "The staphylococcal tetracycline macrolide-lincosamide-streptogramin B resistance plasmid PST2 is an RSA mediated in vivo recombination product."
 RT product."
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ888003; CAI59791.1; -; Genomic_DNA.
 KW Hypothetical protein; Plasmid.
 SQ SEQUENCE 19 AA; 2219 MW; 13FEE3D9897F3A7B CRC64;

Query Match 28.0%; Score 33; DB 2; Length 19;
 Best Local Similarity 45.5%; Pred. No. 4.8e+02;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 8 VYLYTMHYLN 18
 :|:|:|:|:
 Db 7 FVISTVHYHPN 17

RESULT 2
 Q9EV48_STAUV PRELIMINARY; PRT; 19 AA.
 ID Q9EV48_STAUV PRELIMINARY; PRT; 19 AA.
 AC Q9EV48;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Leader peptide of ErmGM.
 GN Name=leader peptide (LP) of ermGM;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21621309; PubMed=11751136; DOI=10.1128/JAC.46.1.211-215.2002;
 RA Matsushita M., Inoue M., Nakajima Y., Endo Y.;
 RT "New erm Gene in Staphylococcus aureus clinical isolates."
 RL Antimicrob. Agents Chemother. 46:211-215 (2002).
 DR EMBL; AB014481; BAB20747.1; -; Genomic_DNA.
 SQ SEQUENCE 19 AA; 2195 MW; 605CBAD99E4B6B7F CRC64;

Query Match 28.0%; Score 33; DB 2; Length 19;
 Best Local Similarity 40.0%; Pred. No. 4.8e+02;
 Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 4 NVKXYLYTMHYLN 18
 :|:|:|:|:
 Db 3 NCSLPIVINTVHYQPN 17

RESULT 3
 Q9S8A2_HELAN PRELIMINARY; PRT; 15 AA.
 ID Q9S8A2_HELAN PRELIMINARY; PRT; 15 AA.
 AC Q9S8A2;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE Oleosin (Fragment).
 OS Helianthus annuus (Common sunflower).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Campanulids; Asterales; Asteraceae; Asteroideae; Helianthaceae;
 OC Helianthus.
 OX NCBI_TaxID=4232;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=96195148; PubMed=8660304;
 RA Millichip M., Tatham A.S., Jackson F., Griffiths G., Shewry P.R.,
 RA Scobart A.K.;
 RT "Purification and characterization of oil-bodies (oleosomes) and oil-body boundary proteins (oleosins) from the developing cotyledons of sunflower (Helianthus annuus L.)."
 RT Biochem. J. 314:333-337 (1996).
 RL Biochem. J. 314:333-337 (1996).
 SQ SEQUENCE 15 AA; 1619 MW; CDC28A062F7F8704 CRC64;

Query Match 27.1%; Score 32; DB 2; Length 15;
 Best Local Similarity 75.0%; Pred. No. 5.4e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 16 YLNNGATR 23
 :|:|:|:|:
 Db 8 FLNNGAFR 15

RESULT 4
 Q4XS28_PLACH PRELIMINARY; PRT; 20 AA.
 ID Q4XS28_PLACH PRELIMINARY; PRT; 20 AA.
 AC Q4XS28;
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN ORFNames=PC106693.00.0;
 OS Plasmodium chabaudi.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5825;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
 RA Bertrian M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Jense C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RT "A comprehensive survey of the Plasmodium life cycle by genomic, transcriptomic, and proteomic analyses."
 RT Science 307:82-86 (2005).
 RL Science 307:82-86 (2005).
 CC -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
 DR EMBL; CAJ01003410; CAH79964.1; -; Genomic_DNA.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 20 AA; 2488 MW; C628661F489812F9 CRC64;

Query Match 27.1%; Score 32; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 7.3e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 8 VYLYTMHYLN 17
 :|:|:|:|:
 Db 11 YLYICVYI 20

RESULT 5
 Q4YWF2_PLABE PRELIMINARY; PRT; 20 AA.
 ID Q4YWF2_PLABE PRELIMINARY; PRT; 20 AA.
 AC Q4YWF2;
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Hypothetical protein (Fragment).

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GN ORFNames=PB105101.00.0;
OS Plasmidium berghel.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmidium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Jansse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,
RT "A comprehensive survey of the Plasmidium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAI01002093; CAH97654.1; -; Genomic_DNA.
KM Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 20 AA; 2419 MW; 3ABE7624B6E5F6EA8 CRC64;

Query Match 27.1%; Score 32; DB 2; Length 20;
Best Local Similarity 31.2%; Pred. No. 7.3e+02;
Matches 5; Conservative 6; Mismatches 3; Indels 2; Gaps 1;

OY 4 NNMXXVLYTMHYIANN 19
Db 3 SILIYAIYT--FYFNH 16

RESULT 6
O52135_92222
ID O52135_92222 PRELIMINARY; PRT; 15 AA.
AC O52135;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE ORF; putative.
OS Plasmid PADI.
OC other sequences; plasmids.
OX NCBI_TaxID=2520;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MDLLine=91261999; PubMed=2128961;
RA Clewell D.B., Pontius L.T., An F.Y., Ike Y., Suzuki A., Nakayama J.;
RT "Nucleotide sequence of the sex pheromone inhibitor (IAD1) determinant
RT of Enterococcus faecalis conjugative plasmid PADI.";
RL Plasmid 24:156-161(1990).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA MDLLine=92250408; PubMed=1315730;
RA Pontius L.T., Clewell D.B.;
RT "Conjugative transfer of Enterococcus faecalis plasmid PADI:
RT nucleotide sequence and transcriptional fusion analysis of a region
RT involved in positive regulation.";
RL J. Bacteriol. 174:3152-3160(1992).
DR EMBL; M62888; AAA98040.1; -; Genomic_DNA.
PIR; B41868; B41868.
KM Plasmid.
SQ SEQUENCE 15 AA; 1874 MW; 0D9D073079E3559 CRC64;

Query Match 26.3%; Score 31; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 10 LYTMHYTL 17
Db 1 MYTVHYVI 8
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RESULT 7
O4YVN6_PLABE
ID O4YVN6_PLABE PRELIMINARY; PRT; 21 AA.
AC O4YVN6;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PB105419.00.0;
OS Plasmidium berghel.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmidium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Jansse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,
RT "A comprehensive survey of the Plasmidium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAI01002238; CAH97920.1; -; Genomic_DNA.
KM Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 21 AA; 2441 MW; B79B04782E2A5804 CRC64;

Query Match 26.3%; Score 31; DB 2; Length 21;
Best Local Similarity 33.3%; Pred. No. 1.1e+03;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 4 NNMXXVLYTMHY 15
Db 6 NCLVYIYLQYF 17

RESULT 8
O4Z5L3_PLABE
ID O4Z5L3_PLABE PRELIMINARY; PRT; 18 AA.
AC O4Z5L3;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB101034.00.0;
OS Plasmidium berghel.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmidium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Jansse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,
RT "A comprehensive survey of the Plasmidium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAI0100433; CAH94418.1; -; Genomic_DNA.
KM Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2302 MW; 28C71708F18BA20 CRC64;

Query Match 25.8%; Score 30.5; DB 2; Length 18;
Best Local Similarity 40.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 4; Mismatches 4; Indels 1; Gaps 1;
```

Oy 4 NMXXVLTMYHYLN 18
 ||| : |||
 Db 3 NMVYCNF-VHFFN 16

RESULT 9

O4XG09 PLACH PRELIMINARY; PRT; 15 AA.
 ID O4XG09 PLACH PRELIMINARY;
 AC O4XG09
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=PC401954.00.0;
 OS Plasmodium chabaudi.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NCBI_TaxID=5825;
 RN [1]

NUCLEOTIDE SEQUENCE.

RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
 RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Jansz C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses.";
 RL Science 307:82-86(2005).
 CC -! CAUTION: The sequence shown here is derived from an
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.

DR EMBL; CAAJ01006563; CAH84159.1; -; Genomic_DNA.
 KM Hypothetical protein.

SO SEQUENCE 15 AA; 1776 MW; 05ACF46B687A4482 CRC64;

Query Match 25.4%; Score 30; DB 2; Length 15;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 8 YVLYTM 13
 ||| : |||
 Db 5 YVLYTM 10

RESULT 10

LPRM_STAUP STANDARD; PRT; 19 AA.
 ID LPRM_STAUP STANDARD;
 AC P03063;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE 23S rRNA methylase leader peptide (erythromycin resistance leader
 DE peptide).
 GN Name=ermC;
 OS Staphylococcus aureus.
 OC Plasmid pE194, and Plasmid pT48.
 CC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=1280;
 RN [1]

NUCLEOTIDE SEQUENCE.

RA MEDLINE=DE194;
 RC MEDLINE=81124320; PubMed=6162157;
 RA Gryczan T.J., Grandi G., Hahn J., Grandi R., Dubnau D.;
 RT "Conformational alteration of mRNA structure and the
 RT posttranscriptional regulation of erythromycin-induced drug
 RT resistance.";
 RL Nucleic Acids Res. 8:6081-6097(1980).
 RN [2]

NUCLEOTIDE SEQUENCE.

RC PLASMTD=PE194;
 RX MEDLINE=81175093; PubMed=6938954;
 RA Horinouchi S., Weisblum B.;

RT "Posttranscriptional modification of mRNA conformation: mechanism that
 RT regulates erythromycin-induced resistance.";
 RL Proc. Natl. Acad. Sci. U.S.A. 77:7079-7083(1980).
 RN [3]

NUCLEOTIDE SEQUENCE.

RC PLASMTD=PE194;
 RX MEDLINE=86037248; PubMed=2414456;
 RA Mayford M., Weisblum B.;
 RT "messenger RNA from Staphylococcus aureus that specifies macrolide-
 RT lincosamide-streptogramin resistance. Demonstration of its
 RT conformations and of the leader peptide it encodes.";
 RL J. Mol. Biol. 185:769-780(1985).
 RN [4]

NUCLEOTIDE SEQUENCE.

RC PLASMTD=PE194;
 RX MEDLINE=8919652; PubMed=2467989;
 RA Mayford M., Weisblum B.;
 RT "ermC leader peptide. Amino acid sequence critical for induction by
 RT translational attenuation.";
 RL J. Mol. Biol. 206:69-79(1989).
 RN [5]

NUCLEOTIDE SEQUENCE.

RC PLASMTD=PT48;
 RX MEDLINE=89036120; PubMed=3141573;
 RA Catcampole I., Thomas C., Davies A., Dyke K.G.H.;
 RT "The nucleotide sequence of Staphylococcus aureus plasmid pT48
 RT conferring inducible macrolide-lincosamide-streptogramin B resistance
 RT and comparison with similar plasmids expressing constitutive
 RT resistance.";
 RL J. Gen. Microbiol. 134:697-709(1988).
 CC -!- FUNCTION: This peptide is involved in the control mechanism of the
 CC synthesis of the erythromycin resistance protein.

CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

DR EMBL; V01278; CAA24592.1; -; Genomic_DNA.
 DR EMBL; M37841; AAA98225.1; -; Genomic_DNA.
 DR EMBL; M19652; AAA20193.1; -; Unassigned_DNA.

DR PIR; B93717; LPSAP9.
 KM Antibiotic resistance; Leader peptide; Plasmid.
 SO SEQUENCE 19 AA; 2210 MW; 13FE3D99E4F3A7B CRC64;

Query Match 25.4%; Score 30; DB 1; Length 19;
 Best Local Similarity 45.5%; Pred. No. 1.4e+03;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 8 YVLYTMHYLYN 18
 ||| : ||| : |||
 Db 7 FVLSIVHYQPN 17

RESULT 11

O57313 9STAP PRELIMINARY; PRT; 19 AA.
 ID O57313 9STAP PRELIMINARY;
 AC O57313;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Of1 protein.
 GN Name=orf1;
 OS Staphylococcus equorum subsp. equorum.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=29383;
 RN [1]

NUCLEOTIDE SEQUENCE.

RC MEDLINE=96379895; PubMed=8787908;
 RX Loddar G., Schwarz S., Gregory P., Dyke K.;
 RA "Tandem duplication in ermC translational attenuator of the macrolide-

RT lincosamide-streptogramin B resistance plasmid pSES6 from
 RT Staphylococcus equorum.";
 RL Antimicrob. Agents Chemother. 40:215-217(1996).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=97358486; PubMed=9215582; DOI=10.1016/S0928-8244(97)00016-3;
 RA Loder G., Wercenkenthin C., Schwarz S., Dyke K.;
 RT "Molecular analysis of naturally occurring ermC-encoding plasmids in
 RT staphylococci isolated from animals with and without previous contact
 RT with macrolide / lincosamide antibiotics.";
 RL FEMS Immunol. Med. Microbiol. 18:7-15(1997).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Schwarz S.P.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X82668; CA57984.1; -; Genomic_DNA.
 KW Plasmid.
 SQ SEQUENCE 19 AA; 2237 MW; 13E4CAD99E4F3A7B CRC64;
 QY Query Match 25.4%; Score 30; DB 2; Length 19;
 Best Local Similarity 45.5%; Pred. No. 1.4e+03;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Db 8 VVLYTMHYLYN 18
 7 FVINTVHYQPN 17
 RESULT 12
 ID 0799A5 STAU PRELIMINARY; PRT; 19 AA.
 AC 0799A5;
 DT 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DE Hypothetical protein.
 OS Staphylococcus aureus.
 OC Plasmid pSES31.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OK NCBI_TaxID=1280;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=12;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=12;
 RA Schwarz S.P.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Y17294; CAB46339.1; -; Genomic_DNA.
 KW Hypothetical protein; Plasmid.
 SQ SEQUENCE 19 AA; 2237 MW; 13E4CAD99E4F3A7B CRC64;
 QY Query Match 25.4%; Score 30; DB 2; Length 19;
 Best Local Similarity 45.5%; Pred. No. 1.4e+03;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Db 8 VVLYTMHYLYN 18
 7 FVINTVHYQPN 17
 RESULT 13
 ID 0799E4 STAP PRELIMINARY; PRT; 19 AA.
 AC 0799E4;
 DT 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
 DE Oxf 1 protein.
 RN Name=orf 1;
 OS Staphylococcus epidermidis.

OG Plasmid pSES23.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OK NCBI_TaxID=1282;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=DK20;
 RA Schwarz S.P.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Y15274; CA75561.1; -; Genomic_DNA.
 KW Plasmid.
 SQ SEQUENCE 19 AA; 2210 MW; 13FEE3D99E4F3A7B CRC64;
 QY Query Match 25.4%; Score 30; DB 2; Length 19;
 Best Local Similarity 45.5%; Pred. No. 1.4e+03;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Db 8 VVLYTMHYLYN 18
 7 FVISTVHYQPN 17
 RESULT 14
 ID 07AY86 STAP PRELIMINARY; PRT; 19 AA.
 AC 07AY86;
 DT 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DE Hypothetical protein.
 OS Staphylococcus sciuri.
 OC Plasmid pSCF81.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OK NCBI_TaxID=1296;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22270974; PubMed=12384375;
 RL DOI=10.1128/AAC.46.11.3621-3623.2002;
 RA Schwarz S., Kehrenberg C., Ojo K.K.;
 RT "Staphylococcus sciuri gene erm(33), encoding inducible resistance to
 RT macrolides, lincosamides, and streptogramin B antibiotics, is a
 RT product of recombination between erm(C) and erm(A).";
 RL Antimicrob. Agents Chemother. 46:3621-3623(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Schwarz S.P.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ313523; CAC86409.1; -; Genomic_DNA.
 KW Hypothetical protein; Plasmid.
 SQ SEQUENCE 19 AA; 2237 MW; 13E4CAD99E4F3A7B CRC64;
 QY Query Match 25.4%; Score 30; DB 2; Length 19;
 Best Local Similarity 45.5%; Pred. No. 1.4e+03;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Db 8 VVLYTMHYLYN 18
 7 FVINTVHYQPN 17
 RESULT 15
 ID 045558 BACSH PRELIMINARY; PRT; 19 AA.
 AC 045558;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DE Second leader peptide.
 OS Bacillus sphaericus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OK NCBI_TaxID=1421;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=87083389; PubMed=3025178;

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RA Monod M., Mohan S., Dubnau D.;
RT "Cloning and analysis of ermG, a new macrolide-lincosamide-";
RT streptogramin B resistance element from Bacillus sphaericus.";
RL J. Bacteriol. 169:340-350(1987).
DR EMBL; M1532; AAA2418.1; -; Genomic_DNA.
DR PIR; B26930.
SQ SEQUENCE 19 AA; 2269 MW; F983BD99E4F3A7B CRC64;

Query Match 25.4%; Score 30; DB 2; Length 19;
Best Local Similarity 45.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 8 VLYTYMHYLYN 18
   :|:|:|:|
Db 7 FVISTVHYQPN 17

RESULT 16
Q799W9 STAH0 PRELIMINARY; PRT; 19 AA.
AC Q799W9
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Orf1 protein (Leader peptide).
GN Name=orf1;
OS Staphylococcus hominis.
OC Plasmid pSES5.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1290;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=73153; PLASMID=pSES5;
RA MEDLINE=97358486; PubMed=9215582; DOI=10.1016/S0928-8244(97)00016-3;
RX Loder G., Werschenhuth C., Schwarz S., Dyke K.;
RA "Molecular analysis of naturally occurring ermC-encoding plasmids in
RT staphylococci isolated from animals with and without previous contact
RT with macrolide / lincosamide antibiotics.";
RL FEWS Immunol. Med. Microbiol. 18:7-15(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=73153; PLASMID=pSES5;
RA Schwarz S.P.;
RL Submitted (OCT-1996) to the EMBL/Genbank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96379693; PubMed=8787908;
RA Loder G., Schwarz S., Gregory P., Dyke K.;
RT "Tandem duplication in ermC translational attenuator of the macrolide-
RT lincosamide-streptogramin B resistance plasmid pSES6 from
RT Staphylococcus equorum.";
RL Antimicrob. Agents Chemother. 40:215-217(1996).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Schwarz S.P.;
RL Submitted (NOV-1994) to the EMBL/Genbank/DBJ databases.
DR EMBL; Y09001; CA70205.1; -; Genomic_DNA.
DR EMBL; X82667; CAA57982.1; -; Genomic_DNA.
KW Plasmid.
SQ SEQUENCE 19 AA; 2210 MW; 13FEE3D99E4F3A7B CRC64;

Query Match 25.4%; Score 30; DB 2; Length 19;
Best Local Similarity 45.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 8 VLYTYMHYLYN 18
   :|:|:|:|
Db 7 FVISTVHYQPN 17

RESULT 17
Q4JHNS STAU0 PRELIMINARY; PRT; 19 AA.
ID Q4JHNS STAU0 PRELIMINARY; PRT; 19 AA.

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AC Q4JHNS;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Leader peptide.
GN Name=lep;
OS Staphylococcus aureus.
OC Plasmid pWBG738.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CMRSA;
RA O'Brien F.G., Zaini Z., Grubb M.B.;
RT "The complete sequence of plasmid pWBG738 from the ST1-MRSA-IV lineage
RT of community methicillin-resistant Staphylococcus aureus.";
RL Submitted (JUN-2005) to the EMBL/Genbank/DBJ databases.
DR EMBL; DQ088624; AAY8964.1; -; Genomic_DNA.
KW Plasmid.
SQ SEQUENCE 19 AA; 2210 MW; 13FEE3D99E4F3A7B CRC64;

Query Match 25.4%; Score 30; DB 2; Length 19;
Best Local Similarity 45.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 8 VLYTYMHYLYN 18
   :|:|:|:|
Db 7 FVISTVHYQPN 17

RESULT 18
Q6LEG3 92ZZZ PRELIMINARY; PRT; 19 AA.
ID Q6LEG3 92ZZZ
AC Q6LEG3
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Leader peptide.
OS Plasmid pRJS.
OC Plasmid pRJS.
OC other sequences; plasmids.
OX NCBI_TaxID=31885;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93381457; PubMed=8371109;
RA Oliveira S.S., Murphy E., Gamon M.R., Bastos M.C.;
RT "pRJS: a naturally occurring Staphylococcus aureus plasmid expressing
RT constitutive macrolide-lincosamide-streptogramin B resistance contains
RT a tandem duplication in the leader region of the ermC gene.";
RL J. Gen. Microbiol. 139:1461-1467(1993).
DR EMBL; L04687; AAA92763.1; -; Genomic_DNA.
KW Plasmid.
SQ SEQUENCE 19 AA; 2210 MW; 13FEE3D99E4F3A7B CRC64;

Query Match 25.4%; Score 30; DB 2; Length 19;
Best Local Similarity 45.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 8 VLYTYMHYLYN 18
   :|:|:|:|
Db 7 FVISTVHYQPN 17

RESULT 19
Q79DT6 92ZZZ PRELIMINARY; PRT; 19 AA.
ID Q79DT6 92ZZZ
AC Q79DT6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Leader peptide.
GN Name=ermG;
OS Plasmid pGT633.

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OG Plasmid pGT633.
 OC other sequences; plasmids.
 OX NCBI_TaxID=28406;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=94224982; PubMed=817126; DOI=10.1006/plae.1994.1007;
 RA Tamok G.W., Luchansky J.B., Miller L.A., Connell H.,
 RA Thode-Andersen S., Mercer A.A., Klenhamer T.R.;
 RT "Molecular characterization of a plasmid-borne (pGT633) erythromycin
 resistance determinant (ermGT) from *Lactobacillus reuteri* 100-63.";
 RL Plasmid 31:60-71(1994).
 DR EMBL; M64090; AAA98095.1; -; Genomic_DNA.
 KW Plasmid.
 SQ SEQUENCE 19 AA; 2237 MW; 13E4CAD99E4F3A7B CRC64;
 Query Match 25.4%; Score 30; DB 2; Length 19;
 Best Local Similarity 45.5%; Pred. No. 1.4e+03;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 8 YVLYTMHYLYN 18
 Db 7 FVINTVHQP 17

RESULT 20
 O7PC06 PLAYO PRELIMINARY; PRT; 20 AA.
 ID O7PC06;
 AC O7PC06;
 DT 01-MAR-2004 (TReMBLrel. 26, Created)
 DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN Name=py06333; Synonym=py01707;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
 OX NCBI_TaxID=73239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=17XNL;
 RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
 RA Carlton J.M., Angiolini S.V., Suh B.B., Kooij T.W., Perlea M.,
 RA Sirlin J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kogack D.S., Shumway M.F., Bidwell S.L.,
 RA Shalom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
 RA Cho J.K., Quackenbush J., Sedegah M., Shoabhi A., Cummings L.M.,
 RA Florens L., Yates J.R., III, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.;
 RT "Genome sequence and comparative analysis of the model rodent malaria
 parasite *Plasmodium yoelii yoelii*.";
 RL Nature 419:512-519(2002).
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AABL01002128; EAA18531.1; -; Genomic_DNA.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 20 AA; 2516 MW; DD48FCB3936EA2 CRC64;
 Query Match 25.4%; Score 30; DB 2; Length 20;
 Best Local Similarity 55.6%; Pred. No. 1.5e+03;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 10 LYTMHYLYN 18
 Db 3 LYKMHIFN 11

RESULT 21
 O4Y2F8 PLACH PRELIMINARY; PRT; 21 AA.
 ID O4Y2F8 PLACH PRELIMINARY; PRT; 21 AA.

AC O4Y2F8;
 DT 13-SEP-2005 (TReMBLrel. 31, Created)
 DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=PC102749.00.0;
 OS Plasmodium chabaudi.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
 OX NCBI_TaxID=5825;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
 RA Berrian M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,
 RT "A comprehensive survey of the *Plasmodium* life cycle by genomic,
 RT transcriptomic, and proteomic analyses.";
 RL Science 307:82-86(2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAJ01001590; CAH76652.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 21 AA; 2693 MW; FD162F9CAD7A4A46 CRC64;
 Query Match 25.4%; Score 30; DB 2; Length 21;
 Best Local Similarity 40.0%; Pred. No. 1.6e+03;
 Matches 6; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
 QY 4 NVKXVLYTMHYLYN 18
 Db 6 NVFLFHINHYLYN 20

RESULT 22
 O7GEY8 TOBAC PRELIMINARY; PRT; 21 AA.
 ID O7GEY8;
 AC O7GEY8;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE Ndhb gene product (21 AA) (Fragment).
 OS Nicotiana tabacum (Common tobacco).
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC asterids; lamiales; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Bright yellow 4; TISSUE=leave;
 RX MEDLINE=88210537; PubMed=3329576;
 RA Hayashida N., Matsubayashi T., Shinozaki K., Sugiyama M., Inoue K.,
 RA Hyama T.;
 RT "The gene for the 9 kd polypeptide, a possible apoprotein for the
 RT iron-sulfur centers A and B of the photosystem I complex, in tobacco
 RT chloroplast DNA.";
 RL Curr. Genet. 12:247-250(1987).
 DR EMBL; X05881; CAA29305.1; -; Genomic_DNA.
 DR GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER 21
 SQ SEQUENCE 21 AA; 2547 MW; 0A06CB19BB649FB7 CRC64;
 Query Match 25.4%; Score 30; DB 2; Length 21;
 Best Local Similarity 33.3%; Pred. No. 1.6e+03;
 Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 5 VVKXVLYTMHYLYN 16
 Db 2 VQVLYVETNYF 13

RESULT	23		
OTM447_9MOLL			
ID	OTM447_9MOLL	PRELIMINARY;	PRT; 20 AA.
AC	OTM447_9MOLL		
DT	01-MAR-2004	(TREMBLrel. 26, Created)	
DT	01-MAR-2004	(TREMBLrel. 26, Last sequence update)	
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)	
DE	Crystallin (Fragment).		
OS	Septia esculenta.		
OC	Eukaryota; Metazoa; Mollusca; Cephalopoda; Colecoidea; Neocoleoidea;		
OC	Decapodiformes; Sepioloidea; Sepiidae; Sepia.		
OX	NCBI_TaxID=31210;		
RN	[1]		
RP	PROTEIN SEQUENCE.		
RX	MEDLINE=69351593; PubMed=3255376;		
RA	Chion S.H.;		
RT	"The protein sequence homology of gamma-crystallins among major		
RT	vertebrate classes and their DNA sequence homology to heat-shock		
RT	protein genes.";		
RL	J. Protein Chem. 7:527-534(1988).		
DR	PIR; E60894; E60894.		
DR	NON_TER		
FT	NON_TER	1	
FT	NON_TER	1	
FT	NON_TER	1	
SEQUENCE	20 AA; 2448 MW; 4CD89E874BCB2EE7 CRC64;		

Query Match	24.6%	Score 29	DB 2	Length 20
Best Local Similarity	40.0%	Pred. No. 2.2e+03		
Matches 4; Conservative	3	Mismatches 3	Indels 0	Gaps 0

QY	12	YTMHYLLNNG	20
		:: :	
Db	3	YTLYYENGNG	12

RESULT	24			
ID	Q9ZYB7_9HYPE			
AC	Q9ZYB7_9HYPE	PRELIMINARY;	PRT;	21 AA.
DT	01-MAY-1999	(TREMBLrel. 10, Created)		
DT	01-MAY-1999	(TREMBLrel. 10, Last sequence update)		
DT	01-JUN-2003	(TREMBLrel. 24, Last annotation update)		
DE	Cytochrome oxidase II (Fragment).			
OS	Spiraria sp. MD-1998.			
OC	Mitochondrion.			
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Peerygota;			
OC	Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;			
OC	Braconidae; Rogadinae; Spinarina.			
OX	NCBI_Taxid=77908;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RA	MEDLIN=99152621; PubMed=10028295;			
RT	Dowton M., Austin A.D.,			
RT	"Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in			
RL	the Hymenoptera."			
RL	Mol. Biol. Evol. 16:298-309(1999).			
DR	EMBL; AF072122; AADI7665.1; -; Genomic_DNA.			
GO	GO: GO:0005739; C:mitochondrion; IEA.			
KW	Mitochondrion.			
FT	NON_TER	1		
QO	SEQUENCE	21 AA; 2691 MW; 9445FCDCBA90F8C5 CRC64;		

Query Match	24.6%	Score 29	DB 2	Length 21
Best Local Similarity	25.0%	Pred. No. 2.3e+03		
Matches 4	Conservative 6	Mismatches 6	Indels 0	Gaps 0

```
QY      1 DEXNVMXXVLYTMHYY 16
        :  :  :  :  :  :  :
Db      4 ESDVFLMYLNMVNMYY 19
```

RESULT 25

Q4X6E8	PLACH	PRELIMINARY;	PRT;	21 AA.
ID	Q4X6E8_PLACH	PRELIMINARY;		
AC	Q4X6E8			
DT	13-SEP-2005 (TrEMBLrel. 31, Created)			
DT	13-SEP-2005 (TrEMBLrel. 31, Last sequence update)			
DT	13-SEP-2005 (TrEMBLrel. 31, Last annotation update)			
DE	Hypothetical protein (Fragment).			
GN	ORFNames=PC405819.00.0;			
OS	Plasmodium chabaudi.			
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.			
OX	NCBI_TaxID=5825;			
RN	[1]			
RP	NCULECTIDE SEQUENCE.			
RA	Hall N., Karras M., Raine J.D., Carlton J.M., Koolij T.W.A.,			
RA	Berriman M., Florens L., janssen C.S., Pain A., Christophides G.K.,			
RA	James K., Rutherford K., Harris B., Harris D., Churcher C.,			
RA	Quail M.A., Ormond D., Duggett J., Trueman H.E., Mendoza J.,			
RA	Bitwell S.L., Rajadream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,			
RA	Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,			
RT	"A comprehensive survey of the Plasmodium life cycle by genomic,			
RT	transcriptomic, and proteomic analyses."			
RL	Science 307:82-86(2005).			
CC	-!- CAUTION: The sequence shown here is derived from an			
CC	EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is			
CC	preliminary data.			
CC	EMBL; CAAY01009531; CAH87528.1; -; Genomic_DNA.			
KW	Hypothetical protein.			
FT	NON TER			
FT	SEQUENCE 21 AA; 2608 MW; 803A3B52CC2F369F CRC64;			

Query Match	24.6%	Score 29	DB 2	Length 21
Best Local Similarity	26.7%	Pred. No.	2.3e+03	
Matches 4	Conservative 6	Mismatches 5	Indels 0	Gaps 0

QY 5 VMXVVLVTMHHYLLNN 19
:::|::|::|
Db 2 IILNLYSVFYIFSN 16

Search completed: January 26, 2006, 08:03:57
Job time : 71.4052 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:47:09 ; Search time 57.7414 Seconds
(without alignments)
129.360 Million cell updates/sec

Title: US-09-662-293-10

Perfect score: 83
Sequence: 1 DKLVGMGVFGRAKSIE 17

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378761 residues

Total number of hits satisfying chosen parameters: 897420

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

A_Geneseq_21: *
1: geneseqp1980s: *
2: geneseqp1980s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *
9: geneseqp2005s: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	97.6	17	5	AA52519 House dms
2	81	97.6	17	3	AAU96323 Der HMW-m
3	47	56.6	16	2	AAW45138 Human car
4	42	50.6	15	8	ADL26336 Synthetic
5	42	50.6	20	8	ADM29133 Hepatitis
6	41	49.4	10	4	ABBS5898 Vascular
7	41	49.4	10	4	ABBS6114 Vascular
8	41	49.4	10	4	ABBS5939 Vascular
9	41	49.4	10	4	AAU28751 DPI trypt
10	41	49.4	10	4	AAU28791 DPI trypt
11	41	49.4	10	4	AAU28539 DPI trypt
12	41	49.4	10	4	AAU25095 Schizophr
13	41	49.4	10	4	AAU25399 Depressio
14	41	49.4	10	4	AAU26439 Depressio
15	41	49.4	10	4	AAU26186 Depressio
16	41	49.4	10	4	AAU5439 Schizophr
17	41	49.4	10	4	ABBS2306 Human API
18	41	49.4	10	6	ABBS5912 Alzheimer
19	41	49.4	10	8	ADN31951 Human Alz
20	41	49.4	10	8	ADN31951 Human Alz
21	41	49.4	10	8	ADN31951 Human Alz
22	41	49.4	10	8	ADN31951 Human Alz
23	40	48.2	15	8	ADN31951 Human Alz
24	40	48.2	18	9	ADN31951 Human Alz

25	39	47.0	10	6	ABBS9057	ADBS9057 Alzheimer
26	39	47.0	10	8	ADN31952	ADN31952 Human Alz
27	39	47.0	10	8	ADN31952	ADN31952 Human Alz
28	39	47.0	12	7	ADN31952	ADN31952 Human Alz
29	36	42.2	16	2	AAW45139	AAW45139 Human car
30	35	42.2	8	2	AAW4471	AAW4471 Human car
31	35	42.2	8	3	AAW73124	AAW73124 Hepatitis
32	35	42.2	8	3	AAW73124	AAW73124 Hepatitis
33	35	42.2	8	4	AAU00049	AAU00049 Hepatitis
34	35	42.2	8	4	AAU03907	AAU03907 Hepatitis
35	35	42.2	8	4	AAU01621	AAU01621 Hepatitis
36	35	42.2	8	4	AAU01643	AAU01643 Hepatitis
37	35	42.2	8	4	AAU01110	AAU01110 Hepatitis
38	35	42.2	8	4	AAU00256	AAU00256 Hepatitis
39	35	42.2	8	4	AAU04104	AAU04104 Hepatitis
40	35	42.2	8	4	AAU02138	AAU02138 Hepatitis
41	35	42.2	8	5	ABU00088	ABU00088 HCV deriv
42	35	42.2	8	6	ABO00953	ABO00953 B7-like s
43	35	42.2	8	8	ADJ79584	ADJ79584 CTL epit
44	35	42.2	9	4	AAU00257	AAU00257 Hepatitis
45	35	42.2	9	4	AAU00873	AAU00873 Hepatitis
46	35	42.2	9	4	AAU01752	AAU01752 Hepatitis
47	35	42.2	9	7	ADW32956	ADW32956 HLA bindi
48	35	42.2	9	8	ADV98608	ADV98608 MHC-B40-a
49	35	42.2	9	9	ADZ86801	ADZ86801 Cytotoxic
50	35	42.2	10	4	AAJ02500	AAJ02500 Hepatitis
51	35	42.2	10	7	ADM32957	ADM32957 HLA bindi
52	35	42.2	15	4	AAE02910	AAE02910 Tryptic p
53	35	42.2	21	8	ADH35147	ADH35147 Plasma se
54	34	41.0	13	4	AAE02857	AAE02857 Tryptic p
55	34	41.0	15	6	AAO29829	AAO29829 hTRT MHC
56	34	41.0	16	2	AAK45137	AAK45137 Human car
57	32	38.6	15	5	AECL1322	AECL1322 Escherich
58	32	38.6	18	4	AAW22037	AAW22037 Peptide #
59	32	38.6	18	4	ABBA4423	ABBA4423 Peptide #
60	32	38.6	18	4	AAW38410	AAW38410 Peptide #
61	32	38.6	18	4	ABB27270	ABB27270 Protein #
62	32	38.6	18	4	AAW78165	AAW78165 Human bon
63	32	38.6	18	4	AAW65503	AAW65503 Human bra
64	32	38.6	18	4	ABBS5911	ABBS5911 Human liv
65	31	37.3	9	2	AAW35936	AAW35936 Hepatitis
66	31	37.3	9	4	AAJ02866	AAJ02866 Hepatitis
67	31	37.3	9	4	AAJ02499	AAJ02499 Hepatitis
68	31	37.3	9	6	ABBS4104	ABBS4104 E. coli g
69	31	37.3	11	5	AAU98969	AAU98969 Peptide #
70	31	37.3	20	4	ABBA2376	ABBA2376 Peptide #
71	31	37.3	20	4	AAW36185	AAW36185 Peptide #
72	31	37.3	20	4	ABBS5849	ABBS5849 Protein #
73	31	37.3	20	4	AAW76076	AAW76076 Human bon
74	31	37.3	20	4	AAW63264	AAW63264 Human bra
75	31	37.3	20	4	ABBS7800	ABBS7800 Human liv
76	31	37.3	20	5	ABBS4549	ABBS4549 Human pep
77	31	37.3	20	8	ADM29132	ADM29132 Hepatitis
78	30	36.1	10	8	ADK12127	ADK12127 Maize DUL
79	30	36.1	15	9	ADZ69770	ADZ69770 Botulinum
80	30	36.1	19	3	AAU10670	AAU10670 L. mesent
81	30	36.1	19	4	AAW47234	AAW47234 hMfi Mit
82	30	36.1	19	6	AAU64950	AAU64950 Human Mfn
83	29	34.9	10	5	AAU80236	AAU80236 Unique pe
84	29	34.9	10	5	AAU80237	AAU80237 Unique pe
85	29	34.9	14	2	AAW82998	AAW82998 M. prolif
86	29	34.9	15	1	AAW80518	AAW80518 Synthetic
87	29	34.9	15	5	ABP46746	ABP46746 Human Bly
88	29	34.9	15	7	ADG97573	ADG97573 scFV VHCD
89	29	34.9	15	8	ADBS0945	ADBS0945 Caehew nu
90	29	34.9	16	4	AAW89458	AAW89458 Streptoco
91	29	34.9	16	4	AAW84518	AAW84518 Streptoco
92	29	34.9	16	4	AAW89707	AAW89707 Streptoco
93	29	34.9	16	4	AAW88270	AAW88270 Streptoco
94	29	34.9	16	4	AAW62429	AAW62429 Streptoco
95	29	34.9	16	4	AAW69367	AAW69367 Streptoco
96	29	34.9	16	4	AAJ04119	AAJ04119 Streptoco
97	29	34.9	16	5	ABBS94470	ABBS94470 Streptoco

98	29	34.9	16	5	ABJ11373
99	29	34.9	16	5	ABJ05782
100	29	34.9	16	5	AAU95434

ALIGNMENTS

RESULT 1

AAV52519 standard; peptide; 17 AA.

AAV52519;

22-FEB-2000 (first entry)

House dust mite allergen protein (map) A/B fragment map(9).

Mite allergen protein; map; high molecular weight; HMW-map; allergy;

house dust mite; IgE; immunoglobulin E; allergen; mapA; mapB;

hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;

canine; veterinary; antibody; vaccine; immunisation.

Dermatophagoides farinae.

Key location/Qualifiers

Misc-difference 14 /label= Xaa

/note= "Xaa = any amino acid"

MO9954349-A2.

28-OCT-1999.

16-APR-1999; 99WO-US008524.

17-APR-1998; 98US-00062013.

13-MAY-1998; 98US-0085295P.

02-SEP-1998; 98US-0098909P.

(HESK-) HESKA CORP.

Mccall CA, Hunter SW, Weber ER;

WPI; 2000-052700/04.

Novel high molecular weight Dermatophagoides nucleic acid polypeptides

used to modify an animals' hypersensitivity to mite allergens.

Claim 3; Page 70; 154pp; English.

Sequences AAV52510-V52522 represent proteolytic fragments of

Dermatophagoides Farinae high molecular weight mite allergen protein (HMW-

map) composition. The HMW-map composition was isolated from a D. farinae

homogenate by gel filtration, with each fraction being analysed for the

presence of proteins that bound to IgE present in mite-allergic dog

antisera. The HMW-map composition comprises mapA (a 109 kD protein) and

mapB (98 kD). Mite allergenic proteins and peptides, and nucleic acids

encoding them, may be used in therapeutic compositions to modify an

animal's hypersensitivity reaction to mite allergens. Animals that may be

treated include mammals and birds, especially felines, canines, equines,

humans, other pets, and work or domestic animals. The proteins or

fragments may also be used to diagnose allergies via a skin test. The

proteins and peptides can also be used to raise antibodies, which have a

variety of potential uses. For example, they can be used as vaccines to

passively immunise animals against dust mite hypersensitivity, as

positive controls in test kits and as tools to recover desired dust mite

allergens from a mixture of proteins

Sequence 17 AA;

Query Match 97.6%; Score 81; DB 3; Length 17;

Best Local Similarity 100.0%; Pred. No. 4.1e-08;

Matches	17;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	DKLVMGVFFYGRAXSIE	17						
DB	1	DKLVMGVFFYGRAXSIE	17						

RESULT 2

AAU96323 standard; peptide; 17 AA.

AAU96323;

15-JUL-2002 (first entry)

Der HMW-map polypeptide #10.

Der HMW-map; American house dust mite; antiallergic; mite; IgE;

mite allergenic protein; immunoglobulin E; hypersensitivity;

immunocomplex formation.

Dermatophagoides farinae.

MO200222807-A2.

21-MAR-2002.

14-SEP-2001; 2001WO-US028730.

14-SEP-2000; 2000US-00662293.

(HESK-) HESKA CORP.

Mccall CA, Hunter SW, Weber ER;

WPI; 2002-351888/38.

New mite allergenic protein isolated from Dermatophagoides, designated

Der HMW-map protein, useful as a vaccine for treating mite allergy.

Claim 12; Page 71; 161pp; English.

The invention relates to an isolated mite allergenic protein of

Dermatophagoides, designated Der HMW-map protein, and its related nucleic

acid. The Der HMW-map protein is useful for eliciting an immune response

against Der HMW-map protein. The protein or a reagent comprising a non-

proteinaceous epitope is useful for identifying an animal (e.g., dog,

cat) susceptible to or having an allergic response to a mite. A

therapeutic composition is useful for desensitising a host animal to an

allergic response to a mite. The DNA and protein can be used in the

detection of anti-Der HMW-map antibodies in animal fluids, and inhibition

of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a

disease. Antibodies that bind to Der HMW-map are useful for inhibiting a

binding of proteins to IgE, to prevent immunocomplex formation, thus

reducing hypersensitivity responses to mite allergens, and as vaccines

against mite allergen hypersensitivity. Sequences AAU96314-AAU96342

represent Der HMW-map polypeptides of the invention

Sequence 17 AA;

Query Match 97.6%; Score 81; DB 5; Length 17;

Best Local Similarity 100.0%; Pred. No. 4.1e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKLVMGVFFYGRAXSIE 17

DB 1 DKLVMGVFFYGRAXSIE 17

RESULT 3

AAW45138 standard; peptide; 16 AA.

ID AAW45138

AC AAW45138;
XX
DT 28-APR-1998 (first entry)
XX
DE Human cartilage glycoprotein 39 derived peptide #39.
XX
KM Articular cartilage; immunosuppressive therapy; antigen; autoantigen;
KW immunological tolerance; T-cell; human cartilage glycoprotein 39;
KW HC gp-39; rheumatoid arthritis; epitope.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN MO9740068-A1.
PD 30-OCT-1997.
XX
PF 22-APR-1997; 97WO-EP002051.
XX
PR 24-APR-1996; 96EP-00201106.
XX
PA (ALKU) AKZO NOBEL NV.
XX
PI Boehr AMH, Verheijden GFM;
XX
DR WPI; 1997-535775/49.
XX
PT Peptide suitable for use in antigen specific immunosuppressive therapy -
PT resembles or mimics epitope present on HC gp-39, so inducing systemic
PT immunological tolerance to rheumatoid arthritis auto-antigen.
XX
PS Claim 2; Page 76; 82pp; English.
XX
CC The present sequence represents a peptide which resembles or mimics an
CC epitope present on human cartilage glycoprotein 39 (HC gp-39), an
CC autoantigen in rheumatoid arthritis. The invention relates to peptides
CC consisting of 16-55 amino acid residues comprising at least one of the
CC following 19 sequences: LVCYTSMS; FLCTHITS; IIVFANIS; LKTLISVGG;
CC FRKSVPEFL; FDGLDLAW; LYGGRDQ; YDIKISQH; LDISTMT; FLSMTYDF;
CC FPGQEDAS; YAVGWMLRL; MRLGAPAS; LAYEIDCF; LRGATVHT; YLKROLAG;
CC LAGAWMAL; VVALDLDDF; or LDLDPFQGS. They can be used medicinally in antigen
CC specific immunosuppressive therapy, particularly the treatment of T-cell
CC mediated destruction of articular cartilage in autoimmune diseases (e.g.
CC rheumatoid arthritis). They can also be used to detect activated
CC autoreactive T cells in an individual. The peptides have a specific
CC effect on the autoreactive T cells, thus leaving the other components of
CC the immune system intact, unlike the non-specific suppressive effect of
CC immunosuppressive drugs, and do not cause toxic side effects. The
CC peptides are predominantly recognised by autoreactive T cells from
CC rheumatoid arthritis patients, but rarely by those from healthy donors
XX
SQ Sequence 16 AA;
XX
Query Match 56.6%; Score 47; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.12;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 2 KLVNGVFPYGRA 13
:||||:|
Db 4 KLVNGVFPYGRA 15
XX
RESULT 4
ADL26336
ID ADL26336 standard; peptide; 15 AA.
XX
AC ADL26336;
XX
DT 17-JUN-2004 (first entry)
XX
DE Synthetic peptide C127 derived from a conserved region of HCV.
XX
KM HCV; hepatitis C virus; virucide; vaccine; MHC; HLA;

KW Major histocompatibility complex; human leukocyte antigen.
XX
OS Synthetic.
XX
PN WO2004024182-A2.
XX
PD 25-MAR-2004.
XX
PF 27-AUG-2003; 2003WO-EP009482.
XX
PR 13-SEP-2002; 2002AT-00001376.
PR 27-FEB-2003; 2003WO-EP002005.
PR 11-JUL-2003; 2003EP-00450171.
XX
PA (INTE-) INTERCELL AG.
XX
PI Buschle M, Habel A, Klade C, Matner F, Otava O, Vytvytska O;
PI Zauner W, Zinke S, Kiriappos H;
XX
DR WPI; 2004-269899/25.
XX
PT Isolating Hepatitis C Virus peptides (HVs) which have a binding capacity
PT to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
PT molecule by separating the complex from the HCV-peptides which do not
PT bind to the molecule.
XX
PS Example 1; Page 31; 73pp; English.
XX
CC The invention relates to a novel method for isolating Hepatitis C Virus
CC (HCV) peptides (HVs). The method of the invention has virucide activity,
CC and may be useful in producing a vaccine. The method is useful for
CC isolating Hepatitis C Virus peptides (HVs) which have a binding capacity
CC to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
CC MHC/HLA molecule for preparing a vaccine against HCV infection. The T
CC cells, a T cell clone or a T cell population or preparation is useful for
CC identifying heteroclitic epitopes or for preparing a composition for
CC treating HCV infection. The present sequence represents a synthetic
CC peptide derived from a conserved region of HCV.
XX
SQ Sequence 15 AA;
XX
Query Match 50.6%; Score 42; DB 8; Length 15;
Best Local Similarity 63.6%; Pred. No. 1;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 7 VPFYGRXSIE 17
:||||:|
Db 4 IPFYKALPIE 14
XX
RESULT 5
ADM29133
ID ADM29133 standard; peptide; 20 AA.
XX
AC ADM29133;
XX
DT 01-JUL-2004 (first entry)
XX
DE Hepatitis C virus cellular immune response related peptide.
XX
KM DNA vaccine; vaccine; antigen gene; antigen; hepatitis C virus; HCV;
KW recombinant adenovirus vaccine; adenovirus; HCV infection;
KW hepatitis C virus infection; infection; virucide.
XX
OS Hepatitis C virus.
OS Synthetic.
XX
PN WO2004028563-A1.
XX
PD 08-APR-2004.
XX
PF 24-SEP-2003; 2003WO-KR001951.
XX

PR 27-SEP-2002; 2002KR-00058712.
PR 06-NOV-2002; 2002KR-00068496.
XX
PA (GENE-) GENEXINE INC.
PA (POST-) POSTECH FOUND.
PA (DONG-) DONG-A PHARM CO LTD.
PA (DAEW-) DAEWONG CO LTD.
PA (POSC-) POSCO.
XX
PI Sung YC, Youn J, Yang S, Park S, Lee CG;
XX WPI; 2004-305120/28.
XX
XX New DNA vaccine comprising plasmid containing 2-6 kb of the total antigen
PT gene of hepatitis C virus (HCV), useful in treating or preventing HCV
PT infection.
XX
XX Disclosure; Fig 20d; 165pp; English.
XX
XX The present invention describes a DNA vaccine which comprises a plasmid
CC containing 2-6 kb of the total antigen gene of hepatitis C virus (HCV).
CC Also described: (1) a recombinant adenovirus vaccine including an
CC adenovirus containing 2-6 kb of total antigen gene of HCV; (2) a vaccine
CC administering method; and (3) a method for treating or preventing HCV
CC infection. The DNA vaccine has virucide activity. The DNA vaccine is
CC useful in treating or preventing HCV infection. The present sequence
CC represents a peptide from the HCV peptide pool used for the investigation
CC of cellular immune response in the exemplification of the present
CC invention.
XX
SQ Sequence 20 AA;

Query Match 50.6%; Score 42; DB 8; Length 20;
Best Local Similarity 63.6%; Pred. No. 1.4;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 7 VPFYGRAXSIE 17
Db :||||:|
5 IPFYGAIPLE 15

RESULT 6
ABB55898
ID ABB55898 standard; peptide; 10 AA.
XX
AC ABB55898;
XX
DT 15-FEB-2002 (first entry)
XX
DE Vascular dementia-associated protein isoform (VPI) 98.
XX
KM Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
KM diagnosis; prognosis; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200169261-A2.
XX
PD 20-SEP-2001.
XX
PF 14-MAR-2001; 2001WO-GB001106.
XX
PR 15-MAR-2000; 2000GB-00006285.
PR 24-NOV-2000; 2000GB-00028734.
PR 28-NOV-2000; 2000US-00724391.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Herath HMAc, Parekh RB, Rohlf C;
XX WPI; 2001-557937/62.
XX
PT Screening, diagnosis or prognosis of vascular dementia (VD), useful for

PT determining stage of VD and monitoring the effect of VD therapy,
PT comprises analyzing body fluid by 2-dimensional electrophoresis for
PT features correlated with VD.
XX
XX Claim 6; Page 31; 151pp; English.
XX
XX The invention relates to screening, diagnosis or prognosis of Vascular
CC Dementia (VD) in a subject comprising analysing body fluid from the
CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
CC features containing at least one chosen feature whose relative abundance
CC correlates with the presence, absence, stage or severity of VD or
CC predicts the onset or course of VD, especially detecting in a sample of
CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
CC protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the
CC specification. Detecting VD-associated features and VPI is useful for the
CC screening, diagnosis or prognosis of VD, for determining the stage or
CC severity of VD, for identifying a subject at risk of VD or for monitoring
CC the effect of therapy administered to a subject having VD. Nucleic acids
CC encoding a VPI or inhibiting the function of a VPI are useful for the
CC treatment of VD and for gene therapy
XX
SQ Sequence 10 AA;

Query Match 49.4%; Score 41; DB 4; Length 10;
Best Local Similarity 70.0%; Pred. No. 0.99;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 LVMGVPPYGR 12
Db :||||:|
1 LVMGIPTFGR 10

RESULT 7
ABB56114
ID ABB56114 standard; peptide; 10 AA.
XX
AC ABB56114;
XX
DT 15-FEB-2002 (first entry)
XX
DE Vascular dementia-associated protein isoform (VPI) 314.
XX
KM Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
KM diagnosis; prognosis; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200169261-A2.
XX
PD 20-SEP-2001.
XX
PF 14-MAR-2001; 2001WO-GB001106.
XX
PR 15-MAR-2000; 2000GB-00006285.
PR 24-NOV-2000; 2000GB-00028734.
PR 28-NOV-2000; 2000US-00724391.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Herath HMAc, Parekh RB, Rohlf C;
XX WPI; 2001-557937/62.
XX
PT Screening, diagnosis or prognosis of vascular dementia (VD), useful for
PT determining stage of VD and monitoring the effect of VD therapy, for
PT comprises analysing body fluid by 2-dimensional electrophoresis for
PT features correlated with VD.
XX
XX Claim 6; Page 36; 151pp; English.
XX
XX The invention relates to screening, diagnosis or prognosis of Vascular
CC Dementia (VD) in a subject comprising analysing body fluid from the
CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of

features containing at least one chosen feature whose relative abundance correlates with the presence, absence, stage or severity of VD or predicts the onset or course of VD, especially detecting in a sample of cerebrospinal fluid (CSF) from the subject one of 223 VD-associated protein isoforms (VPIs) (ABR55601-ABR56295) as fully defined in the specification. Detecting VD-associated features and VPI is useful for the screening, diagnosis or prognosis of VD, for determining the stage or severity of VD, for identifying a subject at risk of VD or for monitoring the effect of therapy administered to a subject having VD. Nucleic acids encoding a VPI or inhibiting the function of a VPI are useful for the treatment of VD and for gene therapy

Query Match	49.4%	Score 41	DB 4	Length 10
Best Local Similarity	70.0%	Pred No. 0.99		
Matches 7	Conservative	2	Mismatches 1	Indels 0
			Gaps	0

QY	3	LVMGVPEFYGR	12
		: :	
Db	1	LVMGIPTFGR	10

RESULT 8
ABB55939
ID ABB55939 standard; peptide; 10 AA

AC	ABB55939;
XX	
DT	15-FEB-2002 (First entry)

DE Vascular dementia-associated protein isoform (VPI) 139.

KN Vascular Dementia; VD; VD-associated protein isoform; VPI; screening
KN diagnosis; prognosis; gene therapy.

OS Homo sapiens.
XX
PN WO200169261-A2.

PD 20-SEP-2001.

PF 14-MAR-2001; 2001WO-GB001106.

PR 15-MAR-2000; 2000GB-00006285.

PR 28-NOV-2000; 2000US-00724391.

PA (OXFO-) OXFORD GLYSCSCIENCES

PI Herath HMC, Parekh RB, Rohlf C;

DR WPI; 2001-557937/62.

Screening, diagnosis

PT Features correlated with VD.
XX
PS Claim 6; Page 32; 151pp; English.

The invention relates to screening, diagnosis or prognosis of Vascular Dementia (VD) in a subject comprising analysing body fluid from the subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array

CC predict the onset or course of VD, especially detecting in a sample of
CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
CC protein isoforms (VPIs) (AAB55801-AAB56295) as fully defined in the
CC specification. Detecting VD-associated features and VPI is useful for the
CC screening, diagnosis or prognosis of VD, for determining the stage or
CC severity of VD, for identifying a subject at risk of VD or for monitoring
CC the effect of therapy administered to a subject having VD. Nucleic acids

CC encoding a VPI or inhibiting the function of a VPI are useful for the
CC treatment of VD and for gene therapy
XX
SQ Sequence 10 AA;

Query Match	49.4%	Score 41	DB 4	Length 10
Best Local Similarity	70.0%	Pred. No.	0.99	
Matches 7, Conservative		Mismatches	1	Indels 0
				Gaps 0

QY	3	LVMGVPEFYGR	12
		:	:
Db	1	LVMGIPTFCGR	10

RESULT 9
AAU28751
ID AAU28751 standard; peptide; 10 AA

AC MAU28751;
XX
DT 03-JAN-2002 (first entry)

DE DPI cryptic digest peptide #348

KM Human, depression associated protein isoform, tryptic digest peptide
KM DPl, cerebrospinal fluid; Csf; BAD; bipolar affective disorder;
KM neuropsychiatric disorder; bipolar mood disorder; neuroleptic;
KM manic-depressive illness; schizoaffective disorder.

OS Homo sapiens

PN WO200162787-A1.

PD 30-AUG-2001

PF 23-FEB-2001; 2001WO-GB000786.

PR 24-FEB-2000; 2000GB-00004412.

PR 12-DEC-2000; 2000US-0254830P.
XXPA (OXFO-) OXFORD GLYSCSCIENCES
XX

PI Herath HMAc, Parekh RB, Rohlf C,
xy

WFL; 2001-5/0626/64

PT Novel nucleic acid disorder which is a

PT neuropsychiatric disorders, such as bipolar affective disorder.
XX
PS Disclosure; Page 38, 153pp; English.
XX

CC The present invention relates to the identification of depression
CC associated protein isoforms (DPIs), particularly the tryptic digest
CC peptides of these proteins. Some of the DPIs (AAU28404-AAU28625)

CC increased in BMD subjects. Also described are peptide sequences
CC identified from DPI-45 and DPI-213 and the nucleic acid sequence they are
CC encoded by. The sequences of the invention are useful for clinical
CC screening, diagnosis, prognosis, therapy and prophylaxis of
CC neuropsychiatric disorders e.g. BMD (also known as bipolar mood disorder,
CC BP), manic-depressive illnesses, attention deficit disorders,
CC schizoaffective disorders, and unipolar affective disorders. The present
CC sequence represents one of the DPI tryptic digest peptides of the present
CC invention

```

SQ Sequence 10 AA;
Query Match      49.4%; Score 41; DB 4; Length 10;
Best Local Similarity 70.0%; Pred. No. 0.99;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```
OY 3 LVMGVPPYGR 12
    |||||:|:|
DB 1 LVMGIPTRGR 10

RESULT 10
AAU28791
ID AAU28791 standard; peptide: 10 AA.
AC AAU28791;
DT 03-JAN-2002 (first entry)
DE DPI tryptic digest peptide #388.
XX
XX Human; depression associated protein isoform; tryptic digest peptide;
XX DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;
XX neuropsychiatric disorder; bipolar mood disorder; neuroleptic;
XX manic-depressive illness; schizoaffective disorder.
XX
XX Homo sapiens.
XX
XX MO200162787-A1.
XX
XX 30-AUG-2001.
XX
XX 23-FEB-2001; 2001WO-GB000786.
XX
XX 24-FEB-2000; 2000GB-00004412.
XX 08-DEC-2000; 2000GB-00030050.
XX 12-DEC-2000; 2000US-0254830P.
XX
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
XX Herath HMAc, Parekh RB, Rohlf C, Terrett JA, Tyson KL;
XX WPI; 2001-570626/64.
XX
XX Novel nucleic acid encoding a protein associated with bipolar affective
XX disorder, which is used for diagnosis, prophylaxis and therapy of
XX neuropsychiatric disorders, such as bipolar affective disorder.
XX
XX Disclosure; Page 38; 153pp; English.
XX
XX The present invention relates to the identification of depression
XX associated protein isoforms (DPIs), particularly the tryptic digest
XX peptides of these proteins. Some of the DPIs (AAU28404-AAU28625)
XX described are decreased in the cerebrospinal fluid (CSF) of BAD (bipolar
XX affective disorder) subjects, whilst other DPIs (AAU28626-AAU28887) are
XX increased in BAD subjects. Also described are peptide sequences
XX identified from DPI-45 and DPI-213 and the nucleic acid sequence they are
XX encoded by. The sequences of the invention are useful for clinical
XX screening, diagnosis, prognosis, therapy and prophylaxis of
XX neuropsychiatric disorders e.g. BAD (also known as bipolar mood disorder,
XX BP), manic-depressive illnesses, attention deficit disorders,
XX schizoaffective disorders, and unipolar affective disorders. The present
XX sequence represents one of the DPI tryptic digest peptides of the present
XX invention
XX
XX Sequence 10 AA;
XX
XX Query Match 49.4%; Score 41; DB 4; Length 10;
XX Best Local Similarity 70.0%; Pred. No. 0.99;
XX Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
ID AAU28539 standard; peptide: 10 AA.
XX
XX AAU28539;
AC
XX
XX 03-JAN-2002 (first entry)
DT
XX
XX DPI tryptic digest peptide #136.
DE
XX
XX Human; depression associated protein isoform; tryptic digest peptide;
XX DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;
XX neuropsychiatric disorder; bipolar mood disorder; neuroleptic;
XX manic-depressive illness; schizoaffective disorder.
XX
XX Homo sapiens.
XX
XX MO200162787-A1.
XX
XX 30-AUG-2001.
XX
XX 23-FEB-2001; 2001WO-GB000786.
XX
XX 24-FEB-2000; 2000GB-00004412.
XX 08-DEC-2000; 2000GB-00030050.
XX 12-DEC-2000; 2000US-0254830P.
XX
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
XX Herath HMAc, Parekh RB, Rohlf C, Terrett JA, Tyson KL;
XX WPI; 2001-570626/64.
XX
XX Novel nucleic acid encoding a protein associated with bipolar affective
XX disorder, which is used for diagnosis, prophylaxis and therapy of
XX neuropsychiatric disorders, such as bipolar affective disorder.
XX
XX Disclosure; Page 33; 153pp; English.
XX
XX The present invention relates to the identification of depression
XX associated protein isoforms (DPIs), particularly the tryptic digest
XX peptides of these proteins. Some of the DPIs (AAU28404-AAU28625)
XX described are decreased in the cerebrospinal fluid (CSF) of BAD (bipolar
XX affective disorder) subjects, whilst other DPIs (AAU28626-AAU28887) are
XX increased in BAD subjects. Also described are peptide sequences
XX identified from DPI-45 and DPI-213 and the nucleic acid sequence they are
XX encoded by. The sequences of the invention are useful for clinical
XX screening, diagnosis, prognosis, therapy and prophylaxis of
XX neuropsychiatric disorders e.g. BAD (also known as bipolar mood disorder,
XX BP), manic-depressive illnesses, attention deficit disorders,
XX schizoaffective disorders, and unipolar affective disorders. The present
XX sequence represents one of the DPI tryptic digest peptides of the present
XX invention
XX
XX Sequence 10 AA;
XX
XX Query Match 49.4%; Score 41; DB 4; Length 10;
XX Best Local Similarity 70.0%; Pred. No. 0.99;
XX Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 3 LVMGVPPYGR 12
    |||||:|:|
DB 1 LVMGIPTRGR 10

RESULT 12
AAU25095
ID AAU25095 standard; peptide: 10 AA.
AC AAU25095;
DT 18-DEC-2001 (first entry)
DE Schizophrenia-Associated Protein Isoform (SPI) peptide #324.
XX
```

KM Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240;
 PA neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.
 XX
 OS Homo sapiens.
 XX
 PN WO200162785-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 23-FEB-2001; 2001WO-GB000792.
 XX
 PR 24-FEB-2000; 2000GB-00004415.
 PR 28-DEC-2000; 2000US-00750395.
 XX
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX
 PI Herach HMAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;
 XX
 DR WPI; 2001-570624/64.
 XX
 PT New schizophrenia associated protein isoforms and encoding nucleic acid
 PT molecules; useful for treatment, diagnosis and prognosis of schizophrenia
 PT and screening for potential drugs for treatment and new drug targets.
 XX
 PS Disclosure; Page 35; 148p; English.
 XX
 CC The sequence represents a schizophrenia-associated protein isoform (SPI).
 CC These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable
 CC in cerebrospinal fluid, serum or plasma and are useful markers of
 CC schizophrenia. The sequences can be used for treatment and diagnosis of
 CC schizophrenia, screening, prognosis, monitoring the results of therapy,
 CC identifying patients most likely to respond to a particular therapy and
 CC identification of new targets for drug treatment. SPI DNA is useful as a
 CC nucleic acid probe to detect the presence of nucleic acids or SPIs
 XX
 SQ Sequence 10 AA;
 Query Match 49.4%; Score 41; DB 4; Length 10;
 Best Local Similarity 70.0%; Pred. No. 0.99;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 3 LVMGVPEYGR 12
 Db 1 LVMGIPRFG 10
 RESULT 13
 AAU26399
 ID AAU26399 standard; peptide; 10 AA.
 XX
 AC AAU26399;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Depression-Associated Protein isoform DPI-184 #2.
 XX
 KM Human; Bipolar Affective Disorder; BAD; Depression-Associated feature;
 KM DF; Depression-Associated protein isoform; DPI; Cerebro-spinal fluid;
 KM CSF; antidepressant; antimanic; nootropic; tranquilliser; neuroleptic;
 KM attention deficient disorder; schizoaffective disorder;
 KM unipolar affective disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200163294-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 23-FEB-2001; 2001WO-GB000791.
 XX
 PR 24-FEB-2000; 2000GB-00004412.
 PR 08-DEC-2000; 2000GB-00030050.
 PR 12-DEC-2000; 2000US-0254830P.
 XX

XX
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX
 PI Herach HMAC, Parekh RB, Rohlf C;
 XX
 DR WPI; 2001-582081/65.
 XX
 PT Preparation for diagnosing or treating bipolar affected disorder (BAD) or
 PT unipolar depression, or for screening for modulators, comprises a BAD-
 PT associated protein isoform.
 XX
 PS Claim 8; Page 38; 163p; English.
 XX
 CC The invention relates to a preparation comprising an isolated Bipolar
 CC Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are
 CC used to screen, diagnose or prognosis of BAD or unipolar depression,
 CC determine the stage or severity of BAD or unipolar depression, identify a
 CC subject at risk of developing BAD or unipolar depression, or monitor the
 CC effect of therapy in a subject. They are also used to screen for or
 CC identify agents that interact with a DPI. These agents, antibodies
 CC against the DPIs, and nucleic acids encoding the DPIs are used to treat
 CC or prevent BAD or unipolar depression. Diseases that can be treated are
 CC attention deficient disorder, a schizoaffective disorder, a bipolar or a
 CC unipolar affective disorder. The DPIs are used in proteomics. The
 CC proteomic approach of using DPIs for screening, diagnosis or prognosis of
 CC BAD or unipolar depression overcomes the problems of using gene
 CC expression analysis, such as not being able to obtain central nervous
 CC system (CNS) tissue from a living patient under normal circumstances. The
 CC present sequence is a DIP increased in the CSF (cerebro-spinal fluid) of
 CC subjects having BAD
 XX
 SQ Sequence 10 AA;
 Query Match 49.4%; Score 41; DB 4; Length 10;
 Best Local Similarity 70.0%; Pred. No. 0.99;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 3 LVMGVPEYGR 12
 Db 1 LVMGIPRFG 10
 RESULT 14
 AAU26439
 ID AAU26439 standard; peptide; 10 AA.
 XX
 AC AAU26439;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Depression-Associated Protein isoform DPI-234.
 XX
 KM Human; Bipolar Affective Disorder; BAD; Depression-Associated feature;
 KM DF; Depression-Associated protein isoform; DPI; Cerebro-spinal fluid;
 KM CSF; antidepressant; antimanic; nootropic; tranquilliser; neuroleptic;
 KM attention deficient disorder; schizoaffective disorder;
 KM unipolar affective disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200163294-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 23-FEB-2001; 2001WO-GB000791.
 XX
 PR 24-FEB-2000; 2000GB-00004412.
 PR 08-DEC-2000; 2000GB-00030050.
 PR 12-DEC-2000; 2000US-0254830P.
 XX
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX
 PI Herach HMAC, Parekh RB, Rohlf C;
 XX

PT		unipolar depression, or for screening for modulators, comprises a BAD-
PT		associated protein isoform.
XX		
PS		Claim 8; Page 33; 163pp; English.
XX		
CC	The invention relates to a preparation comprising an isolated Bipolar	
CC	Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are	
CC	used to screen, diagnose or prognose of BAD or unipolar depression,	
CC	determine the stage or severity of BAD or unipolar depression, identify a	
CC	subject at risk of developing BAD or unipolar depression, or monitor the	
CC	effect of therapy in a subject. They are also used to screen for or	
CC	identify agents that interact with a DPI. These agents, antibodies	
CC	against the DPIs, and nucleic acids encoding the DPIs are used to treat	
CC	or prevent BAD or unipolar depression. Diseases that can be treated are	
CC	attention deficient disorder, a schizoaffective disorder, a bipolar or a	
CC	unipolar affective disorder. The DPIs are used in proteomics. The	
CC	proteomic approach of using DPIs for screening, diagnosis or prognosis of	
CC	BAD or unipolar depression overcomes the problems of using gene	
CC	expression analysis, such as not being able to obtain central nervous	
CC	system (CNS) tissue from a living patient under normal circumstances. The	
CC	present sequence is a DIP decreased in the CSF (cerebro-spinal fluid) of	
CC	subjects having BAD	
SQ		
	Sequence 10 AA;	
Query Match	49.4%; Score 41; DB 4; Length 10;	
Best Local Similarity	70.0%; Pred. No. 0.99;	
Matches	7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	
OY	3 LVMGVPFYGR 12 :: : 1 LVMGIPTPRG 10	
Dd		
RESULT 16		
ID	AAU15439 standard; peptide: 10 AA.	
AC	AAU15439;	
XX		
DT	24-OCT-2001 (first entry)	
XX		
DE	Schizophrenia-associated isoform peptide #324.	
XX		
KW	Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder;	
KM	neurological disorder; neuropathy.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200163293-A2.	
XX		
PD	30-AUG-2001.	
XX		
PF	23-FEB-2001; 2001WO-GB000783.	
XX		
PR	24-FEB-2000; 2000GB-00004415.	
XX		
PR	28-DEC-2000; 2000US-00750395.	
XX		
PA	(OXFO-) OXFORD GLYCOSCENCES UK LTD.	
XX		
PI	Herath HMAc, Parekh RB, Rohlf C;	
XX		
DR	WPI; 2001-502868/55.	
XX		
PT	Diagnosing and monitoring Schizophrenia by detecting the presence of	
PT	Schizophrenia Associated Features and Schizophrenia Associated Protein	
XX	Isoforms in samples of cerebrospinal fluid.	
XX		
PS	Claim 6; Page 35; 160pp; English.	
XX		
CC	The invention relates to methods and compositions for screening,	
CC	diagnosis and prognosis of Schizophrenia. The method involves detecting	
CC	the presence of Schizophrenia (SCH) Associated Features (Sfe) and SCH	

CC Associated Protein Isoforms (SPIs) in samples, e.g. by electrophoresis,
CC immunosay or hybridisation assay, for diagnosing and monitoring SCH
CC studying the effectiveness of treatments and for identifying potential
CC therapeutic agents. The method is used for (1) screening or diagnosis of
CC SCH and the relative abundance of at least 1 chosen feature correlates
CC with the presence or absence of SCH; and (2) monitoring the effect of
CC therapy administered to a subject with SCH and the relative abundance of
CC at least 1 chosen feature which correlates with the severity of SCH. The
CC expression and activity of the SPIs, SPIs and related molecules (e.g.
CC secondary messengers) are studied to diagnose SCH, monitor the progress
CC of the disorder and the effectiveness of treatment and as targets to
CC identify and produce potential therapeutic agents for the treatment of
CC SCH. The paucity of detectable neuronal defects distinguishes
CC neuropsychiatric disorders such as SCH from neurological disorders, where
CC manifestations of anatomical and biochemical changes have been identified
CC in many cases. Consequently the identification and characterisation of
CC cellular and/or molecular causative defects and neuropathies are
CC necessary for improved treatment of neuropsychiatric disorders. AAU15114-
CC AAU15762 represent the amino acid sequences of schizophrenia-associated
CC isoforms used in the method of the invention
CC
XX
SQ Sequence 10 AA;

Query Match 49.4%; Score 41; DB 4; Length 10;
Best Local Similarity 70.0%; Pred. No. 0.99;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 3 LVMGVPFYGR 12
|||:|:|
Db 1 LVMGIPTFGR 10

RESULT 17
ABBS2306
ID ABBS2306 standard; peptide: 10 AA.

XX
AC ABBS2306;

XX
DT 08-FEB-2002 (first entry)

XX
DE Human API-41 cryptic digest peptide #1.

XX
KM Human; neuroprotective; nootropic; gene therapy; vaccine;

XX
KM Alzheimer's disease; Alzheimer's Disease-Associated Feature; AP;

XX
KM Alzheimer's Disease-Associated Protein Isoform; API; cryptic digest;

XX
KM Expression Reference Protein Isoform; ERPI; proteolysis.

XX
OS Homo sapiens.

XX
PN WO200175454-A2.

XX
PD 11-OCT-2001.

XX
PF 03-APR-2001; 2001WO-US010908.

XX
PR 03-APR-2000; 2000US-0194504P.

XX
PR 28-NOV-2000; 2000US-0253647P.

XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX
PA (PFIZ) PFIZER INC.

XX
PI Durham LX, Friedman DL, Herath HMC, Kimmel LH, Parekh RB;

XX
PI Potter DM, Rohlf C, Silber BM, Stiger TR, Sunderland PT;

XX
PI Townsend RR, White F, Williams SA;

XX
DR WPI; 2001-639384/73.

XX
PT Screening for Alzheimer's disease in a mammal, by making two-dimensional
XX array of a feature whose relative abundance correlates with disease, and
XX comparing with abundance of the feature in samples of healthy persons.
XX
XX Example; Page 33; 162pp; English.

CC The invention relates to methods for the screening, diagnosis and
CC prognosis of Alzheimer's disease. The methods involve the detection of
CC Alzheimer's disease-Associated Features (AFs) and Alzheimer's Disease-
CC Associated Protein Isoforms (APIs) in cerebrospinal fluid, serum or
CC plasma. The abundance of the AFs and APIs is then normalised to an
CC Expression Reference Protein Isoform (ERPI) in order to determine whether
CC a patient is suffering from, or has a predisposition to, Alzheimer's
CC disease. The relative abundance of the AFs and APIs correlates with the
CC severity of Alzheimer's Disease. The present sequence is a peptide
CC produced from an API by proteolysis
CC
XX
SQ Sequence 10 AA;

Query Match 49.4%; Score 41; DB 4; Length 10;
Best Local Similarity 70.0%; Pred. No. 0.99;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 3 LVMGVPFYGR 12
|||:|:|
Db 1 LVMGIPTFGR 10

RESULT 18
ABRS9112
ID ABRS9112 standard; peptide: 10 AA.

XX
AC ABRS9112;

XX
DT 11-JUL-2003 (first entry)

XX
DE Alzheimer's Disease-associated protein isoform, API-41, SEQ ID 277.

XX
KM Nootropic; Neuroprotective; Alzheimer's disease; API; human;

XX
KM Alzheimer's Disease-associated protein isoform.

XX
OS Homo sapiens.

XX
PN WO2003028543-A2.

XX
PD 10-APR-2003.

XX
PF 03-OCT-2002; 2002WO-US031642.

XX
PR 03-OCT-2001; 2001US-0326708P.

XX
PA (PFIZ) PFIZER PROD INC.

XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX
PI Durham LX, Friedman DL, Herath HMC, Kimmel LH, Parekh RB;

XX
PI Potter DM, Rohlf C, Silber BM, Snyder PJ, Soares HD, Stiger TR;

XX
PI Sunderland PT, Townsend RR, White WF, Williams SA;

XX
DR WPI; 2003-371957/35.

XX
PT Screening or diagnosing of Alzheimer's disease (AD) determine the stage
XX or severity of AD in a subject, comprises analyzing a test sample of body
XX fluid from the subject by 2-dimensional electrophoresis.

XX
PS Claim 2; Page 51; 179pp; English.

XX
CC The present invention relates to methods for screening or diagnosing

XX
CC Alzheimer's disease (AD) to determine the stage or severity of AD in a

XX
CC subject, to identify subject at risk of developing AD, or to monitor the

XX
CC effect of therapy administered. The methods comprise analysing a test

XX
CC sample of body fluid by 2-dimensional electrophoresis to generate a 2-
XX dimensional array of AD-associated features (AFs). The method
XX alternatively comprises quantitatively detecting in a sample of body
XX fluid from the subject, one or more AD-associated protein isoforms (APIs;
XX ABBS58710-ABBS59184)
XX
XX Sequence 10 AA;

Query Match 49.4%; Score 41; DB 6; Length 10;

Best Local Similarity 70.0%; Pred. No. 0.99;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 LVMGVPPYGR 12
| | | | : | : |
Db 1 LVMGIPTFGR 10

RESULT 19
ADN31951
ID ADN31951 standard; peptide; 10 AA.

XX AC ADN31951;

XX DT 01-JUN-2004 (first entry)

XX DE Human Alzheimer's disease-API tryptic digest peptide - SEQ ID 277.

XX KW Alzheimer's disease; neurotrophic; neuroprotective; cerebrospinal fluid;

XX KW CSF; Alzheimer's disease-associated protein isoform; API; tryptic digest;

XX KW human.

XX OS Homo sapiens.

XX PN EP1408333-A2.

XX PD 14-APR-2004.

XX PF 03-OCT-2002; 2002EP-00256893.

XX PR 03-OCT-2002; 2002US-0326708P.

XX PA (PF12) PFIZER PROD INC.
(OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX PI Dutham LK, Friedman DJ, Herath HMA, Kimmel LH, Parekh RB;

XX PI Potter DM, Rohlf C, Silber BM, Snyder PJ, Soares HD, Stigler TR;

XX PI Sunderland PT, Townsend RR, White WF, Williams SA;

XX DR WPI; 2004-318939/30.

XX PT Screening or diagnosis of Alzheimer's disease (AD) in subject,

XX PT determining stage or severity of AD, identifying subject at risk of

XX PT developing AD, or monitoring effect of therapy, by detecting Alzheimer's

XX PT disease-Associated Features.

XX PS Example; SEQ ID NO 277; 208pp; English.

XX CC The invention relates to a novel method for screening or diagnosis of

XX CC Alzheimer's disease (AD) in a subject, determining the stage or severity

XX CC of AD, identifying a subject at risk of developing AD or monitoring the

XX CC effect of therapy administered to a subject having AD, by analyzing body

XX CC fluid to generate a two-dimensional array of Alzheimer's disease-

XX CC associated features (AFs) such as AF-200, AF-201, AF-202, AF-203, AF-204,

XX CC AF-205, etc., and comparing the abundance of AFs with a control. The

XX CC method of the invention has neurotrophic and neuroprotective applications

XX CC and may be useful for screening or diagnosis of Alzheimer's disease (AD)

XX CC in a subject, determining the stage or severity of AD in a subject,

XX CC identifying a subject at risk of developing AD or monitoring the effect

XX CC of therapy administered to a subject having AD. The body fluid is

XX CC cerebrospinal fluid (CSF). The current sequence is that of a human

XX CC Alzheimer's disease-associated protein isoform (API) tryptic digest

XX CC peptide of the invention.

XX SQ Sequence 10 AA;

OY 3 LVMGVPPYGR 12
| | | | : | : |
Db 1 LVMGIPTFGR 10

RESULT 20
AD078706
ID AD078706 standard; peptide; 10 AA.
XX AC AD078706;
XX DT 26-AUG-2004 (first entry)
XX DE Schizophrenia-Associated Protein Isoform (SPI) segid 324.
XX KW neuroleptic; Schizophrenia; immunospecific binding;
XX KW Schizophrenia-Associated Protein Isoform; SPI; schizophrenia screening;
XX KW Schizophrenia diagnosis; schizophrenia prognosis;
XX KW Schizophrenia treatment; drug development; cerebrospinal fluid; human.
XX OS Homo sapiens.
XX PN US2004110938-A1.
XX PD 10-JUN-2004.
XX PF 23-FEB-2001; 2001US-00791377.
XX PR 24-FEB-2000; 2000GB-00044156.
XX PR 28-DEC-2000; 2000US-00750395.
XX PA (PARE/) PAREKH R B.
XX PA (HERA/) CHANDRASIRI HERATH H M A.
XX PA (ROHL/) ROHLFF C.
XX PA (TERR/) TERRETT J A.
XX PA (TYSO/) TYSON K L.
XX PI Parekh RB, Chandrasiri Herath HMA, Rohlf C, Terrett JA, Tyson KL;
XX DR WPI; 2004-440403/41.
XX PT New isolated nucleic acid molecule, useful for diagnosing Schizophrenia,
XX PT for monitoring the effectiveness of Schizophrenia treatment or for
XX PT screening agents for treating Schizophrenia.
XX PS Disclosure; SEQ ID NO 324; 170pp; English.
XX CC The invention describes an isolated nucleic acid molecule (1) that
XX CC hybridises to two short nucleic acid sequences and the 1515 amino acid
XX CC sequence fully defined in the specification. Also described are: a
XX CC preparation comprising an isolated peptide coded for by the nucleic acid
XX CC molecule above, or comprising an isolated human protein comprising one or
XX CC more of the following sequences: Glu-Leu-Asp-Val-Leu-Gln-Gly-Arg, and Gly
XX CC -Ile-Leu-Ile-Leu-Gly-Gln-Gln-Asp-Thr-Leu-Gly-Gly-Arg; methods for
XX CC diagnosing Schizophrenia; antibodies capable of immunospecific binding to
XX CC a Schizophrenia-Associated Protein Isoform (SPI); methods of treating
XX CC Schizophrenia; and methods of screening for agents that modulate a
XX CC characteristic (e.g., expression or binding activity) of an SPI, an SPI
XX CC analogue, or an SPI-related polypeptide. The nucleic acid molecule and
XX CC encoded proteins, as well as the methods and compositions are useful for
XX CC screening, diagnosing, and prognosing Schizophrenia, for monitoring the
XX CC effectiveness of Schizophrenia treatment, for identifying patients most
XX CC likely to respond to a particular therapeutic treatment and for
XX CC developing drug. They are also useful for screening modulators of
XX CC Schizophrenia-Associated Protein Isoform useful for treating
XX CC Schizophrenia. This is the amino acid sequence a schizophrenia-associated
XX CC protein isoform increased in the cerebrospinal fluid of schizophrenia
XX CC patients.
XX SQ Sequence 10 AA;

OY 3 LVMGVPPYGR 12
| | | | : | : |
Db 1 LVMGIPTFGR 10

Db 1 LVWG1PTFGR 10

RESULT 21

ADRL9350
ID ADRL9350 standard; peptide; 10 AA.

XX AC ADRL9350;

DT 04-NOV-2004 (first entry)

DE TRPI derived human tryptic digest peptide, SEQ ID 12.

XX KW Tissue damage; chronic; tissue repair-associated protein isoform; TRPI;
KW antiulcer; vulnerary; chronic dermal ulcer; human; tryptic digest;
XX proteolysis; trypsin.

OS Homo sapiens.

PN WO2004069795-A2.

PD 19-AUG-2004.

PF 02-FEB-2004; 2004WO-US002881.

PR 03-FEB-2003; 2003US-0444600P.

XX (PRIZ) PEIZER PROD INC.

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX PI Butt R, Rumpel K, Williams-Jones BI, Herath HMAC, Rohlf C;

PI Bruce JA, Patel TP;

DR WPI; 2004-604404/58.

PT Diagnosing, or monitoring the effect of therapy of, chronic tissue damage
PT (e.g. chronic dermal ulcer) comprises detecting and/or quantifying tissue
PT Repair-Associated protein isoform in a sample (e.g. wound exudate) from
PT the subject.

XX PS Claim 7; SEQ ID NO 12; 107pp; English.

XX CC The invention relates to a novel method for assessing, screening,
CC diagnosing or prognosing chronic tissue damage in a subject, identifying
CC a subject at risk of developing chronic tissue damage, or monitoring the
CC effect of therapy administered to a subject having chronic tissue damage.
CC The method comprises detecting and/or quantifying in a biological sample
CC from the subject a tissue repair-associated protein isoform (TRPI), given
CC in the specification. The invention further comprises: an isolated or
CC recombinant TRPI selected from the proteins listed in the specification;
CC screening for or identifying an agent capable of modulating the
CC expression or activity of the TRPI or a TRPI-related polypeptide; a
CC pharmaceutical composition comprising the TRPI cited above or an active
CC agent that modulates the expression and/or activity of the TRPI or a TRPI
CC -related polypeptide, and a pharmaceutical carrier, vehicle or diluent;
CC and treating chronic tissue damage. The novel compositions have antiulcer
CC and vulnerary activity. The composition and methods are useful for
CC diagnosing, preventing, prognosing and treating chronic tissue damage,
CC such as a chronic dermal ulcer. These may also be used for drug screening
CC or drug development, or for screening or identifying agents capable of
CC modulating the activity of TRPI or TRPI-related polypeptides. This
CC sequence represents a TRPI derived human tryptic digest peptide. The
CC peptide was produced by proteolysis using trypsin of a tissue repair-
CC associated protein isoform of the invention.

XX SQ Sequence 10 AA;

Query Match 49.4%; Score 41; DB 8; Length 10;
Best Local Similarity 70.0%; Pred. NO. 0.99;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 LVWGVPFYGR 12

Db 1 LVWG1PTFGR 10

RESULT 22

ADL26337
ID ADL26337 standard; peptide; 15 AA.

XX AC ADL26337;

DT 17-JUN-2004 (first entry)

DE Synthetic peptide C128 derived from a conserved region of HCV.

XX KW HCV; hepatitis C virus; virucide; vaccine; MHC, HLA;
KW major histocompatibility complex; human leukocyte antigen.

XX OS Synthetic.

PN WO2004024182-A2.

PD 25-MAR-2004.

PF 27-AUG-2003; 2003WO-EP009482.

PR 13-SEP-2002; 2002AT-00001376.

PR 27-FEB-2003; 2003WO-EP002005.

PR 11-JUL-2003; 2003EP-00450171.

XX PA (INTE-) INTERCELL AG.

XX PI Buschle M, Habel A, Klade C, Mattner F, Ocava O, Vytvytska O;

PI Zauner W, Zinke S, Kiriappos H;

DR WPI; 2004-269899/25.

PT Isolating Hepatitis C Virus peptides (HVs) which have a binding capacity
PT to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
PT molecule by separating the complex from the HCV-peptides which do not
PT bind to the molecule.

XX PS Example 1; Page 31; 73pp; English.

XX CC The invention relates to a novel method for isolating Hepatitis C Virus
CC (HCV) peptides (HVs). The method of the invention has virucide activity,
CC and may be useful in producing a vaccine. The method is useful for
CC isolating Hepatitis C Virus peptides (HVs) which have a binding capacity
CC to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
CC MHC/HLA molecule for preparing a vaccine against HCV infection. The T
CC cells; a T cell clone or a T cell population or preparation is useful for
CC identifying heteroclitic epitopes or for preparing a composition for
CC treating HCV infection. The present sequence represents a synthetic
CC peptide derived from a conserved region of HCV.

XX SQ Sequence 15 AA;

Query Match 48.2%; Score 40; DB 8; Length 15;
Best Local Similarity 54.5%; Pred. NO. 2.4;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 7 VPFYGRAXST 17
Db 4 IPFYGRAXST 14

RESULT 23

ADV22957
ID ADV22957 standard; peptide; 18 AA.

XX AC ADV22957;

DT 10-MAR-2005 (first entry)

XX

DE HCV H77 immunogenic peptide #198.
 XX
 XX Vaccine; virucide; antigen; autoimmune disease; infection;
 KW immune modulation; cancer; neoplasm; cytostatic; melanoma; lung tumor;
 KW breast tumor; uterine cervix tumor; prostatic cancer; colon tumor;
 KW pancreas tumor; stomach tumor; bladder tumor; kidney tumor;
 KW hodgekin's lymphoma.
 KW
 OS Hepatitis C virus strain H77.
 XX
 PN WO2004108753-A1.
 XX
 XX 16-DEC-2004.
 PD
 XX 10-JUN-2004; 2004WO-AU000775.
 PE
 XX 10-JUN-2003; 2003AU-00902875.
 PR 25-MAR-2004; 2004AU-00901589.
 PR
 XX (UYME) UNIV MELBOURNE.
 PA
 XX Kent SJ;
 PI
 DR WPI; 2005-031657/03.
 XX
 PT Use of at least one set of peptides in the preparation of a medicament
 PT for modulating an immune response, and for treating cancer or yeast,
 PT viral, bacterial, protozoal and mycoplasma infections.
 PT
 XX
 PS Disclosure; SEQ ID NO 1377; 645pp; English.
 PS
 XX The invention relates to the use of at least one set of peptides in the
 CC preparation of a medicament for modulating an immune response, where
 CC individual peptides of a respective set comprise different portions of an
 CC amino acid sequence corresponding to a single polypeptide of interest and
 CC display partial sequence identity or similarity to at least one other
 CC peptide of the same set of peptides (i.e. they are overlapping). Also
 CC included are an antigen-presenting cell which has been contacted with the
 CC peptides above and thus presents the peptides, a population of such
 CC antigen-presenting cells, a process for producing antigen-presenting
 CC cells for modulating an immune response to a polypeptide of interest, a
 CC method for producing antigen-specific lymphocytes, a composition
 CC comprising at least one set of the peptides (and a carrier and/or
 CC diluent), a method for modulating an immune response to a polypeptide of
 CC interest comprising administering to a patient in need at least one set
 CC of the peptides, a method for treatment and/or prophylaxis of a disease
 CC or condition associated with the presence of a polypeptide of interest
 CC and a composition of matter for modulating an immune response in a
 CC subject to a target antigen. The polypeptide of interest is also a
 CC disease- or condition-associated polypeptide that is a polypeptide
 CC produced by a pathogenic organism or a cancer, and produced by a
 CC pathogenic organism selected from yeast, viruses, bacteria, helminths,
 CC protozoans and mycoplasmas. The disease- or condition-associated
 CC polypeptide is produced by a cancer selected from melanoma, lung cancer,
 CC breast cancer, cervical cancer, prostate cancer, colon cancer, pancreatic
 CC cancer, stomach cancer, bladder cancer, kidney cancer, post transplant
 CC lymphoproliferative disease (PTLD) or Hodgekin's lymphoma. The uncultured
 CC antigen-presenting cells or their precursors are useful in the
 CC preparation of a medicament for the treatment of a disease or condition
 CC in a subject, which disease or condition is associated with the presence
 CC of aberrant expression of a target antigen, where the antigen-presenting
 CC cells or their precursors have not been subjected to activating
 CC conditions but have been contacted with an antigen that corresponds to
 CC the target antigen to express a processed or modified form of the antigen
 CC for presentation to the subject's immune system. The present sequence is
 CC one of a set of overlapping immunogenic peptides derived from a Hepatitis
 CC C virus protein.
 XX
 XX Sequence 18 AA;
 SQ

Query Match 48.2%; Score 40; DB 9; Length 18;
 Best Local Similarity 54.5%; Pred. No. 3;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 7 VPEYGRAXSIE 17
 :|||:|:|
 Db 8 IPFYGKALPDE 18
 RESULT 24
 ADV22958
 ID ADV22958 standard; peptide; 18 AA.
 XX
 AC ADV22958;
 XX
 DT 10-MAR-2005 (first entry)
 XX
 DE HCV H77 immunogenic peptide #199.
 XX
 KW Vaccine; virucide; antigen; autoimmune disease; infection;
 KW immune modulation; cancer; neoplasm; cytostatic; melanoma; lung tumor;
 KW breast tumor; uterine cervix tumor; prostatic cancer; colon tumor;
 KW pancreas tumor; stomach tumor; bladder tumor; kidney tumor;
 KW hodgekin's lymphoma.
 KW
 OS Hepatitis C virus strain H77.
 XX
 PN WO2004108753-A1.
 XX
 XX 16-DEC-2004.
 PD
 XX 10-JUN-2004; 2004WO-AU000775.
 PE
 XX 10-JUN-2003; 2003AU-00902875.
 PR 25-MAR-2004; 2004AU-00901589.
 PR
 XX (UYME) UNIV MELBOURNE.
 PA
 XX Kent SJ;
 PI
 DR WPI; 2005-031657/03.
 XX
 PT Use of at least one set of peptides in the preparation of a medicament
 PT for modulating an immune response, and for treating cancer or yeast,
 PT viral, bacterial, protozoal and mycoplasma infections.
 PT
 XX
 PS Disclosure; SEQ ID NO 1378; 645pp; English.
 PS
 XX The invention relates to the use of at least one set of peptides in the
 CC preparation of a medicament for modulating an immune response, where
 CC individual peptides of a respective set comprise different portions of an
 CC amino acid sequence corresponding to a single polypeptide of interest and
 CC display partial sequence identity or similarity to at least one other
 CC peptide of the same set of peptides (i.e. they are overlapping). Also
 CC included are an antigen-presenting cell which has been contacted with the
 CC peptides above and thus presents the peptides, a population of such
 CC antigen-presenting cells, a process for producing antigen-presenting
 CC cells for modulating an immune response to a polypeptide of interest, a
 CC method for producing antigen-specific lymphocytes, a composition
 CC comprising at least one set of the peptides (and a carrier and/or
 CC diluent), a method for modulating an immune response to a polypeptide of
 CC interest comprising administering to a patient in need at least one set
 CC of the peptides, a method for treatment and/or prophylaxis of a disease
 CC or condition associated with the presence of a polypeptide of interest
 CC and a composition of matter for modulating an immune response in a
 CC subject to a target antigen. The polypeptide of interest is also a
 CC disease- or condition-associated polypeptide that is a polypeptide
 CC produced by a pathogenic organism or a cancer, and produced by a
 CC pathogenic organism selected from yeast, viruses, bacteria, helminths,
 CC protozoans and mycoplasmas. The disease- or condition-associated
 CC polypeptide is produced by a cancer selected from melanoma, lung cancer,
 CC breast cancer, cervical cancer, prostate cancer, colon cancer, pancreatic
 CC cancer, stomach cancer, bladder cancer, kidney cancer, post transplant
 CC lymphoproliferative disease (PTLD) or Hodgekin's lymphoma. The uncultured
 CC antigen-presenting cells or their precursors are useful in the
 CC preparation of a medicament for the treatment of a disease or condition

CC in a subject, which disease or condition is associated with the presence
 CC or aberrant expression of a target antigen, where the antigen-presenting
 CC cells or their precursors have not been subjected to activating
 CC conditions but have been contacted with an antigen that corresponds to
 CC the target antigen to express a processed or modified form of the antigen
 CC for presentation to the subject's immune system. The present sequence is
 CC one of a set of overlapping immunogenic peptides derived from a Hepatitis
 CC C virus protein.

XX
 XX
 SQ Sequence 18 AA;

Query Match 48.2%; Score 40; DB 9; Length 18;
 Best Local Similarity 54.5%; Pred. No. 3;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 7 VPFYGRAXSIE 17
 :|||:|:
 Db 1 IPFYKAIPL 11

RESULT 25

ABR59057 standard; peptide; 10 AA.

ABR59057;

11-JUL-2003 (first entry)

Alzheimer's Disease-associated protein isoform, API-406, SEQ ID 278.

Neurotrophic; Neuroprotective; Alzheimer's disease; API; human;

Alzheimer's Disease-associated protein isoform.

Homo sapiens.

WO2003028543-A2.

10-APR-2003.

03-OCT-2002; 2002WO-US031642.

03-OCT-2001; 2001US-0326708P.

(PEITZ) PEITZ PROD INC.

(OXFO-) OXFORD GLYCOSCIENCES UK LTD.

Durham LK, Friedman DL, Herath HMA, Kimmel LH, Parekh RB;
 PI Potter DM, Rohlf C, Silber BM, Snyder PJ, Soares HD, Stiger TR;
 PI Sunderland PT, Townsend RR, White WF, Williams SA;

WPI; 2003-371957/35.

Screening or diagnosing of Alzheimer's disease (AD) determine the stage
 PT or severity of AD in a subject, comprises analyzing a test sample of body
 PT fluid from the subject by 2-dimensional electrophoresis.

Claim 2; Page 47; 179pp; English.

XX The present invention relates to methods for screening or diagnosing
 CC Alzheimer's disease (AD) to determine the stage or severity of AD in a
 CC subject, to identify subject at risk of developing AD, or to monitor the
 CC effect of therapy administered. The methods comprise analyzing a test
 CC sample of body fluid by 2-dimensional electrophoresis to generate a 2-
 CC dimensional array of AD-associated features (AFs). The method
 CC alternatively comprises quantitatively detecting in a sample of body
 CC fluid from the subject, one or more AD-associated protein isoforms (APIs;
 CC ABR58710-ABR59184)

SO Sequence 10 AA;

Query Match 47.0%; Score 39; DB 6; Length 10;
 Best Local Similarity 70.0%; Pred. No. 2.4;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 LVMGVPRYGR 12
 :|||:|:
 Db 1 LVMGLPTFRGR 10

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 Job time : 61.7414 secs

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OM protein - protein search, using sw model

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Title: US-09-662-293-10

Perfect score: 83

Sequence: 1 DKLVGVFPYGRAXSIE 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 229350

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA:*

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3: /cgn2_6/ptodata/1/aa/H COMB.pep:*

4: /cgn2_6/ptodata/1/aa/PTUS COMB.pep:*

5: /cgn2_6/ptodata/1/aa/RE COMB.pep:*

6: /cgn2_6/ptodata/1/aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	97.6	17	US-09-292-225-10	Sequence 10, Appl
2	47	56.6	16	US-09-171-705-39	Sequence 39, Appl
3	47	56.6	16	US-09-657-757-39	Sequence 39, Appl
4	36	43.4	16	US-09-171-705-40	Sequence 40, Appl
5	36	43.4	16	US-09-657-757-40	Sequence 40, Appl
6	35	42.2	8	US-09-311-784A-273	Sequence 273, Appl
7	35	42.2	8	US-08-635-886C-146	Sequence 146, Appl
8	35	42.2	8	US-08-974-690C-146	Sequence 146, Appl
9	35	42.2	8	US-08-974-685-146	Sequence 146, Appl
10	34	41.0	12	US-09-709-947-1	Sequence 1, Appl
11	34	41.0	12	US-08-851-843A-171	Sequence 171, Appl
12	34	41.0	15	US-08-974-549A-291	Sequence 291, Appl
13	34	41.0	15	US-08-854-050-171	Sequence 171, Appl
14	34	41.0	15	US-09-403-323-171	Sequence 171, Appl
15	34	41.0	15	US-09-403-181B-291	Sequence 291, Appl
16	34	41.0	15	US-09-721-456-291	Sequence 291, Appl
17	34	41.0	15	US-09-766-253-171	Sequence 171, Appl
18	34	41.0	15	US-10-054-295-171	Sequence 171, Appl
19	34	41.0	16	US-09-438-486A-171	Sequence 171, Appl
20	34	41.0	16	US-09-171-705-38	Sequence 38, Appl
21	34	41.0	16	US-09-657-757-38	Sequence 38, Appl
22	31	37.3	8	US-08-444-818-420	Sequence 420, Appl
23	31	37.3	11	US-10-038-972A-4	Sequence 4, Appl
24	31	37.3	12	US-08-968-542C-22	Sequence 22, Appl
25	30	36.1	10	US-09-554-467A-22	Sequence 22, Appl
26	30	36.1	19	US-09-499-203-7	Sequence 7, Appl
27	30	36.1	19	US-09-499-203-7	Sequence 7, Appl

28	30	36.1	19	US-10-117-846-33	Sequence 33, Appl
29	30	36.1	20	US-08-564-972-23	Sequence 23, Appl
30	29	34.9	14	US-09-731-092-3	Sequence 3, Appl
31	29	34.9	15	US-10-264-303-12	Sequence 12, Appl
32	29	34.9	16	US-09-543-608A-40	Sequence 40, Appl
33	29	34.9	16	US-09-239-043D-2574	Sequence 2574, Ap
34	29	34.9	16	US-09-935-430-653	Sequence 653, Appl
35	29	34.9	17	US-08-166-266-7	Sequence 7, Appl
36	28	33.7	9	US-09-644-600-93	Sequence 93, Appl
37	28	33.7	9	US-09-654-600A-93	Sequence 93, Appl
38	28	33.7	14	US-08-482-228-20	Sequence 20, Appl
39	28	33.7	14	US-08-482-528C-15	Sequence 15, Appl
40	28	33.7	19	US-08-480-229C-15	Sequence 15, Appl
41	28	33.7	19	US-08-659-235C-15	Sequence 15, Appl
42	28	33.7	20	US-09-962-756-751	Sequence 751, Appl
43	28	33.7	20	US-09-962-756-905	Sequence 905, Appl
44	27	32.5	8	US-08-988-842-27	Sequence 27, Appl
45	27	32.5	8	US-08-635-886C-147	Sequence 147, Appl
46	27	32.5	8	US-08-974-690C-147	Sequence 147, Appl
47	27	32.5	8	US-08-974-685-147	Sequence 147, Appl
48	27	32.5	11	US-10-038-972A-2	Sequence 2, Appl
49	27	32.5	12	US-08-705-660-25	Sequence 25, Appl
50	27	32.5	12	US-08-989-045-25	Sequence 25, Appl
51	27	32.5	12	US-08-475-955-66	Sequence 66, Appl
52	27	32.5	12	US-09-315-355A-25	Sequence 25, Appl
53	27	32.5	12	US-07-867-819D-86	Sequence 86, Appl
54	27	32.5	14	US-10-373-090A-12	Sequence 12, Appl
55	27	32.5	14	US-08-974-549A-78	Sequence 78, Appl
56	27	32.5	16	US-08-912-951-78	Sequence 78, Appl
57	27	32.5	16	US-09-402-181B-78	Sequence 78, Appl
58	27	32.5	16	US-09-721-456-78	Sequence 78, Appl
59	27	32.5	19	US-09-441-502B-66	Sequence 66, Appl
60	27	32.5	19	US-10-117-846-30	Sequence 30, Appl
61	27	32.5	19	US-10-117-846-31	Sequence 31, Appl
62	27	32.5	19	US-10-117-846-31	Sequence 31, Appl
63	27	32.5	20	US-09-962-756-833	Sequence 833, Appl
64	27	32.5	20	US-08-962-756-834	Sequence 834, Appl
65	27	32.5	6	US-08-287-717-14	Sequence 14, Appl
66	26	31.3	6	US-08-441-914-14	Sequence 14, Appl
67	26	31.3	6	US-09-657-276-1092	Sequence 1092, Ap
68	26	31.3	6	US-09-623-548A-1092	Sequence 6, Appl
69	26	31.3	2	US-09-239-043D-803	Sequence 803, Appl
70	26	31.3	2	US-09-239-043D-1591	Sequence 1591, Ap
71	26	31.3	9	US-09-239-043D-1842	Sequence 1842, Ap
72	26	31.3	10	US-08-983-157B-26	Sequence 26, Appl
73	26	31.3	10	US-09-239-043D-194	Sequence 194, Ap
74	26	31.3	11	US-08-557-146-17	Sequence 17, Appl
75	26	31.3	11	US-09-154-344-17	Sequence 17, Appl
76	26	31.3	11	US-09-239-043D-107	Sequence 107, Appl
77	26	31.3	11	US-09-239-043D-957	Sequence 957, Appl
78	26	31.3	11	US-09-239-043D-1676	Sequence 1676, Ap
79	26	31.3	11	US-10-038-972A-5	Sequence 5, Appl
80	26	31.3	14	US-08-679-405-4	Sequence 4, Appl
81	26	31.3	14	US-08-842-799-4	Sequence 4, Appl
82	26	31.3	14	PCT-US96-11458-4	Sequence 4, Appl
83	26	31.3	15	US-09-295-186-6	Sequence 6, Appl
84	26	31.3	15	US-09-239-043D-2124	Sequence 2124, Ap
85	26	31.3	15	US-09-112-524D-38	Sequence 38, Appl
86	26	31.3	16	US-08-313-565-25	Sequence 25, Appl
87	26	31.3	16	US-08-631-479-25	Sequence 25, Appl
88	26	31.3	16	US-08-679-405-10	Sequence 10, Appl
89	26	31.3	16	US-08-842-799-10	Sequence 10, Appl
90	26	31.3	16	PCT-US96-11458-10	Sequence 10, Appl
91	26	31.3	17	US-08-940-577-1	Sequence 1, Appl
92	26	31.3	19	US-10-117-846-32	Sequence 32, Appl
93	26	31.3	20	US-09-962-756-1117	Sequence 1117, Ap
94	26	31.3	20	US-09-962-756-1161	Sequence 1161, Ap
95	26	31.3	21	US-09-962-756-593	Sequence 593, Appl
96	26	31.3	21	US-09-962-756-659	Sequence 659, Appl
97	26	31.3	21	US-09-962-756-659	Sequence 659, Appl
98	26	31.3	21	US-09-962-756-659	Sequence 659, Appl
99	26	31.3	21	US-09-962-756-659	Sequence 659, Appl
100	26	31.3	21	US-09-962-756-659	Sequence 659, Appl

ALIGNMENTS

RESULT 1

US-09-292-225-10
; Sequence 10, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
; FEATURE:
; OTHER INFORMATION: At location 14, Xaa = any amino acid
US-09-292-225-10

Query Match

Best Local Similarity 97.6%; Score 81; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKLVMGVPPYGRXSIE 17
|||||

Db 1 DKLVMGVPPYGRXSIE 17
|||||

RESULT 2

US-09-171-705-39
; Sequence 39, Application US/09171705
; Patent No. 6184204
; GENERAL INFORMATION:
; APPLICANT: BOOTS, ANNA M.H.
; APPLICANT: VERHEIDEN, GILBERTUS F.M.
; TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC
; TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC
; FILE REFERENCE: O/96198 US
; CURRENT APPLICATION NUMBER: US/09/171,705
; CURRENT FILING DATE: 1999-02-09
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM
; OTHER INFORMATION: SEQUENCE OF HUMAN CARTILAGE (HC) -39 PROTEIN
US-09-171-705-39

Query Match

Best Local Similarity 56.6%; Score 47; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.037;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KLVMGVPPYGRXA 13
|||

Db 4 KLVMGIPFGRS 15
|||||

RESULT 3

US-09-657-757-39
; Sequence 39, Application US/09657757
; Patent No. 6881824
; GENERAL INFORMATION:
; APPLICANT: BOOTS, ANNA M.H.
; APPLICANT: VERHEIDEN, GILBERTUS F.M.
; TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC
; TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC
; FILE REFERENCE: O/96198 US
; CURRENT APPLICATION NUMBER: US/09/657,757
; CURRENT FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US/09/171,705
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM
; OTHER INFORMATION: SEQUENCE OF HUMAN CARTILAGE (HC) -39 PROTEIN
US-09-657-757-39

Query Match

Best Local Similarity 56.6%; Score 47; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.037;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KLVMGVPPYGRXA 13
|||||

Db 4 KLVMGIPFGRS 15
|||||

RESULT 4

US-09-171-705-40
; Sequence 40, Application US/09171705
; Patent No. 6184204
; GENERAL INFORMATION:
; APPLICANT: BOOTS, ANNA M.H.
; APPLICANT: VERHEIDEN, GILBERTUS F.M.
; TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC
; TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC
; FILE REFERENCE: O/96198 US
; CURRENT APPLICATION NUMBER: US/09/171,705
; CURRENT FILING DATE: 1999-02-09
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM
; OTHER INFORMATION: SEQUENCE OF HUMAN CARTILAGE (HC) -39 PROTEIN
US-09-171-705-40

Query Match

Best Local Similarity 43.4%; Score 36; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 4.2;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 5 MGVPYGRXS 16
|||

Db 1 MGIPFGRSFTL 12
|||

RESULT 5

US-09-657-757-40
; Sequence 40, Application US/09657757

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; Patent No. 6881824
; GENERAL INFORMATION:
; APPLICANT: BOOTS, ANNA M.H.
; APPLICANT: VERHEIJDE, GILBERTUS F.M.
; TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC
; TITLE OF INVENTION: IMMUNOSUPPRESSIVE THERAPY
; FILE REFERENCE: O/96198 US
; CURRENT APPLICATION NUMBER: US/09/657,757
; CURRENT FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US/09/171,705
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM
; OTHER INFORMATION: SEQUENCE OF HUMAN CARTILAGE (HC) -39 PROTEIN
US-09-657-757-40
```

```
Query Match          43.4%; Score 36; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 4.2;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
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QY 5 MGVPFYGRAXSI 16
    |||:|:|:|:|
DB 1 MGIPTFGRSFTL 12
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RESULT 6
US-09-311-784A-273
; Sequence 273, Application US/09311784A
; Patent No. 6534482
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Edimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.01
; CURRENT APPLICATION NUMBER: US/09/311,784A
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 273
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV 1378 (peptide 29.0035)
US-09-311-784A-273
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Query Match          42.2%; Score 35; DB 2; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 7 VPFYGRA 13
    :|:|:|:|
DB 1 IPFYGKA 7
```

```
RESULT 7
US-08-635-886C-146
; Sequence 146, Application US/08635886C
; Patent No. 6555114
```

```
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2752-18
; CURRENT APPLICATION NUMBER: US/08/635,886C
; CURRENT FILING DATE: 1996-04-25
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 146
; LENGTH: 8
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-146
```

```
Query Match          42.2%; Score 35; DB 2; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 7 VPFYGRA 13
    :|:|:|:|
DB 1 IPFYGKA 7
```

```
RESULT 8
US-08-974-690C-146
; Sequence 146, Application US/08974690C
; Patent No. 6613333
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/08/974,690C
; CURRENT FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 146
; LENGTH: 8
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-974-690C-146
```

```
Query Match          42.2%; Score 35; DB 2; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 7 VPFYGRA 13
    :|:|:|:|
DB 1 IPFYGKA 7
```

```
RESULT 9
US-08-974-685-146
; Sequence 146, Application US/08974685
; Patent No. 6689368
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF
```

HEPATITIS C VIRUS STRUCTURAL PROTEINS, PROPHYLACTIC AND
THERAPEUTIC COMPOSITIONS CONTAINING THE SAME

NUMBER OF SEQUENCES: 181
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,685
FILING DATE: 19-NO. 6689368-1997
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS R.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 146:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 146:
US-08-974-685-146

Query Match 42.2%; Score 35; DB 2; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 7 VPFYGRA 13
:|||||
Db 1 IPFYGKA 7

RESULT 10
US-09-709-947-1
Sequence 1, Application US/09709947
Patent No. 6936424
GENERAL INFORMATION:
APPLICANT: Mackinn, Brynmor
TITLE OF INVENTION: Materials and Methods for Detection and Treatment of
FILE REFERENCE: MTP-024
CURRENT APPLICATION NUMBER: US/09/709,947
CURRENT FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: US 60/165,173
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: US 60/172,170
PRIOR FILING DATE: 1999-12-17
PRIOR APPLICATION NUMBER: US 60/178,860
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/201,721
PRIOR FILING DATE: 2000-05-03
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 1
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Tryptic peptide
US-09-709-947-1

HEPATITIS C VIRUS STRUCTURAL PROTEINS, PROPHYLACTIC AND
THERAPEUTIC COMPOSITIONS CONTAINING THE SAME

NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 171:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
OTHER INFORMATION: /note= "motif D peptide from human
telomerase core protein 1 (TcP1)"
US-08-851-843A-171

Query Match 41.0%; Score 34; DB 2; Length 13;
Best Local Similarity 55.6%; Pred. No. 7.9;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 VMGVFPGYGR 12
:|||||
Db 2 LQGFPGYGR 10

RESULT 11
US-08-851-843A-171
Sequence 171, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 171:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
OTHER INFORMATION: /note= "motif D peptide from human
telomerase core protein 1 (TcP1)"
US-08-851-843A-171

Query Match 41.0%; Score 34; DB 2; Length 15;
Best Local Similarity 77.8%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LVNGVPPYG 11
Db 4 LVRGVPEYG 12

RESULT 12
US-08-974-549A-291

Sequence 291, Application US/08974549A
Patent No. 6166178

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

APPLICANT: Lingner, Joachim

APPLICANT: Nakamura, Toru

APPLICANT: Chapman, Karen B.

APPLICANT: Morin, Gregg B.

APPLICANT: Harley, Calvin B.

APPLICANT: Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3634

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/974,549A

FILING DATE: 19-NOV-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002610US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 291:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..15

OTHER INFORMATION: /note= "motif D peptide from human

US-08-974-549A-291 telomerase core protein 1 (FCP1)"

Query Match 41.0%; Score 34; DB 2; Length 15;
Best Local Similarity 77.8%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LVNGVPPYG 11
Db 4 LVRGVPEYG 12

RESULT 13
US-08-854-050-171

Sequence 171, Application US/08854050
Patent No. 6261836

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

APPLICANT: Lingner, Joachim

APPLICANT: Nakamura, Toru

APPLICANT: Chapman, Karen B.

APPLICANT: Morin, Gregg B.

APPLICANT: Harley, Calvin

APPLICANT: Andrews, William H.

TITLE OF INVENTION: No. 6261836el Telomerase

NUMBER OF SEQUENCES: 225

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/854,050

FILING DATE: 09-MAY-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002610US

APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Aueenhue, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 291:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
OTHER INFORMATION: /note= "motif D peptide from human telomerase core protein 1 (TCPI)"
SEQUENCE DESCRIPTION: SEQ ID NO: 291:
US-09-402-181B-291

Query Match 41.0%; Score 34; DB 2; Length 15;
Best Local Similarity 77.8%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 LVMGVPEY 11
Db 4 LVKGVPY 12

RESULT 16
US-09-721-456-291
Sequence 291, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-No. 6617110-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 291:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
OTHER INFORMATION: /note= "motif D peptide from human telomerase core protein 1 (TCPI)"
SEQUENCE DESCRIPTION: SEQ ID NO: 291:
US-09-721-456-291

Query Match 41.0%; Score 34; DB 2; Length 15;
Best Local Similarity 77.8%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 LVMGVPEY 11
Db 4 LVKGVPY 12

RESULT 17
US-09-766-253-171
Sequence 171, Application US/09766253
Patent No. 6808880
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6808880el Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 171:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
OTHER INFORMATION: /note= "motif D peptide from human telomerase core protein 1 (Tcpl)"
SEQUENCE DESCRIPTION: SEQ ID NO: 171:
US-09-766-253-171
Query Match 41.0%; Score 34; DB 2; Length 15;
Best Local Similarity 77.8%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 LVMGVPEYFG 11
DB 4 LVKGVPPEYFG 12
RESULT 18
US-10-054-295-171
Sequence 171, Application US/10054295
Patent No. 6921664
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: NO. 6921664el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 171:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
OTHER INFORMATION: /note= "motif D peptide from human telomerase core protein 1 (Tcpl)"
SEQUENCE DESCRIPTION: SEQ ID NO: 171:
US-10-054-295-171
Query Match 41.0%; Score 34; DB 2; Length 15;
Best Local Similarity 77.8%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 LVMGVPEYFG 11
DB 4 LVKGVPPEYFG 12
RESULT 19
US-09-438-486A-171
Sequence 171, Application US/09438486A
Patent No. 6927285
GENERAL INFORMATION:
APPLICANT: CECCH, THOMAS R.
LINGNER, JOACHIM
APPLICANT: NAKAMURA, TORU
APPLICANT: CHAPMAN, KAREN B.
APPLICANT: MORIN, GREGG B.
APPLICANT: HARLEY, CALVIN
APPLICANT: ANDREWS, WILLIAM H.
TITLE OF INVENTION: GENE FOR HUMAN TELOMERASE REVERSE TRANSCRIPTASE AND
FILE REFERENCE: 018/062
CURRENT APPLICATION NUMBER: US/09/438,486A
CURRENT FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 08/851,843
PRIOR FILING DATE: 1997-05-06
PRIOR APPLICATION NUMBER: 08/846,017
PRIOR FILING DATE: 1997-04-25
PRIOR APPLICATION NUMBER: 08/844,419
PRIOR FILING DATE: 1997-04-18
PRIOR APPLICATION NUMBER: 08/724,643
PRIOR FILING DATE: 1996-10-01
NUMBER OF SEQ ID NOS: 223
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 171
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Recombinant
OTHER INFORMATION: amino acid sequence
US-09-438-486A-171
Query Match 41.0%; Score 34; DB 2; Length 15;

Best Local Similarity 77.8%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LVMGVPRYG 11
|||
Db 4 LVRGVPEYX 12

RESULT 20

US-09-171-705-38
; Sequence 38, Application US/09171705
; Patent No. 6184204
; GENERAL INFORMATION:
; APPLICANT: BOOTS, ANNA M.H.
; TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC
; FILE REFERENCE: O/96198 US
; CURRENT APPLICATION NUMBER: US/09/171,705
; CURRENT FILING DATE: 1999-02-09
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 38
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM
; OTHER INFORMATION: SEQUENCE OF HUMAN CARTILAGE (HC) -39 PROTEIN
US-09-171-705-38

Query Match 41.0%; Score 34; DB 2; Length 16;
Best Local Similarity 85.7%; Pred. No. 10;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLVWGVP 8
|||
Db 10 KLVWGIP 16

RESULT 21
US-09-657-757-38
; Sequence 38, Application US/09657757
; Patent No. 6881824
; GENERAL INFORMATION:
; APPLICANT: BOOTS, ANNA M.H.
; TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC
; FILE REFERENCE: O/96198 US
; CURRENT APPLICATION NUMBER: US/09/657,757
; CURRENT FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US/09/171,705
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 38
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM
; OTHER INFORMATION: SEQUENCE OF HUMAN CARTILAGE (HC) -39 PROTEIN
US-09-657-757-38

Query Match 41.0%; Score 34; DB 2; Length 16;
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLVWGVP 8
|||
Db 10 KLVWGIP 16

RESULT 22

US-08-444-818-420
; Sequence 420, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutey, William J.
; TITLE OF INVENTION: NANV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 420:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-444-818-420

Query Match 37.3%; Score 31; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 VPRYGR 12
:|
Db 3 IPFYGX 8

RESULT 23
US-10-038-972A-4
; Sequence 4, Application US/10038972A
; Patent No. 6962815
; GENERAL INFORMATION:
; APPLICANT: J. Bartlett
; TITLE OF INVENTION: AAV VECTORS AND METHODS
; FILE REFERENCE: 28335/3699605
; CURRENT APPLICATION NUMBER: US/10/038,972A
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/260,124
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

OTHER INFORMATION: Bovine Papilloma Virus Peptide
US-10-038-972A-4

Query Match 37.3%; Score 31; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 6 GVPYGRAXS 15
DB 2 GTPPYLKALS 11

RESULT 24
5460961-8
PATENT NO. 5460961
APPLICANT: DESY, CAROL; PINCEMAIL, JOEL; BOLLIN, ALEX
TITLE OF INVENTION: HUMAN MYELOPEROXIDASE AND ITS
THERAPEUTIC APPLICATION
NUMBER OF SEQUENCES: 13
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/641,678
FILING DATE: 16-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 460,931
FILING DATE: 14-FEB-1990
SEQ ID NO. 8:
LENGTH: 12
5460961-8

Query Match 37.3%; Score 31; DB 6; Length 12;
Best Local Similarity 83.3%; Pred. No. 26;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 MGVPPY 10
DB 1 MGVPPF 6

RESULT 25
US-08-968-542C-22
SEQUENCE 22, Application US/08968542C
PATENT NO. 5981728
GENERAL INFORMATION:
APPLICANT: Myers, et al.
TITLE OF INVENTION: dulli Codes For A No. 5981728el Starch
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mcgregor & Adler, LLP
STREET: 8011 Candle Lane
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word 6.0.1 for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,542C
FILING DATE: No. 5981728ember 12, 1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D6036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
TELEFAX: (713) 777-6908

INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acid residues
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: amino acid
HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE: internal
US-08-968-542C-22

Query Match 36.1%; Score 30; DB 1; Length 10;
Best Local Similarity 62.5%; Pred. No. 33;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 DKLVGVP 8
DB 1 DKSIIVGP 8

Search completed: January 26, 2006, 08:07:02
Job time: 17.1408 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 08:04:12 ; Search time 55.25 Seconds
(without alignments)
128.563 Million cell updates/sec

Title: US-09-662-293-10
Perfect score: 83
Sequence: 1 DKLVWGVPYGRAXSIE 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 389445

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

Published Applications AA Main:.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	97.6	17	4	US-10-218-743-10 Sequence 10, App1
2	41	49.4	10	3	US-09-791-378-324 Sequence 324, App
3	41	49.4	10	3	US-09-826-290-321 Sequence 321, App
4	41	49.4	10	3	US-09-791-383-111 Sequence 111, App
5	41	49.4	10	3	US-09-791-389-111 Sequence 111, App
6	41	49.4	10	3	US-09-791-379-324 Sequence 324, App
7	41	49.4	10	4	US-10-264-309-277 Sequence 277, App
8	41	49.4	10	5	US-10-264-309-277 Sequence 277, App
9	39	47.0	10	4	US-10-264-309-278 Sequence 278, App
10	39	47.0	10	5	US-10-264-309-278 Sequence 278, App
11	35	42.2	8	3	US-09-017-743C-3 Sequence 3, App11
12	35	42.2	8	4	US-10-371-525-273 Sequence 273, App
13	35	42.2	8	4	US-10-371-069-273 Sequence 273, App
14	35	42.2	8	4	US-10-371-645-273 Sequence 273, App
15	35	42.2	8	4	US-10-371-260-273 Sequence 273, App
16	35	42.2	8	4	US-10-651-165-146 Sequence 146, App
17	35	42.2	21	5	US-10-886-084-1 Sequence 1, App11
18	34	41.0	15	3	US-09-843-676-171 Sequence 171, App
19	34	41.0	15	3	US-09-766-253-171 Sequence 171, App
20	34	41.0	15	3	US-09-438-486-171 Sequence 171, App
21	34	41.0	15	4	US-10-053-758-171 Sequence 171, App
22	34	41.0	15	4	US-10-054-295-171 Sequence 171, App
23	34	41.0	15	4	US-10-054-611-171 Sequence 171, App
24	34	41.0	15	4	US-10-282-960-70 Sequence 70, App1
25	34	41.0	15	4	US-10-325-810-291 Sequence 291, App
26	34	41.0	15	5	US-10-877-124-291 Sequence 291, App
27	34	41.0	15	5	US-10-877-022-291 Sequence 291, App

28	34	41.0	15	5	US-10-877-146-291 Sequence 291, App
29	33	39.8	12	4	US-10-328-916-47 Sequence 47, App1
30	32	38.6	15	5	US-10-958-216-843 Sequence 843, App
31	32	38.6	18	3	US-09-864-761-42568 Sequence 42568, A
32	31	37.3	11	4	US-10-038-972A-4 Sequence 4, App11
33	31	37.3	20	3	US-09-864-761-41147 Sequence 41147, A
34	30	36.1	10	4	US-10-634-262-22 Sequence 22, App1
35	30	36.1	15	5	US-10-715-810-45 Sequence 45, App1
36	30	36.1	19	4	US-10-117-846-33 Sequence 33, App1
37	30	36.1	19	4	US-10-417-280A-7 Sequence 26, App1
38	29	34.9	11	3	US-09-965-967-76 Sequence 7, App11
39	29	34.9	14	3	US-09-731-092-3 Sequence 3, App11
40	29	34.9	14	5	US-10-423-855-3 Sequence 3, App11
41	29	34.9	15	3	US-09-880-748-757 Sequence 2757, App
42	29	34.9	15	3	US-10-264-303-12 Sequence 12, App1
43	29	34.9	15	4	US-10-293-418-2757 Sequence 2757, App
44	29	34.9	16	3	US-09-935-430-653 Sequence 653, App
45	29	34.9	16	3	US-09-932-165-1483 Sequence 1483, App
46	29	34.9	16	3	US-09-935-384-711 Sequence 711, App
47	29	34.9	16	3	US-09-942-052-712 Sequence 712, App
48	29	34.9	16	4	US-10-001-469-1405 Sequence 1405, App
49	29	34.9	16	4	US-10-116-118-34 Sequence 34, App1
50	29	34.9	16	4	US-10-062-109A-762 Sequence 762, App
51	29	34.9	16	4	US-10-005-480A-762 Sequence 762, App
52	29	34.9	16	4	US-10-277-292-653 Sequence 653, App
53	29	34.9	16	4	US-10-231-241-27 Sequence 27, App1
54	29	34.9	16	4	US-10-280-340-653 Sequence 653, App
55	29	34.9	16	4	US-10-147-368-81 Sequence 41, App1
56	29	34.9	16	4	US-10-099-460-21 Sequence 21, App1
57	29	34.9	16	4	US-10-024-652-2584 Sequence 2584, App
58	29	34.9	16	4	US-10-013-312-2993 Sequence 2993, App
59	29	34.9	16	4	US-10-087-190-28 Sequence 28, App1
60	29	34.9	16	4	US-10-120-885A-26 Sequence 26, App1
61	29	34.9	16	4	US-10-107-532-3 Sequence 3, App11
62	29	34.9	16	4	US-10-121-016-53 Sequence 53, App1
63	29	34.9	16	4	US-10-114-669-3 Sequence 3, App11
64	29	34.9	16	4	US-10-120-835-45 Sequence 45, App1
65	29	34.9	16	4	US-10-149-138-4225 Sequence 4225, App
66	29	34.9	16	4	US-10-114-432-10 Sequence 40, App1
67	29	34.9	16	4	US-10-306-531-31 Sequence 31, App1
68	29	34.9	16	4	US-10-455-822-99 Sequence 99, App1
69	29	34.9	16	4	US-10-435-751-39 Sequence 39, App1
70	29	34.9	16	4	US-10-149-135-2212 Sequence 2212, App
71	29	34.9	16	4	US-10-120-807A-46 Sequence 46, App1
72	29	34.9	16	4	US-10-418-972-39 Sequence 39, App1
73	29	34.9	16	4	US-10-422-571-16 Sequence 46, App1
74	29	34.9	16	4	US-10-313-972-50 Sequence 50, App1
75	29	34.9	16	4	US-10-415-014-712 Sequence 712, App
76	29	34.9	16	4	US-10-149-138-4225 Sequence 4225, App
77	29	34.9	16	4	US-10-407-484-99 Sequence 99, App1
78	29	34.9	16	4	US-10-149-137A-461 Sequence 461, App
79	29	34.9	16	4	US-10-463-782A-26 Sequence 26, App1
80	29	34.9	16	4	US-10-641-633-28 Sequence 28, App1
81	29	34.9	16	4	US-10-764-390-15 Sequence 15, App1
82	29	34.9	16	5	US-10-830-699-66 Sequence 66, App1
83	29	34.9	16	5	US-10-654-601-2574 Sequence 2574, App
84	29	34.9	16	5	US-10-861-662-66 Sequence 66, App1
85	29	34.9	16	5	US-10-919-654-20 Sequence 20, App1
86	29	34.9	16	5	US-10-837-269-42 Sequence 42, App1
87	29	34.9	16	5	US-10-994-106-65 Sequence 65, App1
88	29	34.9	16	5	US-10-776-773-26 Sequence 26, App1
89	29	34.9	16	5	US-10-990-137-653 Sequence 653, App
90	29	34.9	16	6	US-11-051-411-1489 Sequence 1489, App
91	29	34.9	16	6	US-11-073-349-45 Sequence 45, App1
92	29	34.9	17	3	US-09-935-476-3 Sequence 3, App11
93	29	34.9	20	4	US-10-424-599-151159 Sequence 151159, App
94	28	33.7	9	4	US-10-600-187-93 Sequence 93, App1
95	28	33.7	10	3	US-09-746-371C-28 Sequence 28, App1
96	28	33.7	11	4	US-10-727-737-47 Sequence 47, App1
97	28	33.7	11	4	US-10-727-737-51 Sequence 51, App1
98	28	33.7	14	5	US-10-813-338-1308 Sequence 1308, App
99	28	33.7	15	4	US-10-282-260-25 Sequence 25, App1
100	28	33.7	20	3	US-09-962-756-751 Sequence 751, App

ALIGNMENTS

RESULT 1

US-10-218-743-10
; Sequence 10, Application US/10218743
; Publication No. US20030096799A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
; FEATURE:
; OTHER INFORMATION: At location 14, Xaa = any amino acid
US-10-218-743-10

Query Match

Best Local Similarity 97.6%; Score 81; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 DKLWGVFPYGRXSIE 17
|||||
1 DKLWGVFPYGRXSIE 17

DB

RESULT 2

US-09-791-378-324
; Sequence 324, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: SCHIZOPHRENIA
; FILE REFERENCE: 9195-061-999
; CURRENT APPLICATION NUMBER: US/09/791,378
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 324
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-378-324

Query Match

Best Local Similarity 49.4%; Score 41; DB 3; Length 10;
Best Local Similarity 70.0%; Pred. No. 2.1;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 LVMGVFPYGR 12

Db 1 LVMGIPTFGR 10
|||||

RESULT 3

US-09-826-290-321
; Sequence 321, Application US/09826290
; Patent No. US2002016468A1
; GENERAL INFORMATION:
; APPLICANT: Durham, L. Kathryn
; APPLICANT: Friedman, David L.
; APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
; APPLICANT: Kimmel, Lida H.
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Potter, David M.
; APPLICANT: Rohlf, Christian
; APPLICANT: Silber, B. Michael
; APPLICANT: Stiger, Thomas R.
; APPLICANT: Sunderland, P. Trey
; APPLICANT: Townsend, Robert Reid
; APPLICANT: White, Frost
; APPLICANT: Williams, Stephen A.
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
; TITLE OF INVENTION: Uses Thereof, Including Diagnosis and Treatment of
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 2572-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/826,290
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/194,504
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/253,647
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 321
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapien
US-09-826-290-321

Query Match

Best Local Similarity 49.4%; Score 41; DB 3; Length 10;
Best Local Similarity 70.0%; Pred. No. 2.1;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 LVMGVFPYGR 12
|||||

Db 1 LVMGIPTFGR 10

RESULT 4

US-09-791-393-111
; Sequence 111, Application US/09791393
; Publication No. US20030032200A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; FILE REFERENCE: 2543-1-001 N1
; CURRENT APPLICATION NUMBER: US/09/791,393
; CURRENT FILING DATE: 2002-01-02
; EARLIER APPLICATION NUMBER: GB 0004412.3
; EARLIER FILING DATE: 2000-02-24
; EARLIER APPLICATION NUMBER: GB 0030050.9
; EARLIER FILING DATE: 2000-12-08
; EARLIER APPLICATION NUMBER: US 60/254,830
; EARLIER FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 111
; LENGTH: 10

TYPE: PRT
ORGANISM: homo sapien
US-09-791-393-111

Query Match 49.4%; Score 41; DB 3; Length 10;
Best Local Similarity 70.0%; Pred. No. 2.1;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 LVMGVPPYGR 12
||||:|:|
Db 1 LVMGIPTFGR 10

RESULT 5

US-09-791-389-111
Sequence 111, Application US/09791389
Publication No. US20030032773A1
GENERAL INFORMATION:
APPLICANT: Herath, Herath Mudiyanselage Achula Chandrasiri
APPLICANT: Parekh, Rajesh Bhikhu
APPLICANT: Rohlf, Christian
APPLICANT: Terrett, Jonathan Alexander
APPLICANT: Tyson, Kerry Louise
TITLE OF INVENTION: Proteins, Genes and Their Use for
TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
FILE REFERENCE: 2543-1-001 N2
CURRENT APPLICATION NUMBER: US/09/791,389
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: GB 0004412.3
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: GB 0030050.9
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: US 60/254,830
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 308
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 111
LENGTH: 10
TYPE: PRT
ORGANISM: homo sapien
US-09-791-389-111

Query Match 49.4%; Score 41; DB 3; Length 10;
Best Local Similarity 70.0%; Pred. No. 2.1;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 LVMGVPPYGR 12
||||:|:|
Db 1 LVMGIPTFGR 10

RESULT 6

US-09-791-377-324
Sequence 324, Application US/09791377
Publication No. US20040110938A1
GENERAL INFORMATION:
APPLICANT: Parekh, Rajesh
TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
FILE REFERENCE: 9195-060-999
CURRENT APPLICATION NUMBER: US/09/791,377
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 09/750,395
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 677
SOFTWARE: PatentIn version 3.0
SEQ ID NO 324
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-09-791-377-324

Query Match 49.4%; Score 41; DB 3; Length 10;
Best Local Similarity 70.0%; Pred. No. 2.1;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 LVMGVPPYGR 12
||||:|:|
Db 1 LVMGIPTFGR 10

RESULT 7

US-10-264-309-277
Sequence 277, Application US/10264309
Publication No. US20040022794A1
GENERAL INFORMATION:
APPLICANT: DURHAM, L. KATHRYN
APPLICANT: FRIEDMAN, DAVID L.
APPLICANT: HERATH, HERATH
APPLICANT: KIMMEL, LIDA H.
APPLICANT: PAREKH, RAJESH B.
APPLICANT: POTTER, DAVID M.
APPLICANT: ROHLF, CHRISTIAN
APPLICANT: SILBER, B. MICHAEL
APPLICANT: SNYDER, PETER J.
APPLICANT: SOARES, HOLLY D.
APPLICANT: STIGER, THOMAS R.
APPLICANT: SUNDERLAND, P. TREY
APPLICANT: TOWNSEND, ROBERT R.
APPLICANT: WHITE, W. FROST
TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,
TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE
FILE REFERENCE: POA-002.01
CURRENT APPLICATION NUMBER: US/10/264,309
CURRENT FILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: 60/326,708
PRIOR FILING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 491
SOFTWARE: PatentIn Version 2.1
SEQ ID NO 277
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-10-264-309-277

Query Match 49.4%; Score 41; DB 4; Length 10;
Best Local Similarity 70.0%; Pred. No. 2.1;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 LVMGVPPYGR 12
||||:|:|
Db 1 LVMGIPTFGR 10

RESULT 8

US-10-264-309-277
Sequence 277, Application US/10264309
Publication No. US20050163789A9
GENERAL INFORMATION:
APPLICANT: DURHAM, L. KATHRYN
APPLICANT: FRIEDMAN, DAVID L.
APPLICANT: HERATH, HERATH
APPLICANT: KIMMEL, LIDA H.
APPLICANT: PAREKH, RAJESH B.
APPLICANT: POTTER, DAVID M.
APPLICANT: ROHLF, CHRISTIAN
APPLICANT: SILBER, B. MICHAEL
APPLICANT: SNYDER, PETER J.
APPLICANT: SOARES, HOLLY D.
APPLICANT: STIGER, THOMAS R.
APPLICANT: SUNDERLAND, P. TREY
APPLICANT: TOWNSEND, ROBERT R.
APPLICANT: WHITE, W. FROST
APPLICANT: WILLIAMS, STEPHEN A.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,
TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE
FILE REFERENCE: POA-002.01
CURRENT APPLICATION NUMBER: US/10/264,309
CURRENT FILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: 60/326,708
PRIOR FILING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 491
SOFTWARE: PatentIn Version 2.1
SEQ ID NO 277
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-10-264-309-277

Query Match 49.4%; Score 41; DB 5; Length 10;
Best Local Similarity 70.0%; Pred. No. 2.1;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 LVMGVPEYGR 12
Db 1 LVMGLEPTGR 10

RESULT 9
US-10-264-309-278
Sequence 278, Application US/10264309
Publication No. US20040022794A1
GENERAL INFORMATION:
APPLICANT: DURHAM, L. KATHRYN
APPLICANT: FRIEDMAN, DAVID L.
APPLICANT: HERATH, HERATH
APPLICANT: KIMMEL, LIDA H.
APPLICANT: PAREKH, RAJESH B.
APPLICANT: POTTER, DAVID M.
APPLICANT: ROHLF, CHRISTIAN
APPLICANT: SILBER, B. MICHAEL
APPLICANT: SNYDER, PETER J.
APPLICANT: SOARES, HOLLY D.
APPLICANT: STIGER, THOMAS R.
APPLICANT: SUNDERLAND, P. TREY
APPLICANT: TOWNSEND, ROBERT R.
APPLICANT: WHITE, W. FROST
APPLICANT: WILLIAMS, STEPHEN A.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,
TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE
FILE REFERENCE: POA-002.01
CURRENT APPLICATION NUMBER: US/10/264,309
CURRENT FILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: 60/326,708
PRIOR FILING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 491
SOFTWARE: PatentIn Version 2.1
SEQ ID NO 278
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-10-264-309-278

Query Match 47.0%; Score 39; DB 4; Length 10;
Best Local Similarity 70.0%; Pred. No. 4.8;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 LVMGVPEYGR 12
Db 1 LVMGLEPTGR 10

RESULT 10
US-10-264-309-278
Sequence 278, Application US/10264309
Publication No. US20050163789A9
GENERAL INFORMATION:

APPLICANT: DURHAM, L. KATHRYN
APPLICANT: FRIEDMAN, DAVID L.
APPLICANT: HERATH, HERATH
APPLICANT: KIMMEL, LIDA H.
APPLICANT: PAREKH, RAJESH B.
APPLICANT: POTTER, DAVID M.
APPLICANT: ROHLF, CHRISTIAN
APPLICANT: SILBER, B. MICHAEL
APPLICANT: SNYDER, PETER J.
APPLICANT: SOARES, HOLLY D.
APPLICANT: STIGER, THOMAS R.
APPLICANT: SUNDERLAND, P. TREY
APPLICANT: TOWNSEND, ROBERT R.
APPLICANT: WHITE, W. FROST
APPLICANT: WILLIAMS, STEPHEN A.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,
TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE
FILE REFERENCE: POA-002.01
CURRENT APPLICATION NUMBER: US/10/264,309
CURRENT FILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: 60/326,708
PRIOR FILING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 491
SOFTWARE: PatentIn Version 2.1
SEQ ID NO 278
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-10-264-309-278

Query Match 47.0%; Score 39; DB 5; Length 10;
Best Local Similarity 70.0%; Pred. No. 4.8;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 LVMGVPEYGR 12
Db 1 LVMGLEPTGR 10

RESULT 11
US-09-017-743C-3
Sequence 3, Application US/09017743C
Patent No. US2002017694A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
Sidney, John
Southwood, Scott
TITLE OF INVENTION: HLA Binding Peptides and Their
Uses
NUMBER OF SEQUENCES: 146
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,743C
FILING DATE: 03-Feb-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/590,298
FILING DATE: 23-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 018623-008050US


```
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-017-743C-3

Query Match      42.2% Score 35; DB 3; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      7 VPFYGRA 13
       :||||:|
Db      1 IPFYGKA 7

RESULT 12
US-10-371-525-273
Sequence 273, Application US/10371525
GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Hermanson, Gary G.
APPLICANT: Sette, Alessandro
APPLICANT: Livingston, Brian
APPLICANT: Iehioka, Glenn Y.
APPLICANT: Chesnut, Robert W.
APPLICANT: Epimmune, Inc.
TITLE OF INVENTION: Expression Vectors for Stimulating an
FILE REFERENCE: 39963-20022.01
CURRENT APPLICATION NUMBER: US/10/371,525
PRIOR FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: US 09/311,784
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: US 60/085,751
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 273
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HCV 1378 (peptide 29.0035)
US-10-371-525-273

Query Match      42.2% Score 35; DB 4; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      7 VPFYGRA 13
       :||||:|
Db      1 IPFYGKA 7

RESULT 13
US-10-371-069-273
Sequence 273, Application US/10371069
GENERAL INFORMATION:
APPLICANT: Epimmune, Inc.
APPLICANT: Fikes, John D.
APPLICANT: Hermanson, Gary G.
APPLICANT: Sette, Alessandro
APPLICANT: Iehioka, Glenn Y.
```

```
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert W.
APPLICANT: Epimmune, Inc.
TITLE OF INVENTION: Expression Vectors for Stimulating an
FILE REFERENCE: 39963-20022.10
CURRENT APPLICATION NUMBER: US/10/371,069
PRIOR FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: US 09/078,904
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: US 60/085,751
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 273
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HCV 1378 (peptide 29.0035)
US-10-371-069-273

Query Match      42.2% Score 35; DB 4; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      7 VPFYGRA 13
       :||||:|
Db      1 IPFYGKA 7

RESULT 14
US-10-371-645-273
Sequence 273, Application US/10371645
GENERAL INFORMATION:
APPLICANT: Epimmune, Inc.
APPLICANT: Fikes, John D.
APPLICANT: Hermanson, Gary G.
APPLICANT: Sette, Alessandro
APPLICANT: Iehioka, Glenn Y.
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert W.
APPLICANT: Epimmune, Inc.
TITLE OF INVENTION: Expression Vectors for Stimulating an
FILE REFERENCE: 39963-20022.11
CURRENT APPLICATION NUMBER: US/10/371,645
PRIOR FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: US 09/078,904
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: US 60/085,751
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 273
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HCV 1378 (peptide 29.0035)
US-10-371-645-273

Query Match      42.2% Score 35; DB 4; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      7 VPFYGRA 13
       :||||:|
Db      1 IPFYGKA 7

RESULT 15
```

US-10-371-260-273
; Sequence 273, Application US/10371260
; Publication No. US20030220285A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Cheesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.13 US/10/371,260
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 273
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV 1378 (peptide 29.0035)
US-10-371-260-273

Query Match 42.2%; Score 35; DB 4; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 7 VPFYGRA 13
:||||:
Db 1 IPFYGA 7

RESULT 16
US-10-651-165-146
; Sequence 146, Application US/10651165
; Publication No. US20040047877A1
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELBYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/10/651,165
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/08/974,690C
; PRIOR FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 146
; LENGTH: 8
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-10-651-165-146

Query Match 42.2%; Score 35; DB 4; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 7 VPFYGRA 13
:||||:
Db 1 IPFYGA 7

Db 1 IPFYGA 7
RESULT 17
US-10-888-084-1
; Sequence 1, Application US/10888084
; Publication No. US20050095649A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Ruedi
; APPLICANT: Zhang, Ruedi
; TITLE OF INVENTION: Affinity Capture of Peptides by
; TITLE OF INVENTION: Microarray and Related Methods
; FILE REFERENCE: 66661-113
; CURRENT APPLICATION NUMBER: US/10/888,084
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/486,581
; PRIOR FILING DATE: 2003-07-10
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary peptide
US-10-888-084-1

Query Match 42.2%; Score 35; DB 5; Length 21;
Best Local Similarity 46.2%; Pred. No. 55;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy 4 VMGVFYGAXSI 16
:||||:
Db 1 VGVFYGDARAL 13

RESULT 18
US-09-843-676-171
; Sequence 171, Application US/09843676
; Patent No. US20020164786A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. US20020164786A1e1 Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/843,676
; FILING DATE: 26-Apr-2001
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 171:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
OTHER INFORMATION: /note="motif D peptide from human telomerase core protein 1 (TCPI)"
SEQUENCE DESCRIPTION: SEQ ID NO: 171:
US-09-843-676-171

Query Match 41.0%; Score 34; DB 3; Length 15;
Best Local Similarity 77.8%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LVNGVPEYVG 11
DB 4 LVNGVPEYVG 12

RESULT 19
US-09-766-253-171
Sequence 171, Application US/09766253
Publication No. US20020187471A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
LINGNER, Joachim
NAKAMURA, Toru
CHAPMAN, Karen B.
MORIN, Gregg B.
HARLEY, Calvin
ANDREWS, William H.
TITLE OF INVENTION: No. US20020187471A1 Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 171:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
OTHER INFORMATION: /note="motif D peptide from human telomerase core protein 1 (TCPI)"
SEQUENCE DESCRIPTION: SEQ ID NO: 171:
US-09-766-253-171

Query Match 41.0%; Score 34; DB 3; Length 15;
Best Local Similarity 77.8%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LVNGVPEYVG 11
DB 4 LVNGVPEYVG 12

RESULT 20
US-09-438-486-171
Sequence 171, Application US/09438486
Publication No. US20030009019A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
LINGNER, Joachim
NAKAMURA, Toru
CHAPMAN, Karen B.
MORIN, Gregg B.
HARLEY, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. US20030009019A1 Telomerase
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438,486
FILING DATE: 12-NOV-1999
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002931US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 171:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
OTHER INFORMATION: /note="motif D peptide from human
telomerase core protein 1 (TCP1)"
US-09-438-486-171

Query Match 41.0%; Score 34; DB 3; Length 15;
Best Local Similarity 77.8%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LVMGVPPFG 11
|||
Db 4 LVKGVPFYG 12

RESULT 21
US-10-053-758-171
; Sequence 171, Application US/10053758
; Publication No. US20030032075A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin H.
Andrews, William H.
TITLE OF INVENTION: No. US20030032075A1e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-0029310US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 171:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
OTHER INFORMATION: /note="motif D peptide from human
telomerase core protein 1 (TCP1)"
US-10-053-758-171

Query Match 41.0%; Score 34; DB 4; Length 15;
Best Local Similarity 77.8%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LVMGVPPFG 11
|||
Db 4 LVKGVPFYG 12

RESULT 22
US-10-054-295-171
; Sequence 171, Application US/10054295
; Publication No. US20030044953A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin H.
Andrews, William H.
TITLE OF INVENTION: No. US20030044953A1e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-0029310US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 171:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
OTHER INFORMATION: /note= "motif D peptide from human
telomerase core protein 1 (TCPI)"
SEQUENCE DESCRIPTION: SEQ ID NO: 171:
US-10-054-295-171

Query Match 41.0%; Score 34; DB 4; Length 15;
Best Local Similarity 77.8%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 LVMGVPPYG 11
Db 4 LVRGVPEYG 12

RESULT 23
US-10-054-611-171
Sequence 171, Application US/10054611
Publication No. US20030059787A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030059787A1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,611
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 171:
SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
OTHER INFORMATION: /note= "motif D peptide from human
telomerase core protein 1 (TCPI)"
SEQUENCE DESCRIPTION: SEQ ID NO: 171:
US-10-054-611-171

Query Match 41.0%; Score 34; DB 4; Length 15;
Best Local Similarity 77.8%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 LVMGVPPYG 11
Db 4 LVRGVPEYG 12

RESULT 24
US-10-282-960-70
Sequence 70, Application US/10282960
Publication No. US20030143228A1
GENERAL INFORMATION:
APPLICANT: Chen, Si-Yi
APPLICANT: Zhaoyang, You
APPLICANT: Schroers, Roland
TITLE OF INVENTION: Human Telomerase Reverse Transcriptase as a Class-II Restricted
FILE REFERENCE: P02193US1
CURRENT APPLICATION NUMBER: US/10/282,960
CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: US 60/345,012
PRIOR FILING DATE: 2001-10-29
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patent version 3.1
SEQ ID NO 70
LENGTH: 15
TYPE: PRT
ORGANISM: Human
US-10-282-960-70

Query Match 41.0%; Score 34; DB 4; Length 15;
Best Local Similarity 77.8%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 LVMGVPPYG 11
Db 7 LVRGVPEYG 15

RESULT 25
US-10-325-810-291
Sequence 291, Application US/10325810
Publication No. US20030204069A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California

COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,810
FILING DATE: 20-Dec-2002
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181
FILING DATE: 29-Sep-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-Oct-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Auehue, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 291:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
OTHER INFORMATION: /note= "motif D peptide from human telomerase core protein 1 (TCPI)"
SEQUENCE DESCRIPTION: SEQ ID NO: 291:
US-10-325-810-291
Query Match 41.0%; Score 34; DB 4; Length 15;
Best Local Similarity 77.8%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 LVMGVPEYG 11
Db 4 LVRGVPEYG 12

Search completed: January 26, 2006, 08:38:37
Job time : 56.25 secs

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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:48:50 ; Search time 8.5 Seconds
(without alignments)
192.434 Million cell updates/sec

Title: US-09-662-293-10
Perfect score: 83
Sequence: 1 DKLVGVPFYGRAXSIE 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 4071

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	33.7	7	2	E33932
2	26	31.3	16	2	A12729
3	25	30.1	20	2	B39089
4	24	28.9	14	2	PH1763
5	24	28.9	16	4	I79565
6	24	28.9	17	2	PH1820
7	24	28.9	20	2	I46652
8	23	27.7	12	2	PQ0730
9	23	27.7	19	2	PQ0730
10	22	26.5	9	2	PT0324
11	22	26.5	15	2	PW0004
12	22	26.5	15	2	S57584
13	22	26.5	16	2	PH1782
14	22	26.5	17	2	PH1801
15	22	26.5	17	2	SI6929
16	22	26.5	18	2	A32917
17	22	26.5	19	2	PH1304
18	22	26.5	21	2	S03504
19	22	26.5	21	2	A85712
20	22	25.3	10	2	B49581
21	21	25.3	11	2	B39853
22	21	25.3	11	2	B39853
23	21	25.3	13	2	PS0325
24	21	25.3	13	2	B61620
25	21	25.3	14	2	G44957
26	21	25.3	15	2	PA0026
27	21	25.3	15	2	PH1610
28	21	25.3	15	2	JT0610
29	21	25.3	16	2	H41299

30	21	25.3	17	2	C24166
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33	21	25.3	19	2	A44356
34	21	25.3	19	2	PH1624
35	21	25.3	20	2	PH1338
36	21	25.3	21	2	C49042
37	20	24.1	11	2	A40693
38	20	24.1	13	2	S21152
39	20	24.1	14	2	PA0013
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44	20	24.1	16	2	C49048
45	20	24.1	16	2	A41170
46	20	24.1	17	2	B36727
47	20	24.1	18	2	S09086
48	20	24.1	18	2	I52651
49	20	24.1	18	2	S51734
50	20	24.1	20	2	S50022
51	20	24.1	20	2	S46205
52	20	24.1	20	2	I64036
53	20	24.1	20	2	S53440
54	20	24.1	20	2	A58903
55	20	24.1	21	2	B12055
56	20	24.1	21	2	A27719
57	20	24.1	21	2	S09088
58	20	24.1	21	2	F64121
59	20	24.1	21	2	I52794
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61	19	22.9	10	1	ECLQIM
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63	19	22.9	10	2	S68033
64	19	22.9	10	2	B61033
65	19	22.9	10	2	A24867
66	19	22.9	11	1	ECLQ2M
67	19	22.9	11	2	A26120
68	19	22.9	11	2	S07203
69	19	22.9	11	2	S07201
70	19	22.9	11	2	A61033
71	19	22.9	12	2	C39109
72	19	22.9	12	2	S07436
73	19	22.9	13	2	A32486
74	19	22.9	13	2	D61491
75	19	22.9	13	2	A61361
76	19	22.9	14	2	JN0390
77	19	22.9	14	2	PA0015
78	19	22.9	14	2	B39111
79	19	22.9	14	2	S48685
80	19	22.9	15	1	LEFCP
81	19	22.9	15	2	PA0014
82	19	22.9	15	2	PN0173
83	19	22.9	15	2	PH0808
84	19	22.9	15	2	I40655
85	19	22.9	17	2	S26747
86	19	22.9	17	2	PH1789
87	19	22.9	17	2	B31769
88	19	22.9	17	2	PH0809
89	19	22.9	18	1	DRUPFD
90	19	22.9	18	2	J50647
91	19	22.9	18	2	PT0239
92	19	22.9	18	2	PH1794
93	19	22.9	18	2	A45590
94	19	22.9	19	2	S43960
95	19	22.9	19	2	A28814
96	19	22.9	19	2	PT0332
97	19	22.9	19	2	I49039
98	19	22.9	20	2	A24589
99	19	22.9	20	2	S58382
100	19	22.9	20	2	A85645

photosystem II ext
distal-retinal-pig
proteasome endopep
37k adherens junct
Ig H chain V-D-J r
Ig heavy chain V r
Ig heavy chain V r
transgelin - sheep
tryptophyltin-rela
photosystem II oxy
protein QA600027 -
GLYMA1 - soybean (NADH2 dehydrogenas
T-cell receptor al
T-cell receptor be
photosystem II 6.1
cytochrome c554 -
proteasome chain 5
brain-derived neur
T-cell receptor al
trypsin-like prote
comosain (EC 3.4.2
hypothetical prote
glutathione-bindin
metalloprotease
glyceraledehyde-3-P
trypsin (EC 3.4.21
proteasome chain 7
hypothetical prote
hypothetical BCR/A
fibrinopeptide B -
tachykinin I - mig
tachykinin III - m
cytochrome P450 1A
ranatichykinin B -
scylloethrin I - s
tachykinin II - mi
6-phosphofructokin
upetolein - frog (phylsalaemin - frog
ranatichykinin A -
hypothetical 1.2K
tachykinin - Afric
beta protein - rat
seed protein wa-4
bradykinin-like pe
histamine-releasin
seed storage prote
Ig heavy chain V r
extension protein
phe operon leader
seed storage prote
seed storage prote
T-cell receptor al
livBN leader pepti
Ig heavy chain J r
T-cell receptor al
T-cell receptor de
T-cell receptor al
pigment-dispersing
pheromotropin -
Ig heavy chain CDR
T-cell receptor al
beta-pigment-dispe
Ig mu chain V regi
Ig kappa chain V r
Ig heavy chain CRD
T-cell receptor be
photosystem II chl
hypothetical prote
Amino terminal of

ALIGNMENTS

RESULT 1

E33932

Ig mu chain D region (E7) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 16-Aug-1996

C:Accession: E33932

R:Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.

Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989

A:Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated germ-1

A:Reference number: A33932; MUID:89282823; PMID:2499887

C:Accession: E33932

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-7 <BAC>

A:Cross-references: UNIPARC:UPI000017C6D9; GB:M27106

C:Keywords: immunoglobulin

Query Match 33.7%; Score 28; DB 2; Length 7;

Best Local Similarity 80.0%; Pred. No. 2.8e+05;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PFYGR 12

Db 2 PFYGR 6

RESULT 2

A12729

glutamate dehydrogenase (EC 1.4.1.2) - bluefin tuna (tentative sequence) (fragment)

C:Species: Thunnus thynnus (bluefin tuna)

C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 05-Oct-2004

C:Accession: A12729

R:Veronase, F.M.; Bevilacqua, R.; Boccu, E.; Brown, D.M.

Biochim. Biophys. Acta 445, 1-13, 1976

A:Title: Glutamate dehydrogenase from tuna liver. Purification, characteristics and sequ

A:Reference number: A12729; MUID:7653947; PMID:182270

A:Accession: A12729

A:Molecule type: protein

A:Residues: 1-16 <VER>

A:Cross-references: UNIPROT:P20016; UNIPARC:UPI00001292E1

A:Experimental source: liver

C:Keywords: oxidoreductase

Query Match 31.3%; Score 26; DB 2; Length 16;

Best Local Similarity 35.7%; Pred. No. 3.3e+02;

Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 4 VMGVPFYGRAXSIE 17

Db 3 VVDVDFGAKAGVK 16

RESULT 3

B39089

hydrogenase (EC 1.18.99.1) 34K chain - Thiocapsa roseopersicina (fragment)

C:Species: Thiocapsa roseopersicina

C:Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 23-Jun-1993

C:Accession: B39089

R:Kovacs, K.L.; Tigyil, G.; Thanh, L.T.; Lakatos, S.; Kiss, Z.; Bagyinka, C.

J. Biol. Chem. 266, 947-951, 1991

A:Title: Structural rearrangements in active and inactive forms of hydrogenase from Thic

A:Reference number: A39089; MUID:91093297; PMID:1845998

A:Accession: B39089

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-20 <KOV>

A:Cross-references: UNIPARC:UPI000017AB7F

C:Keywords: oxidoreductase

Query Match 30.1%; Score 25; DB 2; Length 20;

Best Local Similarity 66.7%; Pred. No. 6.2e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VMGVPF 9

Db 10 VIGLGF 15

RESULT 4

PH1763

T cell receptor alpha chain V region (clone 1V alpha 23-2) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C:Accession: PH1763

R:Porcellio, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.

J. Exp. Med. 178, 1-16, 1993

A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood (

A:Reference number: PH1754; MUID:93301585; PMID:8391057

A:Accession: PH1763

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-14 <POR>

A:Cross-references: UNIPARC:UPI000017C36E

Query Match 28.9%; Score 24; DB 2; Length 14;

Best Local Similarity 66.7%; Pred. No. 6.4e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DKLYMG 6

Db 9 DKLIFFG 14

RESULT 5

I79565

hypothetical TCL3/TCRD (T-cell receptor delta chain) mutant fusion protein - human (frag

C:Species: Homo sapiens (man)

C:Date: 28-Jan-2000 #sequence_revision 28-Jan-2000 #text_change 09-Jul-2004

C:Accession: I79565

R:Zutter, M.; Hockett, R.D.; Roberts, C.W.; McGuire, E.A.; Bloomstone, J.; Morton, C.C.;

Proc. Natl. Acad. Sci. U.S.A. 87, 3161-3165, 1990

A:Title: The T(10;14)(q24;q11) of T-cell acute lymphoblastic leukemia juxtaposes the del

A:Reference number: I59162; MUID:90222189; PMID:2336274

A:Accession: I79565

A:Status: translation not shown; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-16 <ZUT>

A:Cross-references: UNIPROT:Q15632; UNIPARC:UPI000007279D; GB:M33602; NID:9339907; PIDN:

C:Comment: This sequence is the hypothetical translation of a chimeric translocation mut

C:Keywords: fusion protein

F.1-5/Region: TCL3 proto-oncogene derived

F.10-16/Region: T-cell receptor delta chain derived

Query Match 28.9%; Score 24; DB 4; Length 16;

Best Local Similarity 66.7%; Pred. No. 7.4e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DKLYMG 6

Db 11 DKLIFFG 16

RESULT 6

PH1820

T cell receptor alpha chain V region (clone 5PBL V alpha 24-3) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C:Accession: PH1820

R:Porcellio, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.

J. Exp. Med. 178, 1-16, 1993

A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A:Reference number: PH1754; MUID:93301585; PMID:8391057
A:Accession: PH1820
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-17 <P>
A:Cross-references: UNIPARC:UPI000017C388

Query Match 28.9%; Score 24; DB 2; Length 17;
Best Local Similarity 66.7%; Pred. No. 7.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DKLVMG 6
|||:|
Db 12 DKLIFG 17

RESULT 7

I46652
T-cell receptor delta-chain J-delta-1 segment - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-Nov-1999
C:Accession: I46652
R:Yang, Y.G.; Ohta, S.; Yamada, S.; Shimizu, M.; Takagaki, Y.
J. Immunol. 155, 1981-1993, 1995
A:Title: Diversity of T cell receptor delta-chain cDNA in the thymus of a one-month-old
A:Reference number: I46623; MUID:95363165; PMID:7636249
A:Accession: I46652
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-20 <Y>
A:Cross-references: UNIPARC:UPI000011B2B7; GB:D49560; NID:G1041172; PIDN:BA08504.1; PIR
C:Keywords: T-cell receptor

Query Match 28.9%; Score 24; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 9.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DKLVMG 6
|||:|
Db 6 DKLIFG 11

RESULT 8

PO0730
unidentified 5.4/35K protein [imported] - rice (fragment)
C:Species: Oryza sativa (rice)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: PO0730
R:Komatsu, S.; Kajiwara, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993
A:Title: A rice protein library; a data-file of rice proteins separated by two-dimension
A:Reference number: PQ0696
A:Accession: PO0730
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <K>
A:Cross-references: UNIPROT:Q7M1U3; UNIPARC:UPI000017B124

Query Match 27.7%; Score 23; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 8.2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 9 FYGRA 13
|||:|
Db 7 FYGBA 11

RESULT 9

PO0780
NADH dehydrogenase (EC 1.6.99.3) 14K chain - fava bean mitochondrion (fragment)
N:Alternate names: complex I 14K chain; NADH-ubiquinone reductase 14K chain
C:Species: mitochondrion Vicia faba (fava bean)
C:Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004

C:Accession: PO0790
R:Letenne, S.; Boutry, M.
Plant Physiol. 102, 435-443, 1993
A:Title: Purification and preliminary characterization of mitochondrial complex I (NADH
A:Reference number: PO0775; MUID:94151437; PMID:8108509
A:Accession: PO0790
A:Molecule type: protein
A:Residues: 1-19 <L>
A:Cross-references: UNIPROT:Q7M2G7; UNIPARC:UPI0000175118
C:Comment: Complex I, mitochondrial NADH-ubiquinone reductase, is the first of the c
ranging from 5K to 75K.
C:Comment: This enzyme catalyzes electron transfer from endogenous NADH to ubiquinone b
C:Genetics:
A:Genome: mitochondrion
C:Superfamily: NADH dehydrogenase
C:Keywords: electron transfer; mitochondrion; oxidoreductase

Query Match 27.7%; Score 23; DB 2; Length 19;
Best Local Similarity 66.7%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 LVMGP 8
|||:|
Db 13 LVSGIP 18

RESULT 10

PT0324
Ig heavy chain CRD3 region (clone J2-106C) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0324
R:Hamada, M.; Maeseman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0324
A:Molecule type: DNA
A:Residues: 1-9 <Y>
A:Cross-references: UNIPARC:UPI000017C217
A:Experimental source: B lymphocyte
C:Keywords: heterotrimer; immunoglobulin

Query Match 26.5%; Score 22; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 7 VPFYGRA 13
|||:|
Db 1 VPGYGS 7

RESULT 11

PM0004
chlorophyll a/b-binding protein 24.5K - green alga (Dunaliella tertiolecta) (fragment)
N:Alternate names: photosystem II light-harvesting chlorophyll 24.5K protein
C:Species: Dunaliella tertiolecta
C:Date: 04-Sep-1998 #sequence_revision 24-Nov-1999 #text_change 24-Nov-1999
C:Accession: PM0004
R:LaRoche, J.; Bennett, J.; Falkowski, P.G.
Gene 95, 165-171, 1990
A:Title: Characterization of a cDNA encoding for the 28.5-kDa LHCI apoprotein from the
A:Reference number: JMW040; MUID:91065528; PMID:2249775
A:Accession: PM0004
A:Molecule type: protein
A:Residues: 1-15 <L>
A:Cross-references: UNIPARC:UPI000017B174
C:Superfamily: chlorophyll a/b-binding protein
C:Keywords: chloroplast; grana; light-harvesting complex; membrane adhesion; membrane p

Query Match 26.5%; Score 22; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 7 VEPYG 11
|||
Db 1 VEPYG 5

RESULT 12

557584
T cell receptor V-D-J junctional alpha chain region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
C:Accession: S57584
R:Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argact, V.P.
submitted to the EMBL Data Library, June 1995
A:Description: T cell receptor repertoire for a viral epitope in humans is diversified b
A:Reference number: S57494
A:Accession: S57584
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-15 <BUR->
A:Cross-references: UNIPARC:UPI0000116747, EMBL:Z49956, NID:g887466, PIDN:CAA90227.1, PI
C:Keywords: T-cell receptor

Query Match 26.5%; Score 22; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 DKLWVG 6
|||
Db 10 DKIRFG 15

RESULT 13

PH1782
T cell receptor alpha chain V region (clone 2DN V alpha 24-3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1782
R:Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood
A:Reference number: PH1754; MUID:93301585; PMID:8391057
A:Accession: PH1782
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-16 <POR->
A:Cross-references: UNIPARC:UPI000017C375

Query Match 26.5%; Score 22; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 DKLWVG 6
|||
Db 11 DKIRFG 16

RESULT 14

PH1801
T cell receptor alpha chain V region (clone 3PBL V alpha 24-7) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1801
R:Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood
A:Reference number: PH1754; MUID:93301585; PMID:8391057
A:Accession: PH1801
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-17 <POR->

A:Cross-references: UNIPARC:UPI000017C383

Query Match 26.5%; Score 22; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 DKLWVG 6
|||
Db 12 DKIRFG 17

RESULT 15

S16929
Flavodoxin A - Azotobacter chroococcum (fragment)
N:Alternate names: ACF1dA
C:Species: Azotobacter chroococcum
C:Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: S16929
R:Bagby, S.; Barker, P.D.; Hill, H.A.O.; Sanghera, G.S.; Dunbar, B.; Ashby, G.A.; Eady, J.
Biochem. J. 277, 313-319, 1991
A:Title: Direct electrochemistry of two genetically distinct flavodoxins isolated from A.
A:Reference number: S16929; MUID:91315397; PMID:1859358
A:Accession: S16929
A:Molecule type: protein
A:Residues: 1-17 <BAG>
A:Experimental source: strain MCD1155
C:Function:
A:Description: acts as an electron donor to the Mo-containing nitrogenase
C:Keywords: electron transfer; flavoprotein; FMN

Query Match 26.5%; Score 22; DB 2; Length 17;
Best Local Similarity 37.5%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 9 FYGRAXSI 16
|||
Db 6 FYGSSGV 13

RESULT 16

A32917
protein phosphatase - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 08-Dec-1989 #sequence_revision 08-Dec-1989 #text_change 30-Sep-1993
C:Accession: A32917
R:Tamura, S.; Yasui, A.; Tsukit, S.
Biochem. Biophys. Res. Commun. 163, 131-136, 1989
A:Title: Expression of rat protein phosphatase 2C (1A) in Escherichia coli.
A:Reference number: A32917; MUID:89374212; PMID:2549985
A:Accession: A32917
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-18 <TAM>
A:Cross-references: UNIPARC:UPI000017C9A7

Query Match 26.5%; Score 22; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DKLWVG 6
|||
Db 13 DQVIMG 18

RESULT 17

PH1304
Ig heavy chain DJ region (clone CA39-111) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1304
R:Masserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992

A>Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A:Reference number: PH1302; MUID:93094761; PMID:1460419

A:Accession: PH1304
A:Molecule type: DNA

A:Residues: 1-19 <WAS>
A:Cross-references: UNIPARC:UPI0000176934

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 26.5%; Score 22; DB 2; Length 19;
Best Local Similarity 60.0%; Pred. No. 2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 6 GVPY 10
| | | |
| | | |
Db 2 GVPY 6

RESULT 18

S03504
T-cell receptor alpha chain J region (TT11) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 23-May-1997

C:Accession: S03504

R:Wino, A.; Mjolsness, S.; Hood, L.

Nature 316, 832-836, 1985

A>Title: Genomic organization of the genes encoding mouse T-cell receptor alpha-chain.

A:Reference number: S03503; MUID:85296332; PMID:2993908

A:Accession: S03504

A:Molecule type: DNA

A:Residues: 1-21 <WIN>

A:Cross-references: UNIPARC:UPI0000176DB6; EMBL:X02858

C:Note: this sequence was determined from the germline gene

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: T-cell receptor

RESULT 19

A85712
Unknown protein encoded by prophage CP-9330 (imported) - Escherichia coli (strain O157:H

C:Species: Escherichia coli

C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C:Accession: A85712

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001

A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: A85712

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-21 <STO>

A:Cross-references: UNIPROT:Q8X4E1; UNIPARC:UPI00000D0DFB; GB:AE005174; NID:g12515036; F

C:Genetic source: strain O157:H7, substrain EDL933

A:Gene: Z2087

Query Match 26.5%; Score 22; DB 2; Length 21;
Best Local Similarity 33.3%; Pred. No. 2.2e+03;
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 5 MGVPYGRAXSI 16
| | | | |
| | | | |
Db 1 MSUDFFERALLPV 12

RESULT 20

B49581
Stalokinin II - yellow fever mosquito

C:Species: Aedes aegypti (yellow fever mosquito)

C>Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004

C:Accession: B49581

R:Chapagne, D.E.; Ribeiro, J.M.
Proc. Natl. Acad. Sci. U.S.A. 91, 138-142, 1994

A>Title: Stalokinin I and II: vasodilatory tachykinins from the yellow fever mosquito A

A:Reference number: A49581; MUID:94105119; PMID:8278354

A:Accession: B49581

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <CHA>

A:Cross-references: UNIPROT:P42635; UNIPARC:UPI0000136FEC

A:Experimental source: Rockefeller, salivary gland

A:Note: sequence extracted from NCBI backbone (NCBI:P:141842)

Query Match 25.3%; Score 21; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 GVPY 11
| | | | |
| | | | |
Db 3 GDRFY 8

RESULT 21
A49581
Stalokinin I - yellow fever mosquito

C:Species: Aedes aegypti (yellow fever mosquito)

C>Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 05-Oct-2004

C:Accession: A49581

R:Chapagne, D.E.; Ribeiro, J.M.
Proc. Natl. Acad. Sci. U.S.A. 91, 138-142, 1994

A>Title: Stalokinin I and II: vasodilatory tachykinins from the yellow fever mosquito A

A:Reference number: A49581; MUID:94105119; PMID:8278354

A:Accession: A49581

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <CHA>

A:Cross-references: UNIPROT:P42634; UNIPARC:UPI0000136FEB

A:Experimental source: Rockefeller, salivary gland

A:Note: sequence extracted from NCBI backbone (NCBI:P:141841)

Query Match 25.3%; Score 21; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 GVPY 11
| | | | |
| | | | |
Db 3 GDRFY 8

RESULT 22
B39853
LuxC protein - Photobacterium phosphoreum (fragment)

C:Species: Photobacterium phosphoreum
C>Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 09-Jul-2004

C:Accession: B39853

R:Perri, S.R.; Melgion, E.A.
J. Biol. Chem. 266, 12852-12857, 1991

A>Title: A lux-specific myristoyl transferase in luminescent bacteria related to eukary.

A:Reference number: A39853; MUID:91302295; PMID:2071574

A:Accession: B39853

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-11 <FER>

A:Cross-references: UNIPROT:P19841; UNIPARC:UPI000016FDC7; GB:M64224; NID:g150701; PIDN

Query Match 25.3%; Score 21; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 DKLVGVYP 8
| | | |
| | | |

Db 4 DKFLVFPV 11

RESULT 23

PS0325 tetrahydroberberine oxidase (EC 1.3.3.8) - rice (strain Nihonbare) (fragment)

C/Species: Oryza sativa (rice)

C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995

C/Accession: PS0325

R/Tungita, A. JIPID, April 1993

Submitted to JIPID, April 1993

A/Reference number: PS0206

A/Accession: PS0325

A/Molecule type: protein

A/Residues: 1-13 <TSU>

A/Cross-references: UNIPARC:UPI000017B121

A/Experimental source: callus

C/Keywords: oxidoreductase

Query Match 25.3%; Score 21; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 KLVMGVPPYG 11
| | | |
| | | |

Db 4 KLFGGLXYG 13

RESULT 24

B61620 locustamyotropin IV - migratory locust

C/Species: Locusta migratoria (migratory locust)

C/Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 09-Jul-2004

C/Accession: B61620

R/SchoofB, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; Kochansky, J.P.; De Loof, A.

Insect Biochem. Mol. Biol. 22, 447-452, 1992

A/Title: Isolation, identification and synthesis of locustamyotropin III and IV, two add

A/Reference number: B61620

A/Accession: B61620

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-13 <SCH>

A/Cross-references: UNIPROT:P41490; UNIPARC:UPI000012E792

C/Keywords: amidated carboxyl end; neuropeptide

F.13/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 25.3%; Score 21; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 6 GVPEYGR 12
| | | |
| | | |

Db 6 GMPSPFR 12

RESULT 25

G44957 photosystem II oxygen-evolving complex protein 2 - common tobacco (cv. Samsum NN) (fragm

C/Species: Nicotiana tabacum (common tobacco)

C/Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Jun-1993

C/Accession: G44957

R/Takeda, S.; Sato, F.; Ida, K.; Yamada, Y.

Plant Cell Physiol. 31, 215-221, 1990

A/Title: Characterization of polypeptides that accumulate in cultured Nicotiana tabacum

A/Reference number: A44957

A/Accession: G44957

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-14 <TRK>

A/Cross-references: UNIPARC:UPI000017B0AD

Query Match 25.3%; Score 21; DB 2; Length 14;

Best Local Similarity 42.9%; Pred. No. 2.2e+03; Indels 0; Gaps 0;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 10 YGRAXSI 16
| | | |
| | | |

Db 2 YGEAANY 8

Search completed: January 26, 2006, 08:05:03
Job time : 9.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 08:05:12 : Search time 3.22414 Seconds
(without alignments)
57.099 Million cell updates/sec

Title: US-09-662-293-10

Perfect score: 83

Sequence: 1 DKUWGVFGRAXSIE 17

Scoring table: BLOSUM62

Searched: Gapop 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters: 37628

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA New:
1: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubppa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	37.3	11	7	US-11-145-035-4	Sequence 4, Appli
2	34.9	15	7	US-11-054-515-2757	Sequence 2757, Ap
3	34.9	16	6	US-10-859-643-762	Sequence 762, App
4	34.9	16	7	US-11-097-864-762	Sequence 762, App
5	34.9	16	7	US-11-097-912-762	Sequence 762, App
6	34.9	16	7	US-11-045-024-14490	Sequence 14490, A
7	33.7	11	6	US-10-665-658-53	Sequence 53, Appli
8	33.7	11	6	US-10-665-658-57	Sequence 57, Appli
9	32.5	11	6	US-10-665-658-54	Sequence 54, Appli
10	32.5	11	7	US-11-145-035-2	Sequence 2, Appli
11	31.3	8	7	US-11-145-035-6	Sequence 6, Appli
12	31.3	10	6	US-10-929-988-156	Sequence 156, App
13	31.3	11	7	US-11-145-035-5	Sequence 5, Appli
14	30.7	19	7	US-11-139-435-4	Sequence 4, Appli
15	30.1	11	6	US-10-665-658-51	Sequence 51, Appli
16	30.1	11	6	US-10-665-658-56	Sequence 56, Appli
17	30.1	12	6	US-10-665-658-58	Sequence 58, Appli
18	30.1	12	6	US-10-665-658-12	Sequence 12, Appli
19	30.1	16	7	US-11-054-515-2893	Sequence 2893, Ap
20	28.9	6	6	US-10-431-638-9	Sequence 9, Appli
21	28.9	8	6	US-10-431-638-10	Sequence 10, Appli
22	28.9	9	6	US-10-859-643-597	Sequence 597, App
23	28.9	9	6	US-10-859-643-685	Sequence 685, App
24	28.9	9	7	US-11-097-864-597	Sequence 597, App
25	28.9	9	7	US-11-097-864-685	Sequence 685, App

26	28.9	9	7	US-11-097-912-597	Sequence 597, App
27	28.9	9	7	US-11-097-912-685	Sequence 685, App
28	28.9	9	7	US-11-136-079-145	Sequence 145, App
29	28.9	10	7	US-11-041-893-56	Sequence 56, Appli
30	28.9	14	6	US-10-431-638-2	Sequence 2, Appli
31	28.9	14	6	US-10-431-638-38	Sequence 38, Appli
32	28.9	14	6	US-10-431-638-46	Sequence 46, Appli
33	28.9	17	6	US-10-945-853-4	Sequence 4, Appli
34	28.9	18	6	US-10-518-441-15	Sequence 15, Appli
35	28.9	18	6	US-10-431-638-19	Sequence 39, Appli
36	28.9	18	6	US-10-431-638-42	Sequence 42, Appli
37	28.9	18	6	US-10-431-638-43	Sequence 43, Appli
38	28.9	18	7	US-11-054-515-2752	Sequence 2752, App
39	28.9	19	7	US-11-033-1321	Sequence 1321, Ap
40	28.9	19	6	US-10-982-891-72	Sequence 72, Appli
41	28.9	20	6	US-10-939-890-174	Sequence 174, App
42	28.9	20	7	US-11-053-100-18	Sequence 18, Appli
43	28.9	12	6	US-10-982-891-55	Sequence 55, Appli
44	23.5	8	7	US-11-066-967-82	Sequence 82, Appli
45	27.7	9	6	US-10-073-301A-5	Sequence 5, Appli
46	27.7	9	7	US-11-203-137-5	Sequence 5, Appli
47	27.7	11	7	US-11-116-144-76	Sequence 76, Appli
48	27.7	12	7	US-11-193-512-42	Sequence 42, Appli
49	27.7	12	7	US-11-089-266-9	Sequence 9, Appli
50	27.7	14	7	US-11-054-515-2755	Sequence 2755, App
51	27.7	16	7	US-11-054-515-2296	Sequence 2296, App
52	27.7	16	7	US-11-054-515-2791	Sequence 2791, App
53	27.7	16	7	US-11-054-515-3047	Sequence 3047, App
54	27.7	16	7	US-11-071-259-16	Sequence 16, Appli
55	27.7	17	7	US-11-097-812-91	Sequence 91, Appli
56	27.7	17	7	US-11-097-812-93	Sequence 93, Appli
57	27.7	17	7	US-11-097-812-94	Sequence 94, Appli
58	27.7	17	7	US-11-097-812-163	Sequence 163, App
59	27.7	17	7	US-11-097-812-166	Sequence 166, App
60	27.7	18	6	US-10-939-890-143	Sequence 143, App
61	27.7	18	7	US-11-054-515-2802	Sequence 2802, App
62	27.7	20	6	US-10-939-890-173	Sequence 173, App
63	27.7	20	6	US-10-901-576-14	Sequence 14, Appli
64	27.7	20	7	US-11-071-259-15	Sequence 15, Appli
65	26.5	9	6	US-10-491-096-44	Sequence 44, Appli
66	26.5	10	6	US-10-491-096-89	Sequence 89, Appli
67	26.5	10	6	US-10-491-096-185	Sequence 185, Appli
68	26.5	10	7	US-11-009-873A-209	Sequence 209, App
69	26.5	10	7	US-11-009-873A-209	Sequence 209, App
70	26.5	12	6	US-10-982-891-53	Sequence 53, Appli
71	26.5	12	7	US-11-033-165-47	Sequence 47, Appli
72	26.5	15	7	US-11-054-515-2292	Sequence 2292, App
73	26.5	16	7	US-11-054-515-2760	Sequence 2760, App
74	26.5	17	7	US-11-054-515-2135	Sequence 2135, App
75	26.5	17	7	US-11-054-515-2156	Sequence 2156, App
76	26.5	18	7	US-11-054-515-3060	Sequence 3060, App
77	26.5	18	7	US-11-041-893-113	Sequence 113, App
78	26.5	18	7	US-11-156-163-11	Sequence 11, Appli
79	26.5	19	6	US-10-503-575-168	Sequence 168, App
80	26.5	19	7	US-11-054-515-2996	Sequence 2996, App
81	26.5	20	6	US-10-901-576-20	Sequence 20, Appli
82	26.5	20	7	US-11-094-142-32	Sequence 32, Appli
83	26.5	20	7	US-11-033-039-932	Sequence 932, Appli
84	26.5	21	7	US-11-113-224-56	Sequence 56, Appli
85	26.5	9	7	US-11-033-039-559	Sequence 559, App
86	26.5	9	7	US-11-033-039-616	Sequence 616, App
87	26.5	9	7	US-11-033-039-746	Sequence 746, App
88	26.5	9	7	US-11-033-039-766	Sequence 766, App
89	26.5	10	7	US-11-125-837-12	Sequence 12, Appli
90	26.5	10	7	US-11-045-024-750	Sequence 750, App
91	26.5	10	7	US-11-097-812-58	Sequence 58, Appli
92	26.5	11	7	US-11-033-165-52	Sequence 52, Appli
93	26.5	11	7	US-11-045-024-898	Sequence 898, App
94	26.5	12	7	US-11-058-133-35	Sequence 35, Appli
95	26.5	13	7	US-11-105-708-16	Sequence 16, Appli
96	26.5	13	7	US-10-929-988-448	Sequence 448, App
97	26.5	14	7	US-11-033-039-759	Sequence 759, App
98	26.5	15	6	US-10-939-890-467	Sequence 467, App

99 21 25.3 15 7 US-11-054-515-2213
100 .21 25.3 15 7 US-11-054-515-2223

Sequence 2213, Ap
Sequence 2223, Ap

ALIGNMENTS

RESULT 1

US-11-145-035-4
; Sequence 4, Application US/11145035
; Publication No. US20050287122A1
; GENERAL INFORMATION:
; APPLICANT: Bartlett et al.
; TITLE OF INVENTION: AAV VECTORS AND METHODS
; FILE REFERENCE: 28335/41335
; CURRENT APPLICATION NUMBER: US/11/145,035
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/038,972
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/260,124
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-145-035-4

Query Match 37.3%; Score 31; DB 7; Length 11;
Best Local Similarity 60.0%; Pred. No. 4.5;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 GVPPYGRAXS 15
| | | | |
Db 2 GTPFLKALSL 11

RESULT 2

US-11-054-515-2757
; Sequence 2757, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2757

; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2757

Query Match 34.9%; Score 29; DB 7; Length 15;
Best Local Similarity 62.5%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 LVMGVPPY 10
| : | | |
Db 5 LITGVPPY 12

RESULT 3

US-10-859-643-762
; Sequence 762, Application US/10859643
; Publication No. US20060002993A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Farie, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 511582006203
; CURRENT APPLICATION NUMBER: US/10/859,643
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 762
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-859-643-762

Query Match 34.9%; Score 29; DB 6; Length 16;
Best Local Similarity 46.2%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DKLVMGVPPYGRA 13
| : : | | | |
Db 4 DSIIGVATYGA 16

RESULT 4

US-11-097-864-762
; Sequence 762, Application US/11097864
; Publication No. US20050265924A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Farie, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 762

LENGTH: 16
TYPE: PRT
ORGANISM: Homo Sapien
US-11-097-864-762

Query Match 34.9%; Score 29; DB 7; Length 16;
Best Local Similarity 46.2%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DKLVGVPFYGRA 13
DB 4 DSILGVAITYGAA 16

RESULT 5
US-11-097-912-762
Sequence 762, Application US/11097912
Publication No. US20050265921A1
GENERAL INFORMATION:
APPLICANT: Challita-Bid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158206204
CURRENT APPLICATION NUMBER: US/11/097,912
CURRENT FILING DATE: 2005-04-01
PRIOR APPLICATION NUMBER: US 10/062,109
PRIOR FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: US 10/005,480
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 765
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 762
LENGTH: 16
TYPE: PRT
ORGANISM: Homo Sapien
US-11-097-912-762

Query Match 34.9%; Score 29; DB 7; Length 16;
Best Local Similarity 46.2%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DKLVGVPFYGRA 13
DB 4 DSILGVAITYGAA 16

RESULT 6
US-11-045-024-14490
Sequence 14490, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Celis, Esben
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: EpiMune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060, 0040007
CURRENT APPLICATION NUMBER: US/11/045,024
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14490
LENGTH: 16
TYPE: PRT
ORGANISM: Streptococcus sp.
US-11-045-024-14490

Query Match 34.9%; Score 29; DB 7; Length 16;
Best Local Similarity 46.2%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DKLVGVPFYGRA 13
DB 4 DSILGVAITYGAA 16

RESULT 7
US-10-665-658-53
Sequence 53, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-Nov-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-Oct-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-Feb-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014RIC1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 53:

SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: Amino Acid
TOPOLOGY: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-10-665-658-53

Query Match 33.7% Score 28; DB 6; Length 11;
Best Local Similarity 62.5%; Pred. No. 16;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GVPPYGRA 13
|: ||| |
Db 1 GIVFYGAA 8

RESULT 8
US-10-665-658-57
Sequence 57, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1CID1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: Amino Acid
TOPOLOGY: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-665-658-57

Query Match 33.7% Score 28; DB 6; Length 11;
Best Local Similarity 62.5%; Pred. No. 16;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GVPPYGRA 13
|: ||| |
Db 1 GIVFYGTA 8

RESULT 9
US-10-665-658-54
Sequence 54, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1CID1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: Amino Acid
TOPOLOGY: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 54:
US-10-665-658-54

Query Match 32.5% Score 27; DB 6; Length 11;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GVPPY 11
|: ||| |
Db 1 GIAPY 6

RESULT 10
US-11-145-035-2
Sequence 2, Application US/11145035
Publication No. US20050287122A1
GENERAL INFORMATION:
APPLICANT: Bartlett et al.
TITLE OF INVENTION: AAV VECTORS AND METHODS
FILE REFERENCE: 28335/4135
CURRENT APPLICATION NUMBER: US/11/145,035
CURRENT FILING DATE: 2005-06-03
PRIOR APPLICATION NUMBER: US 10/038,972
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: US 60/260,124
PRIOR FILING DATE: 2001-01-05


```

; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Bovine Papilloma Virus Peptide
US-11-145-035-2
```

```

Query Match          32.5%; Score 27; DB 7; Length 11;
Best Local Similarity 50.0%; Pred. No. 24;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      6 GVPEYGRAXS 15
      | | | | |
Db      2 GTPEYLRKGLS 11
```

RESULT 11

```

US-11-145-035-6
; Sequence 6, Application US/11145035
; Publication No. US20050287122A1
; GENERAL INFORMATION:
; APPLICANT: Bartlett et al.
; TITLE OF INVENTION: AAV VECTORS AND METHODS
; FILE REFERENCE: 28335/41335
; CURRENT APPLICATION NUMBER: US/11/145,035
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/038,972
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/260,124
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Bovine Papilloma Virus Peptide
US-11-145-035-6
```

```

Query Match          31.3%; Score 26; DB 7; Length 8;
Best Local Similarity 80.0%; Pred. No. 5; 8e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      6 GVPEY 10
      | | | |
Db      2 GTPEY 6
```

RESULT 12

```

US-10-929-988-156
; Sequence 156, Application US/109299988
; Publication No. US20050275588A1
; GENERAL INFORMATION:
; APPLICANT: Cwiria, Steven E.
; APPLICANT: BALU, PALANI
; APPLICANT: DUFFIN, DAVID J.
; APPLICANT: PIPLANI, SUNIL A.
; APPLICANT: MERRILL, BARBARA MCEOMEN
; APPLICANT: SCHATZ, PETER JOSEPH
; TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY
; TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
; FILE REFERENCE: 0300-0014
; CURRENT APPLICATION NUMBER: US/10/929,988
; CURRENT FILING DATE: 2004-08-30
; PRIOR APPLICATION NUMBER: US/09/620,091
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 491
; SOFTWARE: PatentIn Ver. 2.1
```

```

; SEQ ID NO 156
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-929-988-156
```

```

Query Match          31.3%; Score 26; DB 6; Length 10;
Best Local Similarity 40.0%; Pred. No. 32;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      1 DKLVMGPEFY 10
      | | | | |
Db      1 DEMVYTVPPYV 10
```

RESULT 13

```

US-11-145-035-5
; Sequence 5, Application US/11145035
; Publication No. US20050287122A1
; GENERAL INFORMATION:
; APPLICANT: Bartlett et al.
; TITLE OF INVENTION: AAV VECTORS AND METHODS
; FILE REFERENCE: 28335/41335
; CURRENT APPLICATION NUMBER: US/11/145,035
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/038,972
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/260,124
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Bovine Papilloma Virus Peptide
US-11-145-035-5
```

```

Query Match          31.3%; Score 26; DB 7; Length 11;
Best Local Similarity 80.0%; Pred. No. 36;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      6 GVPEY 10
      | | | |
Db      2 GTPEY 6
```

RESULT 14

```

US-11-139-435-4
; Sequence 4, Application US/11139435
; Publication No. US20050287664A1
; GENERAL INFORMATION:
; APPLICANT: Fann, Ming-Ji
; TITLE OF INVENTION: Cellular Proliferation Control Factors
; FILE REFERENCE: 17741-002001
; CURRENT APPLICATION NUMBER: US/11/139,435
; CURRENT FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: US 60/575,611
; PRIOR FILING DATE: 2004-05-27
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: conditioned medium (CM)
US-11-139-435-4
```

Query Match 30.7%; Score 25.5; DB 7; Length 19;
Best Local Similarity 42.9%; Pred. No. 81;
Matches 6; Conservative 4; Mismatches 1; Indels 3; Gaps 1;

QY 4 VMGVPFYGRAXSIE 17
Db 7 ILGVP---RSASIK 17

RESULT 15

US-10-665-658-51
; Sequence 51, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:

APPLICANT: Jardiou, Paula M.
PRESTA, Leonard G.

TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way
CITY: South San Francisco
STATE: California

COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971

FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899

FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745

FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798

FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:

NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447

REFERENCE/DOCKET NUMBER: P1014R1CID1C1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids
TYPE: Amino Acid
TOPOLOGY: <Unknown>

SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-10-665-658-51

Query Match 30.1%; Score 25; DB 6; Length 11;
Best Local Similarity 66.7%; Pred. No. 54;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 GVPPFYG 11
Db 1 GIVFYG 6

RESULT 16
US-10-665-658-56
; Sequence 56, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:

APPLICANT: Jardiou, Paula M.
PRESTA, Leonard G.

TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971

FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899

FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745

FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798

FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:

NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447

REFERENCE/DOCKET NUMBER: P1014R1CID1C1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids
TYPE: Amino Acid
TOPOLOGY: <Unknown>

SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-665-658-56

Query Match 30.1%; Score 25; DB 6; Length 11;
Best Local Similarity 66.7%; Pred. No. 54;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 GVPPFYG 11
Db 1 GIVFYG 6

RESULT 17
US-10-665-658-58
; Sequence 58, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:

APPLICANT: Jardiou, Paula M.
PRESTA, Leonard G.

TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

```

?
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/10/665,658
? FILING DATE: 19-Sep-2003
? CLASSIFICATION: <Unknown>
?
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 60/031971
? FILING DATE: 27-NOV-1996
? APPLICATION NUMBER: 08/974899
? FILING DATE: 20-NOV-1997
? APPLICATION NUMBER: 09/420745
? FILING DATE: 20-OCT-1999
? APPLICATION NUMBER: 09/975798
? FILING DATE: 28-FEB-2001
? ATTORNEY/AGENT INFORMATION:
? NAME: Tan, Lee K.
? REGISTRATION NUMBER: 39,447
? REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 650/225-4462
? TELEFAX: 650/952-9881
? INFORMATION FOR SEQ ID NO: 58:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 11 amino acids
? TYPE: Amino Acid
? TOPOLOGY: <unknown>
? SEQUENCE DESCRIPTION: SEQ ID NO: 58:
?
? US-10-665-658-58
?
? Query Match 30.1%; Score 25; DB 6; Length 11;
? Best Local Similarity 66.7%; Pred. No. 54;
? Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
?
? Qy 6 GVPFYG 11
? 1 GIVFYG 6
?
? Db 1 GIVFYG 6
?
? RESULT 18
? US-10-665-658-12
? Sequence 12, Application US/10665658
? Publication No. US20050276801A1
? GENERAL INFORMATION:
? APPLICANT: Jarden, Paula M.
? TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
? NUMBER OF SEQUENCES: 71
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Genentech, Inc.
? STREET: 1 DNA Way
? CITY: South San Francisco
? STATE: California
? COUNTRY: USA
? ZIP: 94080
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: WinPatIn (Genentech)
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/10/665,658
? FILING DATE: 19-Sep-2003
? CLASSIFICATION: <Unknown>
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 60/031971
? FILING DATE: 27-NOV-1996
? APPLICATION NUMBER: 08/974899
? FILING DATE: 20-NOV-1997
? APPLICATION NUMBER: 09/420745
? FILING DATE: 20-OCT-1999
? APPLICATION NUMBER: 09/975798
? FILING DATE: 28-FEB-2001
? ATTORNEY/AGENT INFORMATION:
? NAME: Tan, Lee K.

```

```

?
? REGISTRATION NUMBER: 39,447
? REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 650/225-4462
? TELEFAX: 650/952-9881
? INFORMATION FOR SEQ ID NO: 12:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 12 amino acids
? TYPE: Amino Acid
? TOPOLOGY: Linear
? SEQUENCE DESCRIPTION: SEQ ID NO: 12:
?
? US-10-665-658-12
?
? Query Match 30.1%; Score 25; DB 6; Length 12;
? Best Local Similarity 66.7%; Pred. No. 60;
? Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
?
? Qy 6 GVPFYG 11
? 1 GIVFYG 6
?
? Db 1 GIVFYG 6
?
? RESULT 19
? US-11-054-515-2893
? Sequence 2893, Application US/11054515
? Publication No. US20050255532A1
? GENERAL INFORMATION:
? APPLICANT: Ruben et al.
? TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
? FILE REFERENCE: PE523P3
? CURRENT APPLICATION NUMBER: US/11/054,515
? CURRENT FILING DATE: 2005-02-10
? PRIOR APPLICATION NUMBER: 60/543,296
? PRIOR FILING DATE: 2004-02-11
? PRIOR APPLICATION NUMBER: 60/580,347
? PRIOR FILING DATE: 2004-06-18
? PRIOR APPLICATION NUMBER: 10/293,418
? PRIOR FILING DATE: 2002-11-14
? PRIOR APPLICATION NUMBER: 60/331,469
? PRIOR FILING DATE: 2001-11-16
? PRIOR APPLICATION NUMBER: 60/340,817
? PRIOR FILING DATE: 2001-12-19
? PRIOR APPLICATION NUMBER: 09/880,748
? PRIOR FILING DATE: 2001-06-15
? PRIOR APPLICATION NUMBER: 60/293,499
? PRIOR FILING DATE: 2001-05-25
? PRIOR APPLICATION NUMBER: 60/277,379
? PRIOR FILING DATE: 2001-03-21
? PRIOR APPLICATION NUMBER: 60/276,248
? PRIOR FILING DATE: 2001-03-16
? PRIOR APPLICATION NUMBER: 60/240,816
? PRIOR FILING DATE: 2000-10-17
? Remaining Prior Application data removed - See File Wrapper or PALM.
? NUMBER OF SEQ ID NOS: 3247
? SEQ ID NO 2893
? LENGTH: 16
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-11-054-515-2893
?
? Query Match 30.1%; Score 25; DB 7; Length 16;
? Best Local Similarity 44.4%; Pred. No. 83;
? Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
?
? Qy 3 LVNGVFPYVG 11
? 5 ILNGVYVYVG 13
?
? Db 5 ILNGVYVYVG 13
?
? RESULT 20
? US-10-431-638-9
? Sequence 9, Application US/10431638
? Publication No. US20060003939A1

```

```

; GENERAL INFORMATION:
; APPLICANT: The Rockefeller Institute
; APPLICANT: Steller, Hermann
; TITLE OF INVENTION: PEPTIDES AND METHODS FOR CELL DEATH REGULATION
; FILE REFERENCE: P-5004-US
; CURRENT APPLICATION NUMBER: US/10/431.638
; CURRENT FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-431-638-9
```

```

Query Match      28.9%; Score 24; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      7 VPFY 10
       |||
Db      2 VPFY 5
```

```

RESULT 21
; Sequence 10, Application US/10431638
; Publication No. US20060003939A1
; GENERAL INFORMATION:
; APPLICANT: The Rockefeller Institute
; APPLICANT: Steller, Hermann
; TITLE OF INVENTION: PEPTIDES AND METHODS FOR CELL DEATH REGULATION
; FILE REFERENCE: P-5004-US
; CURRENT APPLICATION NUMBER: US/10/431.638
; CURRENT FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-431-638-10
```

```

Query Match      28.9%; Score 24; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      7 VPFY 10
       |||
Db      2 VPFY 5
```

```

RESULT 22
US-10-859-643-597
; Sequence 597, Application US/10859643
; Publication No. US20060002993A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 511582006203
; CURRENT APPLICATION NUMBER: US/10/859.643
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: US 10/005.480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
```

```

; SEQ ID NO 597
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-859-643-597
```

```

Query Match      28.9%; Score 24; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      7 VPFY 10
       |||
Db      1 VPFY 4
```

```

RESULT 23
US-10-859-643-685
; Sequence 685, Application US/10859643
; Publication No. US20060002993A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 511582006203
; CURRENT APPLICATION NUMBER: US/10/859.643
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: US 10/005.480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 685
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-859-643-685
```

```

Query Match      28.9%; Score 24; DB 6; Length 9;
Best Local Similarity 44.4%; Pred. No. 5.8e+04;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      2 KLVNGVPFY 10
       ::::
Db      1 ELTGTLDYF 9
```

```

RESULT 24
US-11-097-864-597
; Sequence 597, Application US/11097864
; Publication No. US20050265924A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097.864
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062.109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005.480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
```

SEQ ID NO 597
LENGTH: 9
TYPE: PRT
ORGANISM: Homo Sapien
US-11-097-864-597

Query Match 28.9%; Score 24; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VPFY 10
|||
Db 1 VPFY 4

RESULT 25
US-11-097-864-685
Sequence 685, Application US/11097864
Publication No. US20050265924A1
GENERAL INFORMATION:
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 511582006205
CURRENT APPLICATION NUMBER: US/11/097,864
CURRENT FILING DATE: 2005-04-01
PRIOR APPLICATION NUMBER: US 10/062,109
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 10/005,480
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 765
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 685
LENGTH: 9
TYPE: PRT
ORGANISM: Homo Sapien
US-11-097-864-685

Query Match 28.9%; Score 24; DB 7; Length 9;
Best Local Similarity 44.4%; Pred. No. 5.8e+04;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLWGVVPFY 10
|||
Db 1 ELTGGLDPY 9

Search completed: January 26, 2006, 08:39:07
Job time : 4.22414 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:47:56 ; Search time 50.5603 Seconds
(without alignments)
237.221 Million cell updates/sec

Title: US-09-662-293-10
Perfect score: 83
Sequence: 1 DKLVGVPFYGRAXSIE 17

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 15779

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	33.7	16	2	099898 HUMAN
2	27	32.5	21	2	04YWI1 PLABE
3	26	31.3	12	2	Q7AU55 GAGAM
4	26	31.3	16	1	DHE2_THROT
5	25	30.1	16	2	Q9S8A0 PINMO
6	24	28.9	14	1	TY13 BOWVA
7	24	28.9	16	2	015632 HUMAN
8	24	28.9	16	2	Q9AUA1 GBRAS
9	24	28.9	20	2	Q9S8H8 BRANA
10	24	28.9	21	2	Q4XLR5 PLACH
11	23	27.7	8	2	06LID23 MOUSE
12	23	27.7	12	2	Q7M1U3 ORYSA
13	23	27.7	13	2	Q7S2J9 NEUCR
14	23	27.7	14	2	Q8AXQ7 XENLA
15	23	27.7	15	2	Q9BXQ0 HUMAN
16	23	27.7	18	2	Q7TSR9 MOUSE
17	23	27.7	19	2	Q7M2G7 VICFA
18	23	27.7	19	2	06LIDN4 RHOC
19	23	27.7	19	2	08K3K5 MOUSE
20	23	27.7	20	1	OM4VA_VIBAL
21	23	27.7	20	1	TL19_SPTOL
22	23	27.7	20	2	Q9TWN3 THESE
23	23	27.7	20	2	P81896 SOLTU
24	23	27.7	21	1	TL19 ARATH
25	23	27.7	21	2	Q7RZ21 NEUCR
26	23	27.7	21	2	Q9RF21 MYCMS
27	23	27.7	21	2	Q5C9K1 MYCMY
28	23	27.7	21	2	Q80817 GDELA
29	22	26.5	9	2	Q5IA44 GARAE
30	22	26.5	10	2	Q6JL97 NEISGO
31	22	26.5	12	2	Q50019 MYCLE

32	22	26.5	13	1	CRBL_ICASP	P17237 icaria sp.
33	22	26.5	13	1	SOVO_SEPOF	P83567 sepiia offic
34	22	26.5	16	2	Q4X7B4 PLACH	Q4X7B4 plasmodium
35	22	26.5	16	2	Q8H929 SVIRU	Q8H929 bacterioph
36	22	26.5	16	2	Q9QVU1 GMDRI	Q9QVU1 mus sp. s
37	22	26.5	17	1	FLAW_AZOC	P23002 azotobacter
38	22	26.5	17	2	Q7S3B2 NEUCR	Q7S3B2 neurospora
39	22	26.5	17	2	Q7RBC2 PLAVO	Q7RBC2 plasmodium
40	22	26.5	17	2	Q7RTN3 PLATO	Q7RTN3 plasmodium
41	22	26.5	18	2	Q8NFB4 HUMAN	Q8NFB4 homo sapien
42	22	26.5	18	2	Q9R7B8 BORBU	Q9R7B8 borellia bu
43	22	26.5	18	2	Q9R7B9 BORBU	Q9R7B9 borellia bu
44	22	26.5	19	2	Q6XMK6 MACNG	Q6XMK6 macaca nigr
45	22	26.5	19	2	Q9TR77 RABIT	Q9TR77 oryctolagus
46	22	26.5	20	1	FLAW_AZOVI	P52964 azotobacter
47	22	26.5	21	2	Q6W8P8 HUMAN	Q6W8P8 homo sapien
48	22	26.5	21	2	Q4YXH0 PLABE	Q4YXH0 plasmodium
49	22	26.5	21	2	Q9TRK1 CANFA	Q9TRK1 canis famil
50	22	26.5	21	2	Q8X4E1 ECOS7	Q8X4E1 escherichia
51	22	26.5	21	2	Q57019 ARATH	Q57019 arabidopsis
52	21.5	25.9	18	2	Q09258 SYNFB	Q09258 synecococc
53	21	25.3	10	1	TKS1_AEDAE	P42634 aedes aegyp
54	21	25.3	10	1	TKS2_AEDAE	P42635 aedes aegyp
55	21	25.3	10	2	Q8YV66 EUCGR	Q8YV66 eucalyptus
56	21	25.3	11	2	Q9UAR8_AEDAE	Q9UAR8 aedes aegyp
57	21	25.3	12	1	GRAR_RANRU	P40754 rana rugosa
58	21	25.3	13	1	FLWT_LWFT	P82064 limodryast
59	21	25.3	13	1	LMT4_LOCFI	P41490 locusta mig
60	21	25.3	13	1	PSBP_PINPS	P81668 pinus pinas
61	21	25.3	13	1	TEMA_RANTE	P56917 rana tempor
62	21	25.3	15	2	Q7M2Q2 SHEEP	Q7M2Q2 ovis aries
63	21	25.3	15	2	Q9RGQ3 MYCCA	Q9RGQ3 mycoplasma
64	21	25.3	15	2	Q9TH04 GRUM	Q9TH04 grus americ
65	21	25.3	16	2	Q8LIY8 GCVAN	Q8LIY8 oscillatori
66	21	25.3	17	2	Q7RDV1 PLAVO	Q7RDV1 plasmodium
67	21	25.3	18	1	PDM_PANBO	P01209 pandanus bo
68	21	25.3	19	2	Q6XMK0 MACSL	Q6XMK0 macaca sile
69	21	25.3	19	2	Q9RF27 MYCCA	Q9RF27 mycoplasma
70	21	25.3	20	1	FERA_PARDE	P84468 paracoccu
71	21	25.3	20	1	PSAL_SYNVU	P25937 synecococc
72	21	25.3	20	2	Q9UWH0 9EURY	Q9UWH0 thermococc
73	21	25.3	20	2	Q8NED5 HUMAN	Q8NED5 homo sapien
74	21	25.3	20	2	Q9SAH6 HUMAN	Q9SAH6 homo sapien
75	21	25.3	20	2	Q8WLP7 MACNU	Q8WLP7 macaca mula
76	21	25.3	21	2	Q52SL0 PTG	Q52SL0 sus. scrofa
77	21	25.3	21	2	Q5C9K4 MYCMY	Q5C9K4 mycoplasma
78	20.5	24.7	16	2	Q04246 9PARA	Q04246 sendai viru
79	20.5	24.7	16	2	Q88249 9PARA	Q88249 sendai viru
80	20.5	24.7	16	2	Q88250 9PARA	Q88250 sendai viru
81	20.5	24.7	16	2	Q99154 9PARA	Q99154 sendai viru
82	20.5	24.7	21	2	Q84204 9PARA	Q84204 sendai viru
83	20.5	24.7	10	1	ANGT1 BOTVA	Q10561 bothriops ja
84	20	24.1	11	2	TKU2 DREUN	P40752 urechis uni
85	20	24.1	11	2	Q7M2V7 SHEEP	Q7M2V7 ovis aries
86	20	24.1	12	1	H2AX_ONCMY	P83337 oncohychnu
87	20	24.1	13	2	Q7LZ51 PHYBI	Q7LZ51 phyllomedus
88	20	24.1	14	1	TKN1_SCHGR	P82470 schistocerc
89	20	24.1	14	2	Q9UH91 HUMAN	Q9UH91 homo sapien
90	20	24.1	14	2	P82219 BONMO	P82219 bombyx mori
91	20	24.1	15	2	Q9UWG1 9EURY	Q9UWG1 pyrococcus
92	20	24.1	15	2	Q7M1W4 ARATH	Q7M1W4 arabidopsis
93	20	24.1	15	2	Q7M2B5 SOYAN	Q7M2B5 glycine max
94	20	24.1	15	2	Q3S1B8 TOBAC	Q3S1B8 nicotiana t
95	20	24.1	15	2	Q9RQ22 SALTI	Q9RQ22 salmonella
96	20	24.1	15	2	Q9PRZ9 MICCN	Q9PRZ9 micropogoni
97	20	24.1	16	1	TRYP_FELCA	P81071 felis silve
98	20	24.1	16	2	Q4W373 GLECA	Q4W373 dolichouene
99	20	24.1	16	2	Q4W373 GLECA	Q4W373 dolichouene
100	20	24.1	16	2	Q7MLU4_CHLKE	Q7MLU4 chlamydomon

ALIGNMENTS

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RESULT 1
098988 HUMAN PRELIMINARY; PRT; 16 AA.
ID Q59898
AC Q59898
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE Mutant Soc isoform 1 (Fragment).
GN Name=hSOS1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OC NCBI_TaxID=9606;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Brain;
RX MEDLINE=96239588; PubMed=8649768;
RA Rojas J.M., Coque J.J., Guerrero C., Arco P., de Mora J.F.,
de la Cruz X., Lorenzi M.V., Esteban L.M., Santos E.;
RT "A 15 amino acid stretch close to the Grb2-binding domain defines two
RT differentially expressed hSOS1 isoforms with markedly different Grb2
RT binding affinity and biological activity.";
RL Oncogene 12:2291-2300(1996).
DR EMBL; S82270; AAB47139.2; -; mRNA.
FT NON TER
FT NON TER
SQ SEQUENCE 16 AA; 1701 MW; 0D019B3983244198 CRC64;

Query Match 33.7%; Score 28; DB 2; Length 16;
Best Local Similarity 44.4%; Pred. No. 1.3e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 8 PFYGRAXSI 16
Db 5 PFHSRSASV 13

RESULT 2
04YWI1 PLABE PRELIMINARY; PRT; 21 AA.
ID Q4YWI1
AC Q4YWI1;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB105279.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OC NCBI_TaxID=5821;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RP Hall N., Karras M., Raine J.D., Carlson J.M., Kooij T.W.A.,
Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
James K., Rubinfeld K., Harris B., Harris D., Churcher C.,
Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
Jahse C.J., Bartell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -i- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; CAI01002172; CAH97795.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON TER
FT NON TER
SQ SEQUENCE 21 AA; 2553 MW; BDEE331C6A53146B CRC64;

Query Match 32.5%; Score 27; DB 2; Length 21;
Best Local Similarity 37.5%; Pred. No. 2.5e+03;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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Oy 3 LVMGVPEY 10
Db 13 IITGPFPF 20

RESULT 3
07AUS5 9GAMM PRELIMINARY; PRT; 12 AA.
ID 07AUS5
AC 07AUS5
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Putative transposase (Fragment).
GN Name=tnp1006;
OS Acinetobacter sp. BM3.
OC Plasmid pK14207.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=106395;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BM3;
RX PubMed=15073307; DOI=10.1099/mic.0.26844-0;
RA Kholodii G., Mindlin S., Gorienko Z., Petrova M., Hobman J.,
Nikiforov V.;
RT "Translocation of transposition-deficient [Tn(d) pK142-like]
RT transposons in the natural environment: mechanistic insights from the
RT study of adjacent DNA sequences.";
RL Microbiology 150:979-992(2004).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=BM3;
RC Kholodii G.Y.;
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ486856; CAD31077.1; -; Genomic_DNA.
KW Plasmid.
FT NON TER
FT NON TER
SQ SEQUENCE 12 AA; 1457 MW; E5832A70F8F40871 CRC64;

Query Match 31.3%; Score 26; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 8 PFYGR 12
Db 3 PFHGR 7

RESULT 4
DHE2 THUTH STANDARD; PRT; 16 AA.
ID DHE2 THUTH
AC P20016;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-MAY-2005 (Rel. 47, Last annotation update)
DE NAD-specific glutamate dehydrogenase (EC 1.4.1.2) (NAD-GDH)
(Fragment).
OS Thunnus thynnus (Bluefin tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8237;
OX [1]
RN PROTEIN SEQUENCE.
RP TISSUE=Liver;
RX MEDLINE=76253947; PubMed=182270; DOI=10.1016/0005-2744(76)90156-X;
RA Veronese F.M., Bevilacqua R., Boccu E., Brown D.M.;
RT "Purification, characteristics and sequence of a peptide containing an
RT essential lysine residue.";
RL Biochim. Biophys. Acta 445:1-13(1976).
CC -i- CATALYTIC ACTIVITY: L-glutamate + H(2)O + NAD(+) = 2-oxoglutarate

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CC      + NH(3) + NADH.
CC      -1- SIMILARITY: Belongs to the Glu/Leu/Phe/Val dehydrogenases family.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
CC      PIR: A12729; A12729.
CC      InterPro: IPR006095; GLFV_dehydrog.
CC      InterPro: IPR006097; GLFV_dehydrog_N.
CC      Pfam: PF02812; ELFV_dehydrog_N.1.
CC      DR PROSITE: PS00074; GLFV_DEHYDROGENASE; PARTIAL.
CC      Direct protein sequencing; NAD; Oxidoreductase.
CC      ACT_Site 12
CC      FT 12
CC      FT NON_TER 1
CC      FT TER 16
CC      SQ SEQUENCE 16 AA; 1518 MW; FF299AA7C5F1062F CRC64;

Query Match 31.3%; Score 26; DB 1; Length 16;
Best Local Similarity 35.7%; Pred. No. 2.8e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Oy 4 VMGVPFYGRAXSIE 17
    |||||
Db 3 VVDVFFGAKAGVK 16

RESULT 5
09S8A0_PINMO PRELIMINARY; PRT; 16 AA.
AC 09S8A0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Ribulose BIPHOSPHATE carboxylase small subunit (Fragment).
OS Pinus monticola (Western white pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Strobus.
OX NCBI_TaxID=3345;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=96213005; PubMed=8665095;
RA Ekramoddoullah A.K., Taylor D.W.;
RT "Seasonal variation of western white pine (Pinus monticola D. Don)
RT foliage protein.";
RL Plant Cell Physiol. 37:189-199(1996).
SQ SEQUENCE 16 AA; 1803 MW; 27D4934C881717DE CRC64;

Query Match 30.1%; Score 25; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 4.3e+03;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 8 PFYGRAXSIE 17
    |||||
Db 5 PFYGNAAKFE 14

RESULT 6
TY13_BOMVA STANDARD; PRT; 14 AA.
ID TY13_BOMVA
AC P84215;
DT 01-FEB-2005 (Rel. 46, Created)
DT 01-FEB-2005 (Rel. 46, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Tyriophyllin-13.
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archaeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=8348;
RN [1]
RP PROTEIN SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY,

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RP AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RK PubMed=15134346; DOI=10.1515/BC.2004.027;
RA Marenah L., Platt P.R., Orr D.F., McClean S., Shaw C.,
RA Abdel-Wahab Y.H.;
RT "Skin secretion of the toad Bombina variegata contains multiple
RT insulin-releasing peptides including bombesin and entirely novel
RT insulinotropic structures.";
RL Biol. Chem. 385:315-321(2004).
CC -1- FUNCTION: Possesses insulin-releasing activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the skin glands.
CC -1- MASS SPECTROMETRY: MW=1650.5; METHOD=Electrospray; RANGE=1-14;
CC NOTE=Ref.1.
CC -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
CC      DR GO: GO:0005576; C:extracellular region; IDA.
CC      DR GO: GO:0005179; F:hormone activity; TAS.
CC      DR GO: GO:0006952; P:defense response; TAS.
CC      DR GO: GO:0050796; P:regulation of insulin secretion; IDA.
CC      KM Amphibian defense peptide; Direct protein sequencing.
CC      SQ SEQUENCE 14 AA; 1651 MW; 23C4809C33A0DC77 CRC64;

Query Match 28.9%; Score 24; DB 1; Length 14;
Best Local Similarity 80.9%; Pred. No. 5.6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 6 GVPPY 10
    |||||
Db 1 GKPPY 5

RESULT 7
Q15632_HUMAN PRELIMINARY; PRT; 16 AA.
ID Q15632_HUMAN
AC Q15632;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE TCl3 oncogene (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=90222189; PubMed=2326274;
RA Zutter M., Hockett R.D., Roberts C.W., McGuire E.A., Bloomstone J.,
RA Morton C.C., Deaven L.L., Crist W.W., Carroll A.J., Kormeyer S.J.;
RT "The t(10;14)(q24;q11) of T-cell acute lymphoblastic leukemia
RT juxtaposes the delta T-cell receptor with TCl3, a conserved and
RT activated locus at 10q24.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:3161-3165(1990).
DR EMBL: M33602; AAA6450.1; -, Genomic_DNA.
DR PIR: I79565; I79565.
CC FT NON_TER 1
CC FT TER 16
CC SQ SEQUENCE 16 AA; 1812 MW; EBCF0A05EAE77D24 CRC64;

Query Match 28.9%; Score 24; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 6.4e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 DKLVWG 6
    |||||
Db 11 DKLVFG 16

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RESULT 8
Q9ADU1_9BRAS PRELIMINARY; PRT; 16 AA.
ID Q9ADU1_9BRAS PRELIMINARY; PRT; 16 AA.
AC Q9ADU1;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE Chalcone synthase (Fragment).
OS Arabis pauciflora.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabis.
OX NCBI_TaxID=81980;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2141848; PubMed=11557794;
RA Koch M.A., Weisshaar B., Kroymann J., Haubold B., Mitchell-Olds T.;
RT "Comparative genomics and regulatory evolution: conservation and
function of the Chs and Apat1a3 promoters.";
RL Mol. Biol. Evol. 18:1882-1891(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Koch M., Kroymann J., Haubold B., Weisshaar B., Mitchell-Olds T.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF248998; AAK31933.1; -; Genomic_DNA.
FT NON_TER
SQ SEQUENCE 16 AA; 1763 MW; 7D744974539F6176 CRC64;

Query Match 28.9%; Score 24; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 6.4e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 LVMGVP 8
Db 1 MVMGTP 6

RESULT 9
Q9S8H8_BRANA PRELIMINARY; PRT; 20 AA.
ID Q9S8H8_BRANA PRELIMINARY; PRT; 20 AA.
AC Q9S8H8;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Myrosinase-binding protein 50 (Fragment).
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=95218603; PubMed=7766044; DOI=10.1007/BF00202596;
RA Falk A., Taipaleensuu J., Ek B., Lenman M., Raek L.;
RL Planta 195:387-395(1995).
DR InterPro; IPR001229; Jaccalin_lectin.
DR Pfam; PF01419; Jaccalin.1.
SQ SEQUENCE 20 AA; 2101 MW; A12000918972901A CRC64;

Query Match 28.9%; Score 24; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 8e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 7 VPFYGRA 13
Db 2 IGPHGRA 8

RESULT 10
Q4XLT5_PLACH PRELIMINARY; PRT; 21 AA.
ID Q4XLT5_PLACH PRELIMINARY; PRT; 21 AA.
AC Q4XLT5;
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DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORPNames=PC10911.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berrian M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Duggett J., Trueman H.E., Mendoza J.,
RA Buiwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Jansz C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -! CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; CAU01004799; CAH82127.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 21 AA; 2641 MW; 98FCAF5AC6E06614 CRC64;

Query Match 28.9%; Score 24; DB 2; Length 21;
Best Local Similarity 33.3%; Pred. No. 8.4e+03;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 KLVMGVPFY 10
Db 3 KMTATITFY 11

RESULT 11
Q6LD23_MOUSE PRELIMINARY; PRT; 8 AA.
ID Q6LD23_MOUSE PRELIMINARY; PRT; 8 AA.
AC Q6LD23;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Interferon alpha/beta receptor (Fragment).
GN Name=Ifnar1; Synonyms=IFNAR;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95047447; PubMed=7958966; DOI=10.1016/0378-1119(94)90710-2;
RA Lutfialla G., Uze G.;
RT "Structure of the murine interferon alpha/beta receptor-encoding gene:
high-frequency rearrangements in the interferon-resistant Li210 cell
line.";
RL Gene 148:343-346(1994).
DR EMBL; U06237; AAA65003.1; -; Genomic_DNA.
DR MGI; MGI:107658; Ifnar1.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
KW Receptor.
FT NON_TER
FT NON_TER
SQ SEQUENCE 8 AA; 999 MW; CSBBS9D76059D76A CRC64;

Query Match 27.7%; Score 23; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 VPFY 10
Db 1
```

Db 4 IPFY 7

RESULT 12

Q7MU3_ORYSA PRELIMINARY; PRT; 12 AA.

AC Q7MU3_

DT 01-MAR-2004 (TReMBLrel. 26, Created)

DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)

DE Unidentified 5.4/35K protein (Fragment).

OS Oryza sativa (Rice).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; OC Euphorbiaceae; Oryzae; Oryza.

NCBI_TaxID=4530;

OX NCBI_TaxID=4530;

NP [1]

PROTEIN SEQUENCE.

RA Komatsu S., Kajiwara H., Hirano H.;

RT "A rice protein library; a data-file of rice proteins separated by RT two-dimensional electrophoresis."

RL Theor. Appl. Genet. 86:935-942(1993).

DR PIR; PQ0730; PQ0730.

DR Gramene; Q7MU3; -.

FT NON_TER

FT NON_TER

FT NON_TER

SEQUENCE 12 AA; 1316 MW; SED102D36E59C9C3 CRC64;

Query Match 27.7%; Score 23; DB 2; Length 12;

Best Local Similarity 80.0%; Pred. No. 7.1e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 FYGRA 13

Db 7 FYGRA 11

RESULT 13

Q7S2J9_NEUCR PRELIMINARY; PRT; 13 AA.

ID Q7S2J9_

AC Q7S2J9_

DT 01-MAR-2004 (TReMBLrel. 26, Created)

DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)

DE Predicted protein.

GN Name=NCU04977.1;

OS Neurospora crassa.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

NCBI_TaxID=5141;

OX NCBI_TaxID=5141;

NP [1]

NUCLEOTIDE SEQUENCE.

RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M., RA Qui D., Iankilev P., Pedersen D., Nelson M., Washburne M., RA Seltzer J., Jedd G., Kewes W., Straben C., Marcotte E., Greenberg D., RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S., RA Kamal M., Kamysseles M., Mauceli E., Bielke C., Rudd S., Frisman D., RA Kyrkoclova S., Karmann C., Metzner R.L., Perkins D.D., Kroken S., RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmari S.A., RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R., RA Varden O., Plamann M., Seltzer S., Dunlap J., Radford A., Aramayo R., RA Natvig P.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M., RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B., RA "The Genome Sequence of the Filamentous Fungus Neurospora crassa.", RL Nature 0:0-0(2003).

CC -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL; AABX01000422; EAA29651.1; -; Genomic_DNA.

SEQ SEQUENCE 13 AA; 1703 MW; 099245360492586B CRC64;

Query Match 27.7%; Score 23; DB 2; Length 13;

Best Local Similarity 42.9%; Pred. No. 7.7e+03;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 MGVPFYG 11

Db 1 MAIDYVG 7

RESULT 14

Q8AXO7_XENLA PRELIMINARY; PRT; 14 AA.

ID Q8AXO7_

AC Q8AXO7_

DT 01-MAR-2003 (TReMBLrel. 23, Created)

DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)

DE Mannose-binding lectin-associated serine protease (Fragment).

GN Name=MASP;

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; OC Xenopodinae; Xenopus; Xenopus.

NCBI_TaxID=8355;

OX NCBI_TaxID=8355;

NP [1]

NUCLEOTIDE SEQUENCE.

RA MEDLINE=22593355; PubMed=12707349;

RA Endo Y., Nonaka M., Suga H., Kakimura Y., Matsueita A., Takahashi M., RA Matsushita M., Fujita T.;

RT "Origin of mannose-binding lectin complement pathway traced back to RT and MASP-3 involved in the lectin complement pathway traced back to RT the invertebrate, amphioxus."

RL J. Immunol. 170:4701-4707(2003).

DR EMBL; AB078909; BAC41345.1; -; Genomic DNA.

DR GO; GO:0008233; F:peptidase activity; IEA.

DR GO; GO:0005529; F:sugar binding; IEA.

KM Lectin; Protease.

FT NON_TER

FT NON_TER

FT NON_TER

SEQUENCE 14 AA; 1533 MW; 99DD285F40C2B15 CRC64;

Query Match 27.7%; Score 23; DB 2; Length 14;

Best Local Similarity 50.0%; Pred. No. 8.3e+03;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 GVPFYGRA 13

Db 2 GVPFYRS 9

RESULT 15

Q9BXO0_HUMAN PRELIMINARY; PRT; 15 AA.

ID Q9BXO0_

AC Q9BXO0_

DT 01-JUN-2001 (TReMBLrel. 17, Created)

DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)

DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)

DE Tissue transglutaminase (EC 2.3.2.13) (Fragment).

GN Name=TM62;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; OC Homo.

NCBI_TaxID=9606;

OX NCBI_TaxID=9606;

NP [1]

NUCLEOTIDE SEQUENCE.

RA TISSUE=Brain;

RA Cilton B.A., Santa Cruz K.S., Davies P.J.A., Pestoff B.W.;

RT "Intron-exon swapping of transglutaminase mRNA and neuronal tau aggregation in Alzheimer's disease.";

RL J. Biol. Chem. 0:0-0(2001).

EMBL; AF311286; AAK15272.1; -; mRNA.

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DR GO: GO:0005622; C:intracellular; NAS.
DR GO: GO:0005524; F:ATP binding; TAS.
DR GO: GO:0005525; F:GTP binding; TAS.
DR GO: GO:0003924; F:GTPase activity; TAS.
DR GO: GO:0003810; F:protein-glutamine gamma-glutamyltransferase. . . ; TAS.
DR GO: GO:0006916; F:anti-apoptosis; TAS.
DR GO: GO:0019933; P:cytokine-mediated signaling; TAS.
DR GO: GO:0019221; P:cytokine and chemokine mediated signaling P. . . ; NAS.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IMP.
DR GO: GO:0018276; P:leucopetide cross-linking via N6-glycyl-L-ly. . . ; IDA.
DR GO: GO:0012501; P:programmed cell death; TAS.
KM Acyltransferase; Transferase.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1641 MW; C340982AFBFB851 CRC64;

Query Match 27.7%; Score 23; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 9e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 PFYGRA 13
DB 3 PFSGKA 8

RESULT 16
Q7TSR9 MOUSE PRELIMINARY; PRT; 18 AA.
AC Q7TSR9;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Candidate plasticity gene 15 (Fragment).
GN Name=Cpg15;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
RX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Fujino T., Lee W.-C.A., Nedivi E.;
RT "Regulation of cpg15 by Signaling Pathways that Mediate Synaptic
RT Plasticity.";
RL Mol. Cell. Neurosci. 24:538-554(2003).
DR EMBL; AY150584; AAN64528.1; -; Genomic_DNA.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2002 MW; ACC71930108873CC CRC64;

Query Match 27.7%; Score 23; DB 2; Length 18;
Best Local Similarity 41.7%; Pred. No. 1.1e+04;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5 MGVPFYGRAXSI 16
DB 1 MGLKLNKGRYISL 12

RESULT 17
Q7M2G7 VICFA PRELIMINARY; PRT; 19 AA.
AC Q7M2G7;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE NAH2 dehydrogenase (EC 1.6.99.3) 14K chain (Fragment).
OS Vicia faba (Broad bean).
OG Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eustosids 1; Fabales; Fabaceae; Papilionoideae; Viciae; Vicia.
OX NCBI_TaxID=3906;
RN [1]

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RP PROTEIN SEQUENCE.
RX MEDLINE=94151437; PubMed=8108509; DOI=10.1104/jp.102.2.435;
RA Letenne S., Boutry M.;
RT "Purification and preliminary characterization of mitochondrial
RT complex I (NADH:ubiquinone reductase) from broad bean (Vicia faba
RT L.) .";
RL Plant Physiol. 102:435-443(1993).
DR PIR; P00790; P00790.
DR GO: GO:0003954; F:NADH dehydrogenase activity; IEA.
FT NON_TER 1
SQ SEQUENCE 19 AA; 1913 MW; 4113C369A5F11704 CRC64;

Query Match 27.7%; Score 23; DB 2; Length 19;
Best Local Similarity 66.7%; Pred. No. 1.1e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LVWGVP 8
DB 13 LVSGIP 18

RESULT 18
Q6LDN4 RHOCA PRELIMINARY; PRT; 19 AA.
ID Q6LDN4 RHOCA PRELIMINARY;
AC Q6LDN4;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE R. capsulata nifHDK operon. (Fragment).
OS Bacteroides capsulatus (Rhodopseudomonas capsulata).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1061;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88313675; PubMed=3410321; DOI=10.1016/0378-1119(88)90463-5;
RA Pollock D., Bauer C.E., Scolnik P.A.;
RT "Transcription of the Rhodobacter capsulatus nifHDK operon is
RT modulated by the nitrogen source: Construction of plasmid expression
RT vectors based on the nifHDK promoter.";
RL Gene 65:269-275(1988).
DR EMBL; M29400; AAA26142.1; -; Genomic_DNA.
FT NON_TER 19
SQ SEQUENCE 19 AA; 2012 MW; 61392A571F316AB7 CRC64;

Query Match 27.7%; Score 23; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 VPFYGR 12
DB 7 IAFYK 12

RESULT 19
Q8KXKS MOUSE PRELIMINARY; PRT; 19 AA.
ID Q8KXKS MOUSE PRELIMINARY;
AC Q8KXKS;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Arginase I (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
RX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/SvJ;
RX PubMed=15922518; DOI=10.1016/j.gene.2005.04.004;
RX Gray M.J., Poljakovic M., Kepka-Lenhart D., Morris S.M. Jr.;

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RT "Induction of arginase I transcription by IL-4 requires a composite DNA response element for STAT6 and C/EBPbeta."

RL Gene 353:98-106(2005).
DR EMBL; AY074884; AAL79623.1; -; Genomic_DNA.

FT NON_TER 19
SQ SEQUENCE 19 AA; 2005 MW; B4D0E34BB3508F90 CRC64;

Query Match 27.7%; Score 23; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 VMGVVF 9
Db 10 ITGAPF 15

RESULT 20
OM4VA_VIBAL STANDARD; PRT; 20 AA.

AC P83149;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Outer membrane protein 40Va (Omp40Va) (Fragment).
OS Vibrio alginolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=663;

RP PROTEIN SEQUENCE.
RC STRAIN=NCIMB 1903T;
RA Ochi M., Hirabayashi J., Suzuki S.;
RT "Characterization of major outer membrane proteins of Vibrio alginolyticus and the stability against proteases.";
RL Microbes Environ. 0:0-0(2002).
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Outer membrane.

CC -1- SIMILARITY: Belongs to the Gram-negative porin family.

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CC Direct protein sequencing; Ion transport; Membrane; Outer membrane;
KW Porin; Transmembrane; Transport.

FT NON_TER 20
SQ SEQUENCE 20 AA; 2229 MW; 4FA95CB24FEC3CDE CRC64;

Query Match 27.7%; Score 23; DB 1; Length 20;
Best Local Similarity 66.7%; Pred. No. 1.2e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 VPFYGR 12
Db 11 VDFYGO 16

RESULT 21
TL19_SPIOI STANDARD; PRT; 20 AA.

AC P82739;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Thylakoid lumenal 18.4 kDa protein (P18.4) (Fragment).
OS Spinacia oleracea (Spinach).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Caryophyllales; Amaranthaceae; Spinacia.

OX NCBI_TaxID=3562;
[1]

RP PROTEIN SEQUENCE.

RA Kieselbach T., Petersson U., Bystedt M., Schroeder W.P.;

RL Submitted (JUL-2000) to Swiss-Prot.

CC -1- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
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CC Chloroplast; Direct protein sequencing; Thylakoid.

FT NON_TER 20
SQ SEQUENCE 20 AA; 2131 MW; 460408C32420991B CRC64;

Query Match 27.7%; Score 23; DB 1; Length 20;
Best Local Similarity 57.1%; Pred. No. 1.2e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FYGRAXS 15
Db 11 YYGTAAAS 17

RESULT 22
O9TWN3_THESE PRELIMINARY; PRT; 20 AA.

AC O9TWN3;
DT 01-MAY-2000 (TRENBLUREL. 13, Created)
DT 01-MAY-2000 (TRENBLUREL. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLUREL. 14, Last annotation update)
DE 45 kDa immunodominant polypeptide (Fragment).
OS Theileria sergenti.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
OC Theileria.

OX NCBI_TaxID=5877;

RP PROTEIN SEQUENCE.

RA Baek B.K., Kim B.S., Rhim B.M., Lee H.I., Park Y.H., Kakoma I.;
RT "Immunogenicity and protective efficacy of solubilized merozoite-enriched Theileria sergenti immunogens. III. Characterization of immunodominant peptides.";
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.

SQ SEQUENCE 20 AA; 2270 MW; 97F9C630713B8284 CRC64;

Query Match 27.7%; Score 23; DB 2; Length 20;
Best Local Similarity 55.6%; Pred. No. 1.2e+04;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DKLVGVVF 9
Db 12 DKVVARDPF 20

RESULT 23
P81896_SOLTU PRELIMINARY; PRT; 20 AA.

AC P81896;
DT 01-JUN-2000 (TRENBLUREL. 14, Created)
DT 01-JUN-2000 (TRENBLUREL. 14, Last sequence update)
DT 01-JUN-2000 (TRENBLUREL. 14, Last annotation update)
DE Dihydroisoprenyl succinyltransferase component of 2-oxoglutarate dehydrogenase complex (EC 2.3.1.61) (E2) (OGDC-E2) (Fragment).
OS Solanum tuberosum (Potato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.

OX NCBI_TaxID=4113;

RP PROTEIN SEQUENCE.

RC STRAIN=cv. ROMANO; TISSUE=TUBER;
RX MEDLINE=99441232; PubMed=10510296; DOI=10.1042/0264-6021:3430327;
RA Miller A.H., Hill S.A., Leaver C.J.;

RT "Plant mitochondrial 2-oxoglutarate dehydrogenase complex:
RT purification and characterization in potato.";
RL Biochem. J. 343:327-334(1999).
CC -1- FUNCTION: THE 2-OXOGLUTARATE DEHYDROGENASE COMPLEX CATALYZES THE
CC OVERALL CONVERSION OF 2-OXOGLUTARATE TO SUCCINYL-COA & CO(2). IT
CC CONTAINS MULTIPLE COPIES OF 3 ENZYMAIC COMPONENTS: 2-OXOGLUTARATE
CC DEHYDROGENASE (E1), DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE (E2) AND
CC LIPOAMIDE DEHYDROGENASE (E3).
CC -1- CATALYTIC ACTIVITY: SUCCINYL-COA + DIHYDROLIPOAMIDE = COA + S-
CC SUCCINYLDIHYDROLIPOAMIDE.
CC -1- COFACTOR: THE E2 COMPONENT CONTAINS ONE COVALENTLY-BOUND LIPOYL
CC COFACTOR.
CC -1- SUBUNIT: FORMS A 24-POLYPEPTIDE STRUCTURAL CORE WITH OCTAHEDRAL
CC SYMMETRY (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.
CC -1- CAUTION: X IN THE SEQUENCE MIGHT BE CYS RESIDUE.
CC -1- SIMILARITY: TO OTHER SPECIES E2 COMPONENT.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0008415; F:acylttransferase activity; IEA.
DR GO; GO:0004149; F:dihydrolipoyllysine-residue succinyltransferase. . ; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006096; F:glycolysis; IEA.
KM Acyltransferase; Glycolysis; Lipoyl; Mitochondrion; Transferase.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2050 MW; 9256BE292E26A344 CRC64;

Query Match 27.7%; Score 23; DB 2; Length 20;
Best Local Similarity 44.4%; Pred. No. 1.2e+04;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 7 VPFYGRAXS 15
||| :|| :||
DB 12 VPMGESIS 20

RESULT 24
TL19_ARATH STANDARD; PRT; 21 AA.
AC P82658;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 05-JUL-2004 (Rel. 44; Last annotation update)
DE Thylakoid lumenal 19 kDa protein (P19) (Fragment).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=cv. Columbia;
RA Kieselbach T., Bystedt M., Schroeder W.P.;
RL Submitted (JUL-2000) to Swiss-Prot.
CC -1- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC Chloroplast; Direct proteoin sequencing; Thylakoid.
KM NON_TER 21
SQ SEQUENCE 21 AA; 2199 MW; EAA1345E72C00054 CRC64;

Query Match 27.7%; Score 23; DB 1; Length 21;
Best Local Similarity 57.1%; Pred. No. 1.3e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 9 FYGRAXS 15
:||| :||| :|||
DB 9 YYGTAAS 15

RESULT 25
Q7RZ21_NEUCR PRELIMINARY; PRT; 21 AA.
ID Q7RZ21_NEUCR
AC Q7RZ21;
DT 01-MAR-2004 (TREMBlrel. 26; Created)
DT 01-MAR-2004 (TREMBlrel. 26; Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26; Last annotation update)
DE Predicted protein.
GN Name=NCU10082.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrenikoff C.P., Kinsey J.A., Braun E.L., Zeller A., Schulte U.,
RA Koue G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysassilis M., Mauceli E., Bielke C., Rudd S., Frisman D.,
RA Krystofova S., Rasmussen C., Metznerberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA Desouza C.C., Glase L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbel D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa."
RL Nature 0:0-0(2003).
CC -1- CAUTION: The sequence shown here is derived from an
CC preliminary data.
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
DR EMBL; AABX0100651; EAA28603.1; -; Genomic DNA.
SQ SEQUENCE 21 AA; 2379 MW; E1CE7FEAD658B6D5 CRC64;

Query Match 27.7%; Score 23; DB 2; Length 21;
Best Local Similarity 50.0%; Pred. No. 1.3e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 5 MGVPFYGR 12
||| :||| :|||
DB 1 MGTVPFGR 8

Search completed: January 26, 2006, 08:04:00
Job time : 53.5603 secs

98	31	28.4	21	3	AAV90155	UPAR	targ
99	30.5	28.0	14	2	AAW88603	Secreterd	
100	30	27.5	8	8	ADT92805	Consensus	

ALIGNMENTS

RESULT 1

AAV52520 ID AAV52520 standard; peptide; 19 AA.

XX AAV52520;

XX 22-FEB-2000 (first entry)

XX House dust mite allergen protein (map) A/B fragment map(10).

XX Mite allergen protein; map; high molecular weight; HMW-map; allergy;

XX house dust mite; IGE; immunoglobulin E; allergen; mapA; mapB;

XX hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;

XX canine; veterinary; antibody; vaccine; immunisation.

XX Dermatophagoides farinae.

XX MO9954349-A2.

XX 28-OCT-1999.

XX 16-APR-1999; 99WO-US008524.

XX 17-APR-1998; 98US-00062013.

XX 13-MAY-1998; 98US-0085295P.

XX 02-SEP-1998; 98US-0098909P.

XX (HESK-) HESKA CORP.

XX Mccall CA, Hunter SW, Weber ER;

XX WPI; 2000-052700/04.

XX Novel high molecular weight Dermatophagoides nucleic acid polypeptides

XX used to modify an animals' hypersensitivity to mite allergens.

XX Claim 3; Page 70; 154pp; English.

XX Sequences AAV52510-Y52522 represent proteolytic fragments of

XX Dermatophagoides farinae high molecular weight mite allergen protein (HMW

XX -map) composition. The HMW-map composition was isolated from a D. farinae

XX homogenate by gel filtration, with each fraction being analysed for the

XX presence of proteins that bound to IGE present in mite-allergic dog

XX antisera. The HMW-map composition comprises mapA (a 109 kD protein) and

XX mapB (98 kD). Mite allergenic proteins and peptides, and nucleic acids

XX encoding them, may be used in therapeutic compositions to modify an

XX animal's hypersensitivity reaction to mite allergens. Animals that may be

XX treated include mammals and birds, especially felines, canines, equines,

XX humans, other pets, and work or domestic animals. The proteins or

XX fragments may also be used to diagnose allergies via a skin test. The

XX proteins and peptides can also be used to raise antibodies, which have a

XX variety of potential uses. For example, they can be used as vaccines to

XX passively immunise animals against dust mite hypersensitivity, as

XX positive controls in test kits and as tools to recover desired dust mite

XX allergens from a mixture of proteins

XX Sequence 19 AA;

XX Query Match 100.0%; Score 109; DB 3; Length 19;

XX Best Local Similarity 100.0%; Pred. No. 4e-11;

XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 DIPHPTNIHKYLVCSVNG 19

XX 1 DIPHPTNIHKYLVCSVNG 19

XX Db

RESULT 2
AAU96324 ID AAU96324 standard; peptide; 19 AA.

XX AAU96324;

XX 15-JUL-2002 (first entry)

XX Der HMW-map polypeptide #11.

XX Der HMW-map; American house dust mite; antiallergic; mite; IGE;

XX mite allergenic protein; immunoglobulin E; hypersensitivity;

XX immunocomplex formation.

XX Dermatophagoides farinae.

XX MO200222807-A2.

XX 21-MAR-2002.

XX 14-SEP-2001; 2001WO-US028730.

XX 14-SEP-2000; 2000US-00662293.

XX (HESK-) HESKA CORP.

XX Mccall CA, Hunter SW, Weber ER;

XX WPI; 2002-351888/38.

XX New mite allergenic protein isolated from Dermatophagoides, designated

XX Der HMW-map protein, useful as a vaccine for treating mite allergy.

XX Claim 12; Page 71; 161pp; English.

XX The invention relates to an isolated mite allergenic protein of

XX Dermatophagoides, designated Der HMW-map protein, and its related nucleic

XX acid. The Der HMW-map protein is useful for eliciting an immune response

XX against Der HMW-map protein. The protein or a reagent comprising a non-

XX proteinaceous epitope is useful for identifying an animal (e.g., dog,

XX cat) susceptible to or having an allergic response to a mite. A

XX therapeutic composition is useful for desensitising a host animal to an

XX allergic response to a mite. The DNA and protein can be used in the

XX detection of anti-Der HMW-map antibodies in animal fluids, and inhibition

XX of immunoglobulin (IgE or Der HMW-map protein activity associated with a

XX disease. Antibodies that bind to Der HMW-map are useful for inhibiting

XX binding of proteins to IGE, to prevent immunocomplex formation, thus

XX reducing hypersensitivity responses to mite allergens, and as vaccines

XX against mite allergen hypersensitivity. Sequences AAU96314-AAU96342

XX represent Der HMW-map polypeptides of the invention

XX Sequence 19 AA;

XX Query Match 100.0%; Score 109; DB 5; Length 19;

XX Best Local Similarity 100.0%; Pred. No. 4e-11;

XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 DIPHPTNIHKYLVCSVNG 19

XX 1 DIPHPTNIHKYLVCSVNG 19

XX Db

XX RESULT 3

XX AAV52512 ID AAV52512 standard; peptide; 20 AA.

XX AC AAV52512;

XX 22-FEB-2000 (first entry)

XX House dust mite allergen protein (map) A/B fragment map(2).

XX


```

XX      Mite allergen protein; map: high molecular weight; HMW-map; allergy;
KM      house dust mite; IGE; immunoglobulin E; allergen; mapA; mapB;
KM      hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;
KM      canine; veterinary; antibody; vaccine; immunisation.
XX      Dermatophagoides farinae.
XX      WO9954349-A2.
XX      PD
XX      28-OCT-1999.
XX      PF
XX      16-APR-1999; 99WO-US008524.
XX      PR
XX      17-APR-1998; 98US-00062013.
XX      PR
XX      13-MAY-1998; 98US-0085295P.
XX      PR
XX      02-SEP-1998; 98US-0098909P.
XX      PA
XX      (HESK-) HESKA CORP.
XX      PI
XX      Mccall CA, Hunter SW, Weber ER;
XX      WPI; 2000-052700/04.
XX      DR
XX      Novel high molecular weight Dermatophagoides nucleic acid polypeptides
PT      used to modify an animals' hypersensitivity to mite allergens.
XX      PS
XX      Claim 3; Page 69; 154pp; English.
XX      CC
XX      Sequences AA52510-Y52522 represent proteolytic fragments of
CC      Dermatophagoides farinae high molecular weight mite allergen protein (HMW
CC      -map) composition. The HMW-map composition was isolated from a D. farinae
CC      homogenate by gel filtration, with each fraction being analysed for the
CC      presence of proteins that bound to IGE present in mite-allergic dog
CC      antisera. The HMW-map composition comprises mapA (a 109 kD protein) and
CC      mapB (98 kD). Mite allergenic proteins and peptides, and nucleic acids
CC      encoding them, may be used in therapeutic compositions to modify an
CC      animal's hypersensitivity reaction to mite allergens. Animals that may be
CC      treated include mammals and birds, especially felines, canines, equines,
CC      humans, other pets, and work or domestic animals. The proteins or
CC      fragments may also be used to diagnose allergies via a skin test. The
CC      proteins and peptides can also be used to raise antibodies, which have a
CC      variety of potential uses. For example, they can be used as vaccines to
CC      passively immunise animals against dust mite hypersensitivity, as
CC      positive controls in test kits and as tools to recover desired dust mite
CC      allergens from a mixture of proteins
XX      CC
XX      SQ
XX      Sequence 20 AA;
XX      Query Match 100.0%; Score 109; DB 3; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 4.2e-11;
XX      Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX      QY
XX      1 DIPHPNHHKYLVCESYNG 19
XX      1 DIPHPNHHKYLVCESYNG 19
XX      DB
XX      1 DIPHPNHHKYLVCESYNG 19
XX      RESULT 4
XX      ID AAU96316
XX      AAU96316 standard; peptide: 20 AA.
XX      AC
XX      AAU96316;
XX      DT
XX      15-JUL-2002 (first entry)
XX      DE
XX      Der HMW-map polypeptide #3.
XX      KM
XX      Der HMW-map; American house dust mite; antiallergic; mite; IGE;
XX      KM
XX      mite allergenic protein; immunoglobulin E; hypersensitivity;
XX      KM
XX      immunocomplex formation.
XX      OS
XX      Dermatophagoides farinae.

```

```

XX      WO200222807-A2.
XX      PN
XX      21-MAR-2002.
XX      PD
XX      PF
XX      14-SEP-2001; 2001WO-US028730.
XX      PR
XX      14-SEP-2000; 2000US-00662293.
XX      PA
XX      (HESK-) HESKA CORP.
XX      PI
XX      Mccall CA, Hunter SW, Weber ER;
XX      WPI; 2002-351888/38.
XX      DR
XX      PT
XX      New mite allergenic protein isolated from Dermatophagoides, designated
PT      Der HMW-map protein, useful as a vaccine for treating mite allergy.
XX      PS
XX      Claim 12; Page 70; 161pp; English.
XX      CC
XX      The invention relates to an isolated mite allergenic protein of
CC      Dermatophagoides, designated Der HMW-map protein, and its related nucleic
CC      acid. The Der HMW-map protein is useful for eliciting an immune response
CC      against Der HMW-map protein. The protein or a reagent comprising a non-
CC      proteinaceous epitope is useful for identifying an animal (e.g., dog,
CC      cat) susceptible to or having an allergic response to a mite. A
CC      therapeutic composition is useful for desensitising a host animal to an
CC      allergic response to a mite. The DNA and protein can be used in the
CC      detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
CC      of immunoglobulin (Ig) E or Der HMW-map protein activity associated with a
CC      disease. Antibodies that bind to Der HMW-map are useful for inhibiting
CC      binding of proteins to IGE, to prevent immunocomplex formation, thus
CC      reducing hypersensitivity responses to mite allergens, and as vaccines
CC      against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
XX      CC
XX      SQ
XX      Sequence 20 AA;
XX      Query Match 100.0%; Score 109; DB 5; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 4.2e-11;
XX      Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX      QY
XX      1 DIPHPNHHKYLVCESYNG 19
XX      1 DIPHPNHHKYLVCESYNG 19
XX      DB
XX      1 DIPHPNHHKYLVCESYNG 19
XX      RESULT 5
XX      ID AAM18898
XX      AAM18898 standard; protein: 20 AA.
XX      AC
XX      AAM18898;
XX      DT
XX      12-OCT-2001 (first entry)
XX      DE
XX      Peptide #5332 encoded by probe for measuring cervical gene expression.
XX      KM
XX      Probe; human; microarray; gene expression; cervical epithelial cell;
XX      KM
XX      cervical cancer.
XX      OS
XX      Homo sapiens.
XX      PN
XX      WO200157278-A2.
XX      PD
XX      09-AUG-2001.
XX      PF
XX      30-JUN-2001; 2001WO-US000670.
XX      PR
XX      04-FEB-2000; 2000US-0180312P.
XX      PR
XX      26-MAY-2000; 2000US-0207456P.
XX      PR
XX      30-JUN-2000; 2000US-00608408.
XX      PR
XX      03-AUG-2000; 2000US-00632366.
XX      PR
XX      21-SEP-2000; 2000US-0234687P.

```

PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488901/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human cervical epithelial cells.
XX
PS Claim 27; SEQ ID NO 23724; 487bp; English.
XX
CC The present invention relates to human single exon nucleic acid probes
CC (SENPs: see AAI10068-AI128459). The present sequence is a peptide encoded
CC by one such probe. The SENPs are derived from human Hela cells. The SENPs
CC can be used to produce a single exon microarray, which can be used for
CC measuring human gene expression in a sample derived from human cervical
CC epithelial cells. By measuring gene expression, the probes are therefore
CC useful in grading and/or staging of diseases of the cervix, notably
CC cervical cancer. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 AA;
XX
Query Match 34.4%; Score 37.5; DB 4; Length 20;
Best Local Similarity 42.9%; Pred. No. 58;
Matches 6; Conservative 5; Mismatches 2; Indels 1; Gaps 1;
Oy 2 IPHPTNIHKYLVCE 15
: ||| : | : ||| :
Db 8 LPHP-HSHTHLQC 20
XX
RESULT 6
ID ABB38020 standard; peptide; 20 AA.
XX
AC ABB38020;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #5526 encoded by human foetal liver single exon probe.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PE 30-JAN-2001; 2001WO-US000669.
XX
PF 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
XX

PS Claim 27; SEQ ID NO 30655; 639pp + Sequence listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 AA;
XX
Query Match 34.4%; Score 37.5; DB 4; Length 20;
Best Local Similarity 42.9%; Pred. No. 58;
Matches 6; Conservative 5; Mismatches 2; Indels 1; Gaps 1;
Oy 2 IPHPTNIHKYLVCE 15
: ||| : | : ||| :
Db 8 LPHP-HSHTHLQC 20
XX
RESULT 7
ID AAM31434 standard; protein; 20 AA.
XX
AC AAM31434;
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #5471 encoded by probe for measuring placental gene expression.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
XX genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PE 30-JAN-2001; 2001WO-US000663.
XX
PF 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
PS Claim 27; SEQ ID NO 31703; 654pp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENPs:
CC see AAI33315-AI57546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders
XX
SQ Sequence 20 AA;
XX
Query Match 34.4%; Score 37.5; DB 4; Length 20;
Best Local Similarity 42.9%; Pred. No. 58;
Matches 6; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

Matches 6; Conservative 5; Mismatches 2; Indels 1; Gaps 1;
QY 2 IPHPTNHHKYLVE 15
:||||:|:|:|:
DB 8 LPHP-HSHTHLLCQ 20

RESULT 8
ABB23254
ID ABB23254 standard; protein; 20 AA.

AC ABB23254;

DT 23-JAN-2002 (first entry)

DE Protein #5253 encoded by probe for measuring heart cell gene expression.

KW Human; gene expression; heart; microarray; vascular system;

KW cardiovascular disease; hypertension; cardiac arrhythmia;

KW congenital heart disease.

OS Homo sapiens.

PN WO200157274-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000666.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-488899/53.

XX Single exon nucleic acid probes for analyzing gene expression in human

PT heart.

XX Claim 15; SEQ ID NO 25024; 530bp; English.

XX The present invention relates to single exon nucleic acid probes for

CC measuring human gene expression in a sample derived from human heart (see

CC ABA21535-ABA11305). The present sequence is a protein encoded by one such

CC probe. The probes may be used for predicting, measuring and displaying

CC gene expression in samples derived from the human heart via microarrays.

CC By measuring gene expression, the probes are useful for predicting,

CC diagnosing, grading, staging, monitoring and prognosing diseases of the

CC human heart and vascular system e.g. cardiovascular disease.

CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The

CC sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 20 AA;

XX Query Match 34.4%; Score 37.5; DB 4; Length 20;

XX Best Local Similarity 42.9%; Pred. No. 58;

XX Matches 6; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 2 IPHPTNHHKYLVE 15

:||||:|:|:|:

DB 8 LPHP-HSHTHLLCQ 20

RESULT 9

AAM71153
ID AAM71153 standard; protein; 20 AA.

AC AAM71153;

DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 31459.

KW Human; bone marrow expressed exon; gene expression analysis; probe;

KW microarray; cancer; leukaemia; lymphoma; myeloma.

OS Homo sapiens.

PN WO200157276-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000668.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-488900/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human bone marrow.

XX Example 4; SEQ ID NO 31459; 658bp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid

CC probes which are derived from genomic sequences expressed in the human

CC bone marrow. They can be used to measure gene expression in bone marrow

CC samples, which may enable the improved diagnosis and treatment of cancers

CC such as lymphoma, leukaemia and myeloma. The present sequence is a

CC protein encoded by one of the probes of the invention

XX Sequence 20 AA;

XX Query Match 34.4%; Score 37.5; DB 4; Length 20;

XX Best Local Similarity 42.9%; Pred. No. 58;

XX Matches 6; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 2 IPHPTNHHKYLVE 15

:||||:|:|:|:

DB 8 LPHP-HSHTHLLCQ 20

RESULT 10

AAM58647

ID AAM58647 standard; protein; 20 AA.

AC AAM58647;

DT 05-NOV-2001 (first entry)

DE Human brain expressed single exon probe encoded protein SEQ ID NO: 30752.

KW Human; brain expressed exon; gene expression analysis; probe; microarray;

KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.

OS Homo sapiens.

PN WO200157275-A2.

XX 09-AUG-2001.
PD
FF 30-JAN-2001, 2001WO-US0000667.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
XX
PS Example 4; SEQ ID NO 30752; 650bp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention
XX
SQ Sequence 20 AA;

Query Match	34.4%;	Score 37.5;	DB 4;	Length 20;
Best Local Similarity	42.9%;	Pred. No. 58;		
Matches	6;	Conservative	5;	Mismatches 2;
				Indels 1;
				Gaps 1
QY	2	IPHPNTINKYLACE	15	
	:		:	
	:		:	
Db	8	LPHF-HSHTHLLCQ	20	
RESULT	11			
ID	ABG52865			
XX	ABG52865	standard; peptide; 20 AA.		
AC	ABG52865;			
XX				
DT	25-FEB-2003	(first entry)		
XX				
DE	Human liver peptide, SEQ ID NO 31513.			
XX				
KW	Human, liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;			
KM	hypercholesterolaemia; coronary heart disease.			
XX				
OS	Homo sapiens.			
XX				
PN	WO200157273-A2.			
XX				
PD				
XX				
09-AUG-2001.				
XX				
PF	30-JAN-2001; 2001WO-US000664.			
XX				
XX				
PR	04-FEB-2000; 2000US-0180312P.			
PR	26-MAY-2000; 2000US-0207456P.			
PR	30-JUN-2000; 2000US-00608408.			
PR	03-AUG-2000; 2000US-00632366.			
PR	21-SEP-2000; 2000US-0234687P.			
PR	27-SEP-2000; 2000US-0236359P.			
PR	04-OCT-2000; 2000GB-00024263.			
XX				
PA	(MOLE-) MOLECULAR DYNAMICS INC.			

XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-488898/53.
 XX
 DR
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human adult liver.
 XX
 PS Claim 27; SEQ ID NO 31513; 658bp; English.
 XX
 CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
 CC measuring human gene expression in a sample derived from human adult
 CC liver, comprising one of 1109 defined nucleotide sequences given in the
 CC specification (or complements/ fragments). The probe hybridizes at high
 CC stringency to a nucleic acid molecule expressed in the human adult liver.
 CC (I) may be used for predicting, measuring and displaying gene expression
 CC in samples derived from human adult liver. The genes identified may be
 CC involved in genetic, liver diseases such as cirrhosis,
 CC hyperlipoproteinemia, hyperlipidemia and hypercholesterolaemia which is
 CC associated with coronary heart disease. ABG47348-ABG5930 represent human
 CC liver single exon encoded peptides of the invention. Note: The sequence
 CC information for this patent does not appear in the printed specification
 CC but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 AA;
 XX

Query Match		34.4%	Score 37.5;	DB 4;	Length 20;
Best Local Similarity		42.9%	Pred. No. 58;		
Matches	6;	Conservative	5;	Mismatches	2; Indels 1; Gaps 1.
OY	2 IPHPTNIHKYLVC	E 15	:	:	:
	: : : :				
Dd	8 LPH- HSHTHLLCQ	20			
RESULT 12					
ID	ABG40950				
AC	ABG40950 standard; peptide: 20 AA.				
XX	ABG40950;				
DT	19-AUG-2002 (first entry)				
DE	Human peptide encoded by genome-derived single exon probe SEQ ID 30615.				
XX					
KW	Human; single exon probe; asthma; lung cancer; COPD; ILD;				
KM	chronic obstructive pulmonary disease; interstitial lung disease;				
KW	familial idiopathic pulmonary fibrosis; neurofibromatosis;				
KM	tuberosus sclerosis; Gaucher's disease; Niemann-Pick disease;				
KW	Hernandez-Pudak syndrome; sarcoidosis; pulmonary haemosiderosis;				
KM	pulmonary histiocytosis; lymphangioleiomyomatosis; Karsenger syndrome;				
KW	pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;				
KM	primary ciliary dyskinesia; pulmonary hypertension;				
XX	hyaline membrane disease.				
OS	Homo sapiens.				
PN	WO200186003-A2.				
PD	15-NOV-2001.				
PF	30-JAN-2001; 2001WO-US000665.				
PR	04-FEB-2000; 2000US-0180312P.				
PR	26-MAY-2000; 2000US-0207456P.				
PR	30-JUN-2000; 2000US-00608408.				
PR	03-AUG-2000; 2000US-00632366.				
PR	21-SEP-2000; 2000US-0234687P.				
PR	27-SEP-2000; 2000US-0236359P.				
PA	04-OCT-2000; 2000GB-00024263.				
(MOLE-)	MOLECULAR DYNAMICS INC.				

PI	Penn SG, Hanzel DK, Chen W, Rank DR;
XX	WPI, 2002-114183/15.
DR	
XX	
PT	Spatially-addressable set of single exon nucleic acid probes, used to
XX	measure gene expression in human lung samples.
PS	
XX	Claim 27; SEQ ID NO 30615; 634pp; English.
CC	
CC	The invention relates to a spatially-addressable set of single exon
CC	nucleic acid probes for measuring gene expression in a sample derived
CC	from human lung comprising single exon nucleic acid probes having one of
CC	12614 nucleic acid sequences mentioned in the specification, or their
CC	complements or the 12387 open reading frames derived from the 12614
CC	probes. Also included are a microarray comprising the novel set of probes
CC	; the novel set of probes which hybridise at high stringency to a nucleic
CC	acid expressed in the human lung; measuring gene expression in a sample
CC	derived from human lung, comprising (a) contacting the array with a
CC	collection of detectably labeled nucleic acids derived from human lung
CC	mRNA, and (b) measuring the label detectably bound to each probe of the
CC	array; identifying exons in a eukaryotic genome, comprising (a)
CC	algorithmically predicting at least one exon from genomic sequences of
CC	the eukaryote; and (b) detecting specific hybridisation of detectably
CC	labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC	having a fragment identical to the predicted exon, the probe is included
CC	in the above mentioned microarray; assigning exons to a single gene,
CC	comprising (a) identifying exons from genomic sequence by the method
CC	above and (b) measuring the expression of each of the exons in several
CC	tissues and/or cell types using hybridisation to a single exon
CC	microarray having a probe with the exon, where a common pattern of
CC	expression of the exons in the tissues and/or cell types indicates that
CC	the exons should be assigned to a single gene; a peptide comprising one
CC	of 12011 sequences, mentioned in the specification, or encoded by the
CC	probes/open reading frames (ORF). The probes are used for gene expression
CC	analysis, and for identifying exons in a gene, particularly using human
CC	lung derived mRNA and for the study of lung diseases such as asthma, lung
CC	cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC	disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC	tuberosus sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC	Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC	histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
CC	Kartagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC	dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC	present sequence is a peptide/protein encoded by a single exon probe of
CC	the invention. Note: The sequence data for this patent did not form part
CC	of the printed specification, but was obtained in electronic format
CC	directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX	
SO	Sequence 20 AA;
Query Match	34.4%; Score 37.5; DB 5; Length 20;
Best Local Similarity	42.9%; Pred. No. 59;
Matches	6; Conservative 5; Mismatches 2; Indels 1; Gaps 1
Qy	2 IPHPTNIHKYLVCE 15
Db	8 LPHR-HSHTHLCCQ 20
RESULT 13	
ID	ADC27861
AC	ADC27861 standard; peptide; 7 AA.
XX	ADC27861;
DT	18-DEC-2003 (first entry)
XX	
DE	Synthetic stain targeting peptide Seq ID54.
XX	
KW	target stain; phenol oxidising enzyme; redox reaction;
KW	detergent industry; paper and pulp industry; textile industry;
KW	food industry; laccase enzyme; textile; carotenoid stain; fabric;

KW	skin cosmetic; food; fruit ripening agent; oxidase protein;
KV	stain targeting peptide.
XX	
OS	Synthetic.
PN	WO2003023067-A1.
XX	
PD	20-MAR-2003.
XX	
PF	03-SEP-2002; 2002WO-US027993.
XX	
PR	12-SEP-2001; 2001US-00954385.
XX	
PA	(GENENCOR INT INC.
XX	
PI	Aeble W, Baldwin TL, Janesen GG, Murray CJ, Van Gastel FJC,
PI	Wang H, Winetzkys DS,
XX	
DR	WPI; 2003-532545/50.
XX	
PT	Novel binding peptide useful for enhancing the binding of a laccase
PT	enzyme to a target stain, to target a stain on a textile, and in skin
PT	cosmetics.
XX	
PS	Claim 1; SEQ ID NO 54; 50pp; English.
XX	
CC	This invention relates to novel peptides which bind to a target stain.
CC	The invention comprises phenol oxidizing enzyme-binding peptide complexes
CC	wherein the binding peptide is attached to the C-terminus of the phenol
CC	oxidizing enzyme or its inserted or substituted into the phenol oxidizing
CC	enzyme. Phenol oxidizing enzymes function by catalysis of redox reactions
CC	and are used for a wide range of applications (detergent industry, paper
CC	and pulp industry, textile industry and food industry). The invention is
CC	useful for enhancing the binding of a laccase enzyme to a target stain on
CC	a textile, where the peptide binds to the stain and not the surface. This
CC	may be useful for bleaching a carotenoid stain on a fabric or surface.
CC	The invention is useful in skin cosmetics and in food as fruit ripening
CC	agents. The present sequence is that of a stain targeting peptide of the
CC	invention.
XX	
SO	Sequence 7 AA:
QY	Query Match 32.1%; Score 35; DB 7; Length 7;
	Best Local Similarity 83.3%; Pred. No. 2e+06;
	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0
DB	3 PHPTNI 8
	1 PHTNWL 6
XX	
RESULT 14	
ID	ADY56230 standard; peptide; 7 AA.
AC	ADY56230;
DT	02-JUN-2005 (first entry)
DE	Carotenoid-binding phage display cyclic 7-mer peptide. SEQ ID NO:54.
KW	Enzyme engineering; surfactant; textile; phage display; cyclic.
OS	Synthetic.
FN	US2005058996-A1.
PD	17-MAR-2005;
PF	03-SEP-2002; 2002US-00235043.
PR	03-SEP-2002; 2002US-00235043.
XX	

PA (WOLF/) WOLFGANG A.
PA (BALD/) BALDWIN T M.
PA (VGA/) VAN CASTEL F J C.
PA (JANS/) JANSSEN G G.
PA (MURR/) MURRAY C J.
PA (WANG/) WANG H.
PA (WINE/) WINEZKY D S.
XX
PI Wolfgang A, Baldwin TM, Van Castel FJC, Janssen GG, Murray CJ,
PI Wang H, Winezky DS;
XX WPI; 2005-222220/23.
XX
PT New peptides that bind to carotenoid compounds, useful as detergents for
PT targeting or removing stains on textiles or fabrics, in personal care or
PT food industry applications, or in various diagnostic applications.
XX
XX
PS Claim 1; SEQ ID NO 54; 107pp; English.
XX
XX The invention relates to 432 cyclic or linear carotenoid-binding phage
CC display peptides (ADY56178-ADY56609), to carotenoid-binding peptides
CC which comprise a repeatable motif selected from PPP, SSP, SSK, SPT, PTP,
CC SLH, SLP, TTT, NTS, APS, TYP or a motif shown in ADY56623-ADY56651, and
CC to a complex comprising a phenol-oxidizing enzyme (especially a
CC Stachybotrys laccase such as ADY56177 or variants thereof) covalently
CC attached to one of the 432 carotenoid-binding peptides. The invention
CC also relates to polynucleotides encoding a carotenoid-binding peptide,
CC and expression vectors and host cells comprising a polynucleotide
CC encoding a phenol-oxidizing enzyme/carotenoid-binding peptide complex.
CC The carotenoid-binding peptides are useful in complexes with a phenol-
CC oxidizing enzyme for enhancing the selectivity of the enzyme to a target
CC carotenoid stain on a textile or other surface, where the enzyme can then
CC act to bleach the stain. Such enzyme/peptide complexes can be used in
CC detergent or cleaning compositions for targeting or removing food stains
CC (e.g., tomato or paprika) on fabrics, and can also be used in the textile
CC industry in the treatment, processing, finishing, polishing or production
CC of fibers. The enzyme/peptide complexes are additionally useful in
CC personal care applications (e.g., in skin cosmetics as skin tanners), in
CC food industry applications (e.g., as fruit ripening agents) or in
CC diagnostic uses, such as in pharmaceutical applications e.g., to localize
CC the presence of carotenoids in tissues. The present sequence represents a
CC specifically claimed carotenoid-binding cyclic peptide isolated from a
CC phage display library.
XX
SQ Sequence 7 AA;
Query Match 32.1%; Score 35; DB 9; Length 7;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 PHPTNI 8
DB 1 PHPTNL 6
RESULT 15
AEC06055
ID AEC06055 standard; peptide; 10 AA.
XX
AC AEC06055;
XX
DT 20-OCT-2005 (first entry)
XX
DE H3 or D3-acetylated tumor-associated peptide.
XX
KW cytosstatic; vaccine; gene therapy; pharmaceutical; immunotherapy; tumor;
KW cancer; neoplasm.
XX
OS Unidentified.
XX
XX WO2005076009-A2.
XX
PD 18-AUG-2005.

XX
XX 28-JAN-2005; 2005WO-EP000873.
PF
XX
XX 28-JAN-2004; 2004DE-10005273.
PR
XX 06-MAR-2004; 2004DE-10011503.
PR
XX
XX (IMMA-) IMMATICS BIOTECHNOLOGIES GMBH.
XX
XX
PI Lemmel C, Rammensee H;
XX
XX WPI; 2005-618379/63.
XX
XX
PT Identifying and quantifying tumor-associated peptides by chemically
PT identically modifying peptides to generate different physical
PT characteristics, useful for treating tumorous and/or adenomatous
PT diseases.
XX
XX
PS Disclosure; Page 12; 43pp; English.
XX
XX The invention describes a method of identifying and quantifying tumor-
CC associated peptides comprising chemically identically modifying peptides
CC from samples in order to generate different physical characteristics in
CC the peptides from the different samples. The peptides are useful for
CC producing a medicament for the treatment of tumorous diseases and/or
CC adenomatous diseases, such as renal, lung, colon, stomach, pancreatic,
CC breast, prostate, ovarian and/or skin cancer. The peptide is used
CC together with an adjuvant. A peptide bound to an antigen-presenting cell
CC is used. The peptides are also useful for the labeling of leukocytes, in
CC particular of T-lymphocytes, for evaluating the progress of therapy in a
CC tumorous disease, and for producing an antibody. The nucleic acid and/or
CC vector and/or cell are useful in producing a medicament for the treatment
CC of tumorous and/or adenomatous diseases. This is the amino acid sequence
CC of a tumor-associated peptide that binds human MHC class I.
XX
SQ Sequence 10 AA;
Query Match 32.1%; Score 35; DB 9; Length 10;
Best Local Similarity 50.0%; Pred. No. 70;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 DIPHTNIHK 10
DB 1 DAHPNTNVOR 10
RESULT 16
AEC06029
ID AEC06029 standard; peptide; 10 AA.
XX
AC AEC06029;
XX
DT 20-OCT-2005 (first entry)
XX
DE Tumor-associated peptide SEQ ID NO 12.
XX
KW cytosstatic; vaccine; gene therapy; pharmaceutical; immunotherapy; tumor;
KW cancer; neoplasm.
XX
XX Homo sapiens.
OS
XX
XX WO2005076009-A2.
XX
XX
PD 18-AUG-2005.
XX
XX 28-JAN-2005; 2005WO-EP000873.
PF
XX 28-JAN-2004; 2004DE-10005273.
PR
XX 06-MAR-2004; 2004DE-10011503.
PR
XX
XX (IMMA-) IMMATICS BIOTECHNOLOGIES GMBH.
XX
XX Lemmel C, Rammensee H;
XX
XX

DR WPI; 2005-618379/63.

XX Identifying and quantifying tumor-associated peptides by chemically

PT Identically modifying peptides to generate different physical

PT characteristics, useful for treating tumorous and/or adenomatous

PT diseases.

XX

PS Claim 19; SEQ ID NO 12; 43pp; English.

XX

CC The invention describes a method of identifying and quantifying tumor-

CC associated peptides comprising chemically identifying modifying peptides

CC from samples in order to generate different physical characteristics in

CC the peptides from the different samples. The peptides are useful for

CC producing a medicament for the treatment of tumorous diseases and/or

CC adenomatous diseases, such as renal, lung, colon, stomach, pancreatic,

CC breast, prostate, ovarian and/or skin cancer. The peptide is used

CC together with an adjuvant. A peptide bound to an antigen-presenting cell

CC is used. The peptides are also useful for the labeling of leukocytes, in

CC particular of T-lymphocytes, for evaluating the progress of therapy in a

CC tumorous disease, and for producing an antibody. The nucleic acid and/or

CC vector and/or cell are useful in producing a medicament for the treatment

CC of tumorous and/or adenomatous diseases. This is the amino acid sequence

CC of a tumor-associated peptide that binds human MHC class I.

CC

XX

SQ Sequence 10 AA;

Query March 32.1%; Score 35; DB 9; Length 10;

Best Local Similarity 50.0%; Pred. No. 70;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 DHPPTNIHK 10

1 DHPPTNIHK 10

DB 1 DAHPPTNIHK 10

RESULT 17

AAW30771

ID AAW30771 standard; peptide; 15 AA.

XX

AC AAW30771;

XX

DT 27-FEB-1998 (first entry)

XX

DE Prostate Specific Antigen (PSA) derived peptide ABT3.

XX

KW Prostate specific antigen; PSA; immunogenic; human glandular kallikrein;

KW hK2; antigen; antibody; detection; diagnosis; prostate cancer.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9729199-A2.

XX

PD 14-AUG-1997.

XX

PF 06-FEB-1997; 97WO-US001911.

XX

PR 06-FEB-1996; 96US-00595945.

XX

PA (ABBO) ABBOTT LAB.

XX

PI Dowell Bt, Bridon DP, Qiu X, Lilja H, Pitonen T, Vihinen M;

PI Pectersson IK;

XX

DR WPI; 1997-415352/38.

XX

PT Prostate Specific Antigen peptide(s) - useful for diagnosis of prostate

PT cancer.

XX

PS Claim 2; Page 10; 42pp; English.

XX

CC AAW30769-84 are synthetic peptides derived from the prostate specific

CC antigen (PSA) sequence. These peptides are identical to a highly

CC immunogenic region of PSA, and also comprise one or more amino acids

CC identical or non-identical to the amino acid sequence of human glandular

CC kallikrein (hK2). The peptides are used as antigens for the production of

CC antibodies which are used to detect PSA in a test sample (claimed). This

CC is useful for diagnosis of prostate cancer. The peptides enable the

CC production of antisera necessary to determine the amount of total PSA,

CC free PSA and PSA-ACR complex present in a sample and thus improve the

CC ability of the clinician to distinguish, e.g., between BPH (benign

CC prostatic hyperplasia) and prostatic cancer in a patient

CC

XX

SQ Sequence 15 AA;

Query March 32.1%; Score 35; DB 2; Length 15;

Best Local Similarity 36.4%; Pred. No. 1.1e+02;

Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 4 HPTNIHKYLC 14

4 HPTNIHKYLC 14

DB 5 HPQKVTKFMIC 15

5 HPQKVTKFMIC 15

RESULT 18

AAW58054

ID AAW58054 standard; peptide; 15 AA.

XX

AC AAW58054;

XX

DT 11-AUG-1998 (first entry)

XX

DE Human prostate specific antigen peptide SEQ ID NO:72.

XX

KW Human; prostate specific antigen; PSA; epitope; monoclonal antibody;

KW detection; cancer; serine protease.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9810292-A1.

XX

PD 12-MAR-1998.

XX

PF 25-AUG-1997; 97WO-US014909.

XX

PR 06-SEP-1996; 96US-0025404P.

XX

PA (CENZ) CENTOCOR INC.

XX

PI Heavner GA;

PI WPI; 1998-193789/17.

XX

DR

XX

PT Monoclonal antibodies specific for prostate specific antigen - useful,

PT e.g. in screening for prostate or breast cancer and especially to

PT distinguish between benign prostatic hyperplasia and prostate cancer.

XX

XX

Example; Page 59; 84pp; English.

XX

CC The present sequence represents a prostate specific antigen (PSA)

CC peptide. Monoclonal antibodies specific for PSA and hybridomas producing

CC them have been developed. The antibodies: (a) bind to free PSA; (b) are

CC monoclonal antibody 365 binding to amino acids 82-87 of free PSA (LKNRFL)

CC or fragment, and (c) are monoclonal antibodies 10, 11, 16 or 22.2 and

CC 15.2, 156 or 225 binding to amino acids 139-144 (EHLFLTP) and 55-60

CC (SLFHPD) respectively of free and bound PSA, or fragments. The antibodies

CC are useful to detect PSA. For detecting free PSA only, an immunoassay

CC comprising a solid support with attached labelled monoclonal antibody

CC specific for free PSA (especially (b)) and a PSA standard can be used. To

CC detect both free and bound PSA, a second solid support with attached

CC (differently labelled) monoclonal antibody binding free and bound PSA

CC (especially selected from (c)) can be used either with, or in place of,

CC the first solid support. The antibodies are useful in cancer screening,

CC especially prostate and breast cancer. By obtaining total and free PSA

CC values, their ratio can be used to separate prostatic cancer (PCA) from

CC benign prostatic hyperplasia (BHP) patients. Measurement of PSA is also
 CC useful after radical prostatectomy, to predict disease persistence. The
 CC antibodies allow evaluation of PSA free/total ratio, enabling separation
 CC of BPH and PCA patients with PSA values 4-10 ng/ml not previously
 CC possible by total PSA testing, avoiding biopsies
 CC
 SQ Sequence 15 AA;

Query Match 32.1%; Score 35; DB 2; Length 15;
 Best Local Similarity 36.4%; Pred. No. 1.1e+02;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Dy 4 HPTNHHKYLVC 14
 || : ||:
 Db 5 HPQKVTKFMLC 15

RESULT 19
 AAMS8055
 ID AAMS8055 standard; peptide; 15 AA.
 XX
 AC AAMS8055;

XX 11-AUG-1998 (first entry)
 DT
 XX

DE Human prostate specific antigen peptide SEQ ID NO:73.

KM Human, prostate specific antigen; PSA; epitope; monoclonal antibody;
 XX detection; cancer; serine protease.

OS Synthetic.
 OS Homo sapiens.

XX MO9810292-A1.

PN 12-MAR-1998.

PD 25-AUG-1997; 97WO-US014909.

PF 06-SEP-1996; 96US-0025404P.

PR (CENZ) CENTOCOR INC.

PA Heavner GA;

PI WPI; 1998-193789/17.

XX Monoclonal antibodies specific for prostate specific antigen - useful,
 PT e.g. in screening for prostate or breast cancer and especially to
 PT distinguish between benign prostatic hyperplasia and prostate cancer.

XX Example; Page 60; 84pp; English.

XX The present sequence represents a prostate specific antigen (PSA)
 CC peptide. Monoclonal antibodies specific for PSA and hybridomas producing
 CC them have been developed. The antibodies: (a) bind to free PSA; (b) are
 CC monoclonal antibody 365 binding to amino acids 82-87 of free PSA (LKKNFL)
 CC or fragment, and (c) are monoclonal antibodies 10, 11, 16 or 22.2 and
 CC 15.2, 156 or 225 binding to amino acids 139-144 (BBLFUTP) and 55-60
 CC (SLFHNP) respectively of free and bound PSA, or fragments. The antibodies
 CC are useful to detect PSA. For detecting free PSA only, an immunoassay
 CC comprising a solid support with attached labelled monoclonal antibody
 CC specific for free PSA (especially (b)) and a PSA standard can be used. To
 CC detect both free and bound PSA, a second solid support with attached
 CC (differently labelled) monoclonal antibody binding free and bound PSA
 CC (especially selected from (c)) can be used either with, or in place of,
 CC the first solid support. The antibodies are useful in cancer screening,
 CC especially prostate and breast cancer. By obtaining total and free PSA
 CC values, their ratio can be used to separate prostatic cancer (PCA) from
 CC benign prostatic hyperplasia (BHP) patients. Measurement of PSA is also
 CC useful after radical prostatectomy, to predict disease persistence. The
 CC antibodies allow evaluation of PSA free/total ratio, enabling separation
 CC of BPH and PCA patients with PSA values 4-10 ng/ml not previously

CC possible by total PSA testing, avoiding biopsies
 CC
 SQ Sequence 15 AA;

Query Match 32.1%; Score 35; DB 2; Length 15;
 Best Local Similarity 36.4%; Pred. No. 1.1e+02;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Dy 4 HPTNHHKYLVC 14
 || : ||:
 Db 2 HPQKVTKFMLC 12

RESULT 20
 ADM37502
 ID ADM37502 standard; peptide; 15 AA.
 XX
 AC ADM37502;

XX 10-MAR-2005 (first entry)
 DT
 XX

DE HLA binding epitope #8252.

KM Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;
 KM MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
 XX viral disease; cancer.

XX Unidentified.

PN MO203040165-A2.

PD 15-MAY-2003.

PE 18-OCT-2001; 2001WO-US051650.

PR 19-OCT-2000; 2000US-0242350P.

PR 20-APR-2001; 2001US-0285624P.

PA (EPIM-) EPIMMUNE INC.

PI Sette A, Sidney J, Southwood S;

DR WPI; 2003-441519/41.

XX New composition comprising at least one peptide having allele-specific
 PT binding motifs for HLA, useful for preventing, treating or diagnosing
 PT viral diseases and cancer.

XX Claim 1; Page 52-379; 382pp; English.

XX The invention relates to a composition comprising at least one peptide
 CC having an isolated, prepared epitope selected from any of the sequences
 CC from 30 lists given in the specification. Also disclosed is a method for
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a
 CC patient expressing a specific MHC class I allele by contacting cytotoxic
 CC T cells from the patient with the composition cited above. The
 CC composition comprises an epitope that is joined by an amino acid linker.
 CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
 CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
 CC binds to a complex of the HLA molecule and the epitope. Specifically
 CC claimed are peptides having allele-specific binding motifs for HLA. The
 CC compositions and methods are useful for preventing, treating or
 CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
 CC diagnostic agents for evaluating immune responses, for making antibodies
 CC and for evaluating efficacy of a vaccine. Sequences given in ADM29251-
 CC ADM37745 represent epitopes of the invention as given in Tables 2-31.

XX Sequence 15 AA;

Query Match 32.1%; Score 35; DB 7; Length 15;
 Best Local Similarity 36.4%; Pred. No. 1.1e+02;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 4 HPTNHHKYLVC 14
 DB 5 HPQKVTKEFMLC 15

RESULT 21

ADM35209
 ID ADM35209 standard; peptide, 15 AA.

AC ADM35209;

DT 10-MAR-2005 (first entry)

DE HLA binding epitope #5959.

XX Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;

KW MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;

XX viral disease; cancer.

OS Unidentified.

PN WO2003040165-A2.

PD 15-MAY-2003.

PF 18-OCT-2001; 2001WO-US051650.

PR 19-OCT-2000; 2000US-0242350P.

PR 20-APR-2001; 2001US-0285624P.

XX (EPIM-) EPIMMUNE INC.

PI Sette A, Sidney J, Southwood S;

DR WPI; 2003-441519/41.

XX New composition comprising at least one peptide having allele-specific

PT binding motifs for HLA, useful for preventing, treating or diagnosing

PT viral diseases and cancer.

XX Claim 1; Page 52-379; 382pp; English.

CC The invention relates to a composition comprising at least one peptide

CC having an isolated, prepared epitope selected from any of the sequences

CC from 30 lists given in the specification. Also disclosed is a method for

CC inducing a cytotoxic T cell response against a pre-selected antigen in a

CC patient expressing a specific MHC class I allele by contacting cytotoxic

CC T cells from the patient with the composition cited above. The

CC composition comprises an epitope that is joined by an amino acid linker.

CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is

CC bound to an HLA molecule on the antigen-presenting cell, where when an A2

CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL

CC binds to a complex of the HLA molecule and the epitope. Specifically

CC claimed are peptides having allele-specific binding motifs for HLA. The

CC compositions and methods are useful for preventing, treating or

CC diagnosing viral diseases and cancer. The peptide epitopes are useful as

CC diagnostic agents for evaluating immune responses, for making antibodies

CC and for evaluating efficacy of a vaccine. Sequences given in ADM29251-

CC ADM37745 represent epitopes of the invention as given in Tables 2-31.

XX Sequence 15 AA;

XX Query Match 32.1%; Score 35; DB 7; Length 15;

XX Best Local Similarity 36.4%; Pred. No. 1.1e+02;

XX Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

XX DB 4 HPTNHHKYLVC 14

XX 5 HPQKVTKEFMLC 15

XX RESULT 22

ADM33268
 ID ADM33268 standard; peptide, 15 AA.

AC ADM33268;

DT 10-MAR-2005 (first entry)

DE HLA binding epitope #4018.

XX Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;

KW MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;

XX viral disease; cancer.

OS Unidentified.

PN WO2003040165-A2.

PD 15-MAY-2003.

PF 18-OCT-2001; 2001WO-US051650.

PR 19-OCT-2000; 2000US-0242350P.

PR 20-APR-2001; 2001US-0285624P.

XX (EPIM-) EPIMMUNE INC.

PI Sette A, Sidney J, Southwood S;

DR WPI; 2003-441519/41.

XX New composition comprising at least one peptide having allele-specific

PT binding motifs for HLA, useful for preventing, treating or diagnosing

PT viral diseases and cancer.

XX Claim 1; Page 52-379; 382pp; English.

CC The invention relates to a composition comprising at least one peptide

CC having an isolated, prepared epitope selected from any of the sequences

CC from 30 lists given in the specification. Also disclosed is a method for

CC inducing a cytotoxic T cell response against a pre-selected antigen in a

CC patient expressing a specific MHC class I allele by contacting cytotoxic

CC T cells from the patient with the composition cited above. The

CC composition comprises an epitope that is joined by an amino acid linker.

CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is

CC bound to an HLA molecule on the antigen-presenting cell, where when an A2

CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL

CC binds to a complex of the HLA molecule and the epitope. Specifically

CC claimed are peptides having allele-specific binding motifs for HLA. The

CC compositions and methods are useful for preventing, treating or

CC diagnosing viral diseases and cancer. The peptide epitopes are useful as

CC diagnostic agents for evaluating immune responses, for making antibodies

CC and for evaluating efficacy of a vaccine. Sequences given in ADM29251-

CC ADM37745 represent epitopes of the invention as given in Tables 2-31.

XX Sequence 15 AA;

XX Query Match 32.1%; Score 35; DB 7; Length 15;

XX Best Local Similarity 36.4%; Pred. No. 1.1e+02;

XX Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

XX DB 4 HPTNHHKYLVC 14

XX 5 HPQKVTKEFMLC 15

XX RESULT 23

XX ADM33976

XX ID ADM33976 standard; peptide, 15 AA.

XX AC ADM33976;

XX DT 10-MAR-2005 (first entry)

PD 14-AUG-1997.
 XX
 PF 06-FEB-1997; 97MO-US001911.
 XX
 PR 06-FEB-1996; 96US-00595945.
 XX
 PA (ABBOTT) ABBOTT LAB.
 XX
 PI Dowell BL, Bridon DP, Qiu X, Lilja H, Pironen T, Vihinen M;
 PI Pettersson IK;
 XX
 DR WPI; 1997-415352/38.
 XX
 PT Prostate Specific Antigen peptide(s) - useful for diagnosis of prostate
 PT cancer.
 PS Claim 2; Page 10; 42pp; English.
 XX
 XX AA030769-84 are synthetic peptides derived from the prostate specific
 CC antigen (PSA) sequence. These peptides are identical to a highly
 CC immunogenic region of PSA, and also comprise one or more amino acids
 CC identical or non-identical to the amino acid sequence of human glandular
 CC kallikrein (hk2). The peptides are used as antigens for the production of
 CC antibodies which are used to detect PSA in a test sample (claimed). This
 CC is useful for diagnosis of prostate cancer. The peptides enable the
 CC production of antisera necessary to determine the amount of total PSA,
 CC free PSA and PSA-Act complex present in a sample and thus improve the
 CC ability of the clinician to distinguish, e.g., between BPH (benign
 CC prostatic hyperplasia) and prostatic cancer in a patient
 XX
 SQ Sequence 19 AA;

Query Match 32.1%; Score 35; DB 2; Length 19;
 Best Local Similarity 36.4%; Pred. No. 1.5e+02;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 OY 4 HPTNHHKYLVC 14
 DB 9 HPQKVTKFMLC 19

Search completed: January 26, 2006, 07:58:09
 Job time : 68.5345 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:50:06 : Search time 17.8534 Seconds
(without alignments)
87.985 Million cell updates/sec

Title: US-09-662-293-11

Perfect score: 109

Sequence: 1 DIPHPNTHKYLVCESVNG 19

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 229350

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5_COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/6_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/PTCUS_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfillset.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	109	100.0	19	2	US-09-292-225-11
2	109	100.0	20	2	US-09-292-225-3
3	35	32.1	15	2	US-08-595-945-3
4	35	32.1	19	2	US-08-595-945-15
5	35	32.1	20	2	US-09-026-276-20
6	35	32.1	20	2	US-09-964-201A-20
7	34	31.2	15	1	US-07-829-462-6
8	34	29.4	10	2	US-08-159-339A-551
9	32	29.4	15	2	US-09-009-953-109
10	31.5	28.9	21	2	US-09-962-756-51
11	31	28.4	8	1	US-08-529-190B-73
12	31	28.4	16	2	US-09-791-524A-3
13	31	28.4	17	1	US-08-370-567-1
14	31	28.4	17	1	US-08-438-759-1
15	31	28.4	17	1	US-08-538-911-20
16	31	28.4	17	2	US-09-402-641-10
17	31	28.4	17	2	US-09-411-067C-2
18	31	28.4	17	2	US-09-428-082B-196
19	31	28.4	17	2	US-09-155-260C-16
20	31	28.4	17	2	US-09-402-464-1
21	31	28.4	17	2	US-09-791-524A-4
22	31	28.4	17	4	PCT-US94-05591-20
23	31	28.4	17	4	PCT-US94-05684-1
24	31	28.4	20	2	US-09-791-524A-9
25	31	28.4	21	2	US-09-791-524A-10
26	30	27.5	10	2	US-09-139-802-58
27	30	27.5	10	2	US-09-659-786-58

28	30	27.5	10	2	US-08-926-914-58	Sequence 58, Appl
29	30	27.5	15	2	US-09-300-410A-2	Sequence 2, Appl
30	29.5	27.1	20	1	US-08-614-935-75	Sequence 75, Appl
31	29.5	27.1	20	1	US-09-130-287-75	Sequence 75, Appl
32	29	26.6	6	1	US-08-192-243-1	Sequence 1, Appl
33	29	26.6	6	1	US-08-448-059-1	Sequence 1, Appl
34	29	26.6	6	2	US-09-295-996B-15	Sequence 15, Appl
35	29	26.6	6	2	US-09-551-737C-18	Sequence 18, Appl
36	29	26.6	6	2	US-09-295-924B-10	Sequence 10, Appl
37	29	26.6	6	2	US-09-551-738B-15	Sequence 15, Appl
38	29	26.6	11	1	US-07-942-245-195	Sequence 495, Appl
39	29	26.6	11	1	US-08-024-253-16	Sequence 16, Appl
40	29	26.6	11	2	US-09-649-063-16	Sequence 16, Appl
41	29	26.6	20	1	US-08-305-871A-11	Sequence 11, Appl
42	29	26.6	20	1	US-08-797-842-7	Sequence 7, Appl
43	29	26.6	20	2	US-09-100-409A-47	Sequence 47, Appl
44	29	26.6	20	2	US-09-009-953-195	Sequence 195, Appl
45	29	26.6	20	2	US-08-788-822A-14	Sequence 14, Appl
46	29	26.6	20	2	US-09-311-784A-150	Sequence 150, Appl
47	29	26.6	20	2	US-09-239-043D-2566	Sequence 2566, Ap
48	29	26.6	20	2	US-09-701-623C-71	Sequence 71, Appl
49	29	26.6	20	2	US-09-674-183-8	Sequence 8, Appl
50	29	26.6	20	2	US-10-666-480-5	Sequence 5, Appl
51	29	26.6	20	5	US-09-618-592-7	Sequence 7, Appl
52	29	26.6	21	2	US-09-962-756-53	Sequence 53, Appl
53	29	26.6	21	2	US-09-962-756-76	Sequence 76, Appl
54	29	26.6	21	2	US-09-962-756-51	Sequence 51, Appl
55	29	26.6	21	2	US-09-962-756-10	Sequence 10, Appl
56	29	26.6	21	2	US-10-666-480-34	Sequence 34, Appl
57	29	26.6	9	2	US-08-159-339A-526	Sequence 526, Appl
58	28	25.7	11	2	US-09-119-507B-51	Sequence 51, Appl
59	28	25.7	11	2	US-08-897-556A-51	Sequence 51, Appl
60	28	25.7	11	2	US-09-547-693-51	Sequence 51, Appl
61	28	25.7	13	1	US-08-147-011-1	Sequence 1, Appl
62	28	25.7	15	2	US-09-009-953-110	Sequence 110, Appl
63	28	25.7	16	2	US-08-810-009-51	Sequence 51, Appl
64	28	25.7	16	2	US-09-776-490-51	Sequence 51, Appl
65	28	25.7	19	2	US-08-802-981-86	Sequence 86, Appl
66	28	25.7	19	2	US-09-747-287A-121	Sequence 121, Appl
67	28	25.7	19	2	US-09-394-019C-74	Sequence 74, Appl
68	28	25.7	19	2	US-09-394-019C-76	Sequence 76, Appl
69	28	25.7	19	2	US-09-394-019C-83	Sequence 83, Appl
70	28	25.7	19	2	US-09-394-019C-319	Sequence 319, Appl
71	28	25.7	19	2	US-09-394-019C-321	Sequence 321, Appl
72	28	25.7	19	2	US-09-394-019C-328	Sequence 328, Appl
73	28	25.7	21	1	US-07-851-976B-1	Sequence 1, Appl
74	28	25.7	21	1	US-08-291-609-1	Sequence 1, Appl
75	28	25.7	21	1	US-08-401-136-1	Sequence 1, Appl
76	28	25.7	21	2	US-08-850-554-1	Sequence 1, Appl
77	28	25.7	21	2	US-09-962-756-130	Sequence 130, Appl
78	28	25.7	21	6	5459061-6	Patent No. 5459061
79	27	24.8	10	2	US-10-365-908-52	Sequence 52, Appl
80	27	24.8	11	1	US-07-847-311A-19	Sequence 19, Appl
81	27	24.8	12	1	US-09-430-221-9	Sequence 9, Appl
82	27	24.8	14	2	US-08-182-967-23	Sequence 23, Appl
83	27	24.8	14	2	US-09-069-827A-131	Sequence 131, Appl
84	27	24.8	15	2	US-09-117-860-11	Sequence 11, Appl
85	27	24.8	16	2	US-09-428-082B-565	Sequence 565, Appl
86	27	24.8	16	2	US-09-428-082B-573	Sequence 573, Appl
87	27	24.8	16	2	US-09-155-260C-7	Sequence 7, Appl
88	27	24.8	17	1	US-08-451-947-32	Sequence 32, Appl
89	27	24.8	17	1	US-08-424-826A-32	Sequence 32, Appl
90	27	24.8	17	2	US-08-928-594-32	Sequence 32, Appl
91	27	24.8	17	2	US-09-461-325-294	Sequence 294, Appl
92	27	24.8	17	2	US-08-450-842-32	Sequence 32, Appl
93	27	24.8	17	2	US-08-451-390-32	Sequence 32, Appl
94	27	24.8	17	2	US-10-012-442-294	Sequence 294, Appl
95	27	24.8	17	2	US-10-115-123-294	Sequence 294, Appl
96	27	24.8	17	4	PCT-US91-06950-32	Sequence 32, Appl
97	27	24.8	18	1	US-08-232-513A-12	Sequence 12, Appl
98	27	24.8	18	1	US-09-231-159-17	Sequence 17, Appl
99	27	24.8	18	2	US-08-611-307-17	Sequence 17, Appl
100	27	24.8	18	2	US-09-372-425A-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1

US-09-292-225-11
; Sequence 11, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-11

Query Match 100.0%; Score 109; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2,6e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DHPPTNHHKYLVCESVNG 19
Db 1 DHPPTNHHKYLVCESVNG 19

RESULT 2

US-09-292-225-3
; Sequence 3, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-3

Query Match 100.0%; Score 109; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 2,7e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DHPPTNHHKYLVCESVNG 19
Db 1 DHPPTNHHKYLVCESVNG 19

RESULT 3

US-08-595-945-3
; Sequence 3, Application US/08595945
; Patent No. 6143509
; GENERAL INFORMATION:
; APPLICANT: DOWELL, BARRY L.
; APPLICANT: BRIDON, DOMINIQUE P.
; APPLICANT: QIU, XIAOXING
; APPLICANT: LILJA, HANS
; APPLICANT: PIIRONEN, TIMO P.
; APPLICANT: VIHINEN, MAUNO A.
; APPLICANT: PETERSSON, KIM S.I.
; TITLE OF INVENTION: PROSTATE SPECIFIC ANTIGEN PEPTIDES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,945
; FILING DATE: 06-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BECKER, CHERYL L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 5875, US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-935-1729
; TELEFAX: 847-938-2623
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-595-945-3

Query Match 32.1%; Score 35; DB 2; Length 15;
Best Local Similarity 36.4%; Pred. No. 33;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy 4 HPTNHHKYLVC 14
Db 5 HPQKVKFKMLC 15

RESULT 4

US-08-595-945-15
; Sequence 15, Application US/08595945
; Patent No. 6143509
; GENERAL INFORMATION:
; APPLICANT: DOWELL, BARRY L.
; APPLICANT: BRIDON, DOMINIQUE P.
; APPLICANT: QIU, XIAOXING
; APPLICANT: LILJA, HANS

APPLICANT: PIIRONEN, TIMO P.
APPLICANT: VIHINEN, MAURO A.
TITLE OF INVENTION: PROSTATE SPECIFIC ANTIGEN PEPTIDES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,945
FILING DATE: 06-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BECKER, CHERYL L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 5875, US.01
TELEPHONE: 847-935-1729
TELECOMMUNICATION INFORMATION:
TELEFAX: 847-938-2623
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-595-945-15

Query Match 32.1%; Score 35; DB 2; Length 19;
Best Local Similarity 36.4%; Pred. No. 43;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 4 HPTNHHKYLVC 14
|| : : : :
DB 9 HPQKVTKEMLC 19

RESULT 5
US-09-026-276-20
Sequence 20, Application US/09026276
Patent No. 6319503
GENERAL INFORMATION:
APPLICANT: Kenten, John H
APPLICANT: Trimontano, Alfonso
APPLICANT: Pilon, Aprille L
APPLICANT: Lohmas, Gerald L
APPLICANT: Roberts, Steven F
TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM
FILE REFERENCE: U.S. Patent Application No. 6319503 09\026,276
CURRENT APPLICATION NUMBER: US/09/026,276
CURRENT FILING DATE: 1998-02-19
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-09-026-276-20

Query Match 32.1%; Score 35; DB 2; Length 20;
Best Local Similarity 36.4%; Pred. No. 45;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 4 HPTNHHKYLVC 14
|| : : : :
DB 7 HPQKVTKEMLC 17

RESULT 6
US-09-964-201A-20
Sequence 20, Application US/09964201A
Patent No. 6660271
GENERAL INFORMATION:
APPLICANT: Kenten, John H
APPLICANT: Trimontano, Alfonso
APPLICANT: Pilon, Aprille L
APPLICANT: Lohmas, Gerald L
APPLICANT: Roberts, Steven F
TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM
FILE REFERENCE: U.S. Patent Application No. 6660271 09\026,276
CURRENT APPLICATION NUMBER: US/09/964,201A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-09-964-201A-20

Query Match 32.1%; Score 35; DB 2; Length 20;
Best Local Similarity 36.4%; Pred. No. 45;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 4 HPTNHHKYLVC 14
|| : : : :
DB 7 HPQKVTKEMLC 17

RESULT 7
US-07-829-462-6
Sequence 6, Application US/07829462
Patent No. 5453489
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki I.
APPLICANT: Morla, Alex
TITLE OF INVENTION: NOVEL FRAGMENTS OF FIBRONECTIN AND
METHODS TO MODULATE THE ROLE OF FIBRONECTIN IN
EXTRACELLULAR MATRIX ASSEMBLY
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/829,462
FILING DATE: 19920131
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATRYN A.
REGISTRATION NUMBER: 31,547
REFERENCE/DOCKET NUMBER: P-LA 9179
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids

TYPE: AMINO ACID
TOPOLOGY: linear
US-07-829-462-6

Query Match 31.2%; Score 34; DB 1; Length 15;
Best Local Similarity 45.5%; Pred. No. 48;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 PHPTNHYLV 13
| : : | : : | : :
DB 3 PPSHISKYIL 13

RESULT 8

US-08-159-339A-551
Sequence 551, Application US/08159339A

PATENT No. 6037135
GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA

ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:
INFORMATION FOR SEQ ID NO: 551:

SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-551

Query Match 29.4%; Score 32; DB 2; Length 10;
Best Local Similarity 55.6%; Pred. No. 66;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IPHPTNHYK 10
| : : | : : | : :
DB 2 IPHPAGLKK 10

RESULT 9
US-09-009-953-109
Sequence 109, Application US/09009953

PATENT No. 6413517
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
TITLE OF INVENTION: Identification of Broadly
Reactive DR Restricted Epitopes
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA

ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,953
FILING DATE: 21-Jan-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,713
FILING DATE: 23-JAN-1997
APPLICATION NUMBER: US 60/037,432
FILING DATE: 07-FEB-1997

ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-011520US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 109:
US-09-009-953-109

Query Match 29.4%; Score 32; DB 2; Length 15;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IPHPTNHYK 10
| : : | : : | : :
DB 6 IPHPAGLKK 14

RESULT 10
US-09-962-756-51
Sequence 51, Application US/09962756

PATENT No. 6875741
GENERAL INFORMATION:
APPLICANT: PILUTTLA, RENUKA
APPLICANT: BRISSETTE, RENEE
APPLICANT: BLUME, ARTHUR J.
APPLICANT: SCHAFFER, LAUGE
APPLICANT: BRANDT, JAKOB
APPLICANT: GOLDSTEIN, NEIL I.
APPLICANT: SPETZLER, JANE
APPLICANT: OSTERGAARD, SOREN
APPLICANT: HANSEN, PER HERTZ
TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS

FILE REFERENCE: 1878-4051US1
 CURRENT APPLICATION NUMBER: US/09/962,756
 CURRENT FILING DATE: 2001-09-24
 PRIOR APPLICATION NUMBER: 09/538,038
 PRIOR FILING DATE: 2000-03-29
 PRIOR APPLICATION NUMBER: 09/146,127
 PRIOR FILING DATE: 1998-09-02
 NUMBER OF SEQ ID NOS: 2227
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 51
 LENGTH: 21
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-09-962-756-51

Query Match 28.9%; Score 31.5; DB 2; Length 21;
 Best Local Similarity 37.5%; Pred. No. 1.8e+02;
 Matches 6; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

QY 3 PHPTNHYLVCSVN 18
 ||:|:|:|:
 Db 7 PHGSNFDWV-EXIN 21

RESULT 11
 US-08-529-1908-73
 Sequence 73, Application US/085291908
 Patent No. 5833991
 GENERAL INFORMATION:
 APPLICANT: Mabucci, Maria G.
 TITLE OF INVENTION: GLYCINE-CONTAINING SEQUENCES
 TITLE OF INVENTION: CONFERRING INVISIBILITY TO THE IMMUNE SYSTEM
 NUMBER OF SEQUENCES: 76
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Banner & Witcoff, Ltd.
 STREET: One Financial Center
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 OPERATING SYSTEM: DOS
 SOFTWARE: Wordperfect 6.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/529,1908
 FILING DATE: 15-SEP-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: SE9501324-9
 FILING DATE: 10-APR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US08/522,595
 FILING DATE: 01-SEP-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Williams, Ph. D., Kathleen A
 REGISTRATION NUMBER: 34,380
 TELEPHONE: 617-345-9100
 TELEFAX: 617-345-9111
 INFORMATION FOR SEQ ID NO: 73:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-08-529-1908-73

Query Match 28.4%; Score 31; DB 1; Length 8;
 Best Local Similarity 71.4%; Pred. No. 4.6e+05;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 IHKYLVC 14
 ||:|:|:|:
 Db 1 IHRLRC 7

RESULT 12
 US-09-791-524A-3
 Sequence 3, Application US/09791524A
 Patent No. 6911199
 GENERAL INFORMATION:
 APPLICANT: Aventis Pharmaceuticals Products Inc.
 TITLE OF INVENTION: Targeted Adenovirus Vectors for Delivery of Heterologous Genes
 FILE REFERENCE: P26,992-B USA
 CURRENT APPLICATION NUMBER: US/09/791,524A
 PRIOR FILING DATE: 2001-02-22
 PRIOR APPLICATION NUMBER: PCT/IB99/01524
 PRIOR FILING DATE: 1999-08-27
 PRIOR APPLICATION NUMBER: US 60/098,028
 PRIOR FILING DATE: 1998-08-27
 NUMBER OF SEQ ID NOS: 165
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 3
 LENGTH: 16
 TYPE: PRT
 ORGANISM: Adenovirus
 US-09-791-524A-3

Query Match 28.4%; Score 31; DB 2; Length 16;
 Best Local Similarity 45.5%; Pred. No. 1.6e+02;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNHYKL 12
 ||:|:|:|:
 Db 4 MPHSLNFSOYL 14

RESULT 13
 US-08-370-567-1
 Sequence 1, Application US/08370567
 Patent No. 5656726
 GENERAL INFORMATION:
 APPLICANT: Rosenberg, Steven
 APPLICANT: Doyle, Michael
 APPLICANT: Goodson, Robert
 TITLE OF INVENTION: Peptide Inhibitors of Urokinase Receptor
 TITLE OF INVENTION: Activity
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Chiron Corporation
 STREET: 4560 Horton Street
 CITY: Emeryville
 STATE: CA
 COUNTRY: USA
 ZIP: 94608
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/370,567
 FILING DATE:
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/061,514
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Green, Grant D.

REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0941.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-370-567-1

Query Match 28.4%; Score 31; DB 1; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 IPHPTNIHKYL 12
DB 4 MPHSLNFSQYL 14

RESULT 14
US-08-438-759-1
Sequence 1, Application US/08438759
Patent No. 5675782
GENERAL INFORMATION:
APPLICANT: Rosenberg, Steven
APPLICANT: Doyle, Michael
APPLICANT: Goodson, Robert
TITLE OF INVENTION: Peptide Inhibitors of Urokinase Receptor
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESS: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,759
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/370,567
FILING DATE:
APPLICATION NUMBER: US/08/061,514
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0941.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-438-759-1

Query Match 28.4%; Score 31; DB 1; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.7e+02;

Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 IPHPTNIHKYL 12
DB 4 MPHSLNFSQYL 14

RESULT 15
US-08-538-911-20
Sequence 20, Application US/08538911
Patent No. 5750344
GENERAL INFORMATION:
APPLICANT: Doyle, Michael
APPLICANT: Winter, Jill
TITLE OF INVENTION: Method For Selection Of Biologically
TITLE OF INVENTION: Active Peptide Sequences
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESS: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/538,911
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/069,352
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0407.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-538-911-20

Query Match 28.4%; Score 31; DB 1; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 IPHPTNIHKYL 12
DB 4 MPHSLNFSQYL 14

RESULT 16
US-09-402-641-10
Sequence 10, Application US/09402641
Patent No. 6528619
GENERAL INFORMATION:
APPLICANT: BUERGLE, Markus
APPLICANT: GRAEFF, Heinrich
APPLICANT: KESSLER, Horst
APPLICANT: MAGDOLEN, Viktor Robert
APPLICANT: KOENIG, Bernhard
APPLICANT: KOPFITZ, Marcus

```

; APPLICANT: RIEMER, Christoph
; APPLICANT: SCHMITT, Manfred
; APPLICANT: WEIDLE, Ulrich
; APPLICANT: WILHELM, Olaf
; TITLE OF INVENTION: INHIBITORS FOR UROKINASE RECEPTOR
; FILE REFERENCE: Case 20367US
; CURRENT FILING DATE: US/09/402,641
; PRIOR APPLICATION NUMBER: EP97106024.9
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/EP98/02178
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: clone-20 peptide
US-09-402-641-10

```

```

Query Match      28.4%; Score 31; DB 2; Length 17;
Best Local Similarity 45.5%; Pred. NO. 1.7e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      2 IPHPTNIHKYL 12
      :||| :|||
      4 MPHSLNFSQYL 14

```

```

RESULT 17
US-09-411-067C-2
; Sequence 2, Application US/09411067C
; Patent No. 6576610
; GENERAL INFORMATION:
; APPLICANT: NUVAS, LLC
; APPLICANT: HOUSTON, L.L.
; TITLE OF INVENTION: USE OF A CONTEXT-DEPENDENT FUNCTIONAL ENTITY TO ENHANCE THE EFFIC
; TITLE OF INVENTION: AN AGENT
; FILE REFERENCE: NUVAS1140
; CURRENT APPLICATION NUMBER: US/09/411,067C
; CURRENT FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-411-067C-2

```

```

Query Match      28.4%; Score 31; DB 2; Length 17;
Best Local Similarity 45.5%; Pred. NO. 1.7e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      2 IPHPTNIHKYL 12
      :||| :|||
      4 MPHSLNFSQYL 14

```

```

RESULT 18
US-09-428-082B-196
; Sequence 196, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22

```

```

; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 196
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: UKR ANTAGONIST PEPTIDE
US-09-428-082B-196

```

```

Query Match      28.4%; Score 31; DB 2; Length 17;
Best Local Similarity 45.5%; Pred. NO. 1.7e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      2 IPHPTNIHKYL 12
      :||| :|||
      4 MPHSLNFSQYL 14

```

```

RESULT 19
US-09-155-260C-16
; Sequence 16, Application US/09155260C
; Patent No. 6794358
; GENERAL INFORMATION:
; APPLICANT: ROSENBERG, STEVE
; APPLICANT: DOYLE, MICHAEL
; APPLICANT: CHAPMAN, HAROLD
; TITLE OF INVENTION: PEPTIDE LIGANDS OF THE UROKINASE RECEPTOR
; FILE REFERENCE: 014024-0284102
; CURRENT APPLICATION NUMBER: US/09/155,260C
; CURRENT FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: PCT/US97/05199
; PRIOR FILING DATE: 1997-03-28
; PRIOR APPLICATION NUMBER: 08/623,361
; PRIOR FILING DATE: 1996-03-28
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide ligand
US-09-155-260C-16

```

```

Query Match      28.4%; Score 31; DB 2; Length 17;
Best Local Similarity 45.5%; Pred. NO. 1.7e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      2 IPHPTNIHKYL 12
      :||| :|||
      4 MPHSLNFSQYL 14

```

```

RESULT 20
US-09-402-464-1
; Sequence 1, Application US/09402464
; Patent No. 6872702
; GENERAL INFORMATION:
; APPLICANT: Kessler, Horst
; APPLICANT: Graeff, Heinrich
; APPLICANT: Schmitt, Manfred
; APPLICANT: Magdolen, Viktor
; APPLICANT: Wilhelm, Olaf G.
; APPLICANT: Riemer, Christoph
; APPLICANT: Burgle, Markus
; TITLE OF INVENTION: Inhibitors for Urokinase Receptor
; FILE REFERENCE: 100564-09040
; CURRENT APPLICATION NUMBER: US/09/402,464
; CURRENT FILING DATE: 2000-01-07

```

PRIOR APPLICATION NUMBER: EP 97 106 024.9
PRIOR FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 1
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
US-09-402-464-1

Query Match 28.4%; Score 31; DB 2; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNIHKYL 12
:|:|:|:|:
Db 4 MPHSLNFSQYL 14

RESULT 21
US-09-791-524A-4
Sequence 4, Application US/09791524A
Patent No. 6911199
GENERAL INFORMATION:
APPLICANT: Aventis Pharmaceuticals Products Inc.
TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
FILE REFERENCE: P26,992-B USA
CURRENT APPLICATION NUMBER: US/09/791,524A
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/IB99/01524
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: US 60/098,028
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 165
SOFTWARE: Patentln version 3.2
SEQ ID NO 4
LENGTH: 17
TYPE: PRT
ORGANISM: Adenovirus
US-09-791-524A-4

Query Match 28.4%; Score 31; DB 2; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNIHKYL 12
:|:|:|:|:
Db 4 MPHSLNFSQYL 14

RESULT 22
PCT-US94-05591-20
Sequence 20, Application PC/TUS9405591
GENERAL INFORMATION:
APPLICANT: Doyle, Michael V.
TITLE OF INVENTION: Method For Selection Of Biologically
TITLE OF INVENTION: Active Peptide Sequences
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05591
FILING DATE: 19-MAY-1994

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0407.100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
PCT-US94-05591-20

Query Match 28.4%; Score 31; DB 4; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNIHKYL 12
:|:|:|:|:
Db 4 MPHSLNFSQYL 14

RESULT 23
PCT-US94-05684-1
Sequence 1, Application PC/TUS9405684
GENERAL INFORMATION:
APPLICANT: Chiron Corporation
TITLE OF INVENTION: Peptide Inhibitors of Urokinase Receptor
TITLE OF INVENTION: Activity
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05684
FILING DATE: 19 MAY 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0941.100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
PCT-US94-05684-1

Query Match 28.4%; Score 31; DB 4; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNIHKYL 12
:|:|:|:|:

Db 4 MPHSLNFSQYL 14

```

RESULT 24
US-09-791-524A-9
; Sequence 9, Application US/09791524A
; Patent No. 6911199
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Products Inc.
; TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
; FILE REFERENCE: P26,992-B USA
; CURRENT APPLICATION NUMBER: US/09/791,524A
; PRIORITY FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: PCT/IB99/01524
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: US 60/098,028
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Adenovirus
US-09-791-524A-9

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Query Match 28.4%; Score 31; DB 2; Length 20;
 Best Local Similarity 45.5%; Pred. No. 2.1e+02;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNIHKYL 12
 :||| :|||
 Db 6 MPHSLNFSQYL 16

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RESULT 25
US-09-791-524A-10
; Sequence 10, Application US/09791524A
; Patent No. 6911199
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Products Inc.
; TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
; FILE REFERENCE: P26,992-B USA
; CURRENT APPLICATION NUMBER: US/09/791,524A
; PRIORITY FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: PCT/IB99/01524
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: US 60/098,028
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Adenovirus
US-09-791-524A-10

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Query Match 28.4%; Score 31; DB 2; Length 21;
 Best Local Similarity 45.5%; Pred. No. 2.2e+02;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNIHKYL 12
 :||| :|||
 Db 6 MPHSLNFSQYL 16

Search completed: January 26, 2006, 08:07:03
 Job time : 19.0201 secs

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 26, 2006, 08:04:12 ; Search time 61.75 Seconds
(without alignments)
128.563 Million cell updates/sec

Title: US-09-662-293-11

Perfect score: 109
Sequence: 1 DIHPPTNKKYLVCESYNG 19

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 389445

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA Main:*

1: /cgn2_6/ptodata/1/pubpaa/us07_PUBSCOMB.pep:.*
2: /cgn2_6/ptodata/1/pubpaa/us08_PUBSCOMB.pep:.*
3: /cgn2_6/ptodata/1/pubpaa/us09_PUBSCOMB.pep:.*
4: /cgn2_6/ptodata/1/pubpaa/us10_PUBSCOMB.pep:.*
5: /cgn2_6/ptodata/1/pubpaa/us10B_PUBSCOMB.pep:.*
6: /cgn2_6/ptodata/1/pubpaa/us11_PUBSCOMB.pep:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	109	100.0	19	4	US-10-218-743-11 Sequence 11, Appl
2	109	100.0	20	4	US-10-218-743-3 Sequence 3, Appl
3	37.5	34.4	20	3	US-09-864-761-38552 Sequence 36552, A
4	35	32.1	7	3	US-09-954-385-54 Sequence 54, Appl
5	35	32.1	7	5	US-10-912-512-54 Sequence 54, Appl
6	35	32.1	7	5	US-10-235-043-54 Sequence 54, Appl
7	35	32.1	20	3	US-09-964-201A-20 Sequence 20, Appl
8	35	32.1	20	4	US-10-681-389-20 Sequence 20, Appl
9	35	32.1	20	4	US-10-681-388-20 Sequence 20, Appl
10	33	30.3	21	4	US-10-062-710-50 Sequence 50, Appl
11	33	29.4	10	4	US-10-200-708-47 Sequence 47, Appl
12	32	29.4	10	4	US-10-200-708-95 Sequence 95, Appl
13	32	29.4	10	4	US-10-200-708-117 Sequence 117, Appl
14	32	29.4	10	4	US-10-200-708-119 Sequence 119, Appl
15	32	29.4	10	4	US-10-200-708-671 Sequence 671, Appl
16	32	29.4	14	4	US-10-417-895A-36 Sequence 36, Appl
17	32	29.4	14	5	US-10-808-187-2265 Sequence 2265, Ap
18	32	29.4	14	5	US-10-807-807-2265 Sequence 109, Ap
19	32	29.4	15	4	US-10-103-395-109 Sequence 19, Appl
20	32	29.4	16	4	US-10-063-710-19 Sequence 32, Appl
21	32	29.4	17	4	US-10-443-909-32 Sequence 9, Appl
22	32	29.4	20	4	US-10-285-649A-9 Sequence 128, Appl
23	32	29.4	20	6	US-11-008-653-128 Sequence 95, Appl
24	31.5	28.9	17	4	US-10-430-685-95 Sequence 51, Appl
25	31.5	28.9	21	3	US-09-962-756-51 Sequence 51, Appl
26	31.5	28.9	21	4	US-10-253-471-51 Sequence 51, Appl
27	31.5	28.9	21	4	US-10-253-493-51 Sequence 51, Appl

28	31	28.4	12	4	US-10-706-391-29 Sequence 29, Appl
29	31	28.4	15	3	US-09-791-524-3 Sequence 3, Appl
30	31	28.4	17	3	US-09-791-524-4 Sequence 4, Appl
31	31	28.4	17	4	US-10-609-217-196 Sequence 196, Appl
32	31	28.4	17	4	US-10-632-388-196 Sequence 196, Appl
33	31	28.4	17	4	US-10-651-723-196 Sequence 196, Appl
34	31	28.4	17	4	US-10-645-761-196 Sequence 196, Appl
35	31	28.4	17	4	US-10-666-666-196 Sequence 196, Appl
36	31	28.4	17	4	US-10-653-048-196 Sequence 196, Appl
37	31	28.4	17	4	US-10-756-289-1 Sequence 1, Appl
38	31	28.4	17	5	US-10-821-544-16 Sequence 16, Appl
39	31	28.4	17	5	US-10-645-784-196 Sequence 196, Appl
40	31	28.4	18	3	US-09-864-761-44227 Sequence 44227, A
41	31	28.4	20	3	US-09-791-524-9 Sequence 9, Appl
42	31	28.4	21	3	US-09-791-524-10 Sequence 10, Appl
43	31	28.4	9	4	US-10-182-252A-787 Sequence 787, Appl
44	30	27.5	9	4	US-10-182-252A-830 Sequence 830, Appl
45	30	27.5	10	3	US-09-765-086-58 Sequence 58, Appl
46	30	27.5	10	3	US-09-573-822C-160 Sequence 160, Appl
47	30	27.5	10	4	US-10-264-374-58 Sequence 58, Appl
48	30	27.5	10	4	US-10-375-992-58 Sequence 58, Appl
49	30	27.5	10	4	US-10-264-374-58 Sequence 58, Appl
50	30	27.5	10	4	US-10-375-992-58 Sequence 58, Appl
51	30	27.5	10	5	US-10-838-289-549 Sequence 549, Appl
52	30	27.5	15	5	US-10-946-647-769 Sequence 769, Appl
53	30	27.5	16	4	US-10-148-671-10 Sequence 10, Appl
54	30	27.5	20	5	US-10-776-013-463 Sequence 463, Appl
55	29.5	27.1	9	4	US-10-062-109A-123 Sequence 123, Appl
56	29.5	27.1	10	4	US-10-005-480A-123 Sequence 123, Appl
57	29.5	27.1	10	4	US-10-062-109A-164 Sequence 164, Appl
58	29.5	27.1	10	4	US-10-005-480A-164 Sequence 164, Appl
59	29.5	27.1	17	5	US-10-485-788-89 Sequence 89, Appl
60	29	26.6	8	4	US-10-285-354-408 Sequence 408, Appl
61	29	26.6	9	3	US-09-826-290-41 Sequence 41, Appl
62	29	26.6	9	3	US-09-791-393-7 Sequence 7, Appl
63	29	26.6	9	3	US-09-791-389-7 Sequence 7, Appl
64	29	26.6	9	4	US-10-264-309-239 Sequence 239, Appl
65	29	26.6	9	4	US-10-182-252A-232 Sequence 232, Appl
66	29	26.6	9	4	US-10-182-252A-759 Sequence 759, Appl
67	29	26.6	9	4	US-10-182-252A-832 Sequence 832, Appl
68	29	26.6	9	4	US-10-182-252A-866 Sequence 866, Appl
69	29	26.6	9	5	US-10-264-309-239 Sequence 239, Appl
70	29	26.6	11	2	US-08-996-140-16 Sequence 16, Appl
71	29	26.6	11	4	US-10-159-351-80 Sequence 80, Appl
72	29	26.6	11	4	US-10-239-656-9 Sequence 9, Appl
73	29	26.6	11	5	US-10-879-994-59 Sequence 59, Appl
74	29	26.6	12	4	US-10-411-869A-36 Sequence 36, Appl
75	29	26.6	15	4	US-10-283-940-59 Sequence 59, Appl
76	29	26.6	15	6	US-11-022-454-59 Sequence 59, Appl
77	29	26.6	19	4	US-10-481-180-280 Sequence 280, Appl
78	29	26.6	20	3	US-09-466-035-84 Sequence 84, Appl
79	29	26.6	20	3	US-10-103-395-195 Sequence 195, Appl
80	29	26.6	20	4	US-10-225-567A-2221 Sequence 2221, A
81	29	26.6	20	4	US-10-029-386-33390 Sequence 33390, A
82	29	26.6	20	4	US-10-371-525-150 Sequence 150, Appl
83	29	26.6	20	4	US-10-371-089-150 Sequence 150, Appl
84	29	26.6	20	4	US-10-371-645-150 Sequence 150, Appl
85	29	26.6	20	4	US-10-371-260-150 Sequence 150, Appl
86	29	26.6	20	4	US-10-666-480-5 Sequence 5, Appl
87	29	26.6	20	4	US-10-732-962A-232 Sequence 232, Appl
88	29	26.6	20	4	US-10-481-180-283 Sequence 283, Appl
89	29	26.6	20	5	US-10-474-960A-403 Sequence 403, Appl
90	29	26.6	20	5	US-10-654-601-2566 Sequence 2566, Ap
91	29	26.6	20	6	US-11-127-702-5 Sequence 5, Appl
92	29	26.6	21	3	US-09-962-756-53 Sequence 53, Appl
93	29	26.6	21	3	US-09-962-756-56 Sequence 76, Appl
94	29	26.6	21	3	US-09-962-756-56 Sequence 76, Appl
95	29	26.6	21	4	US-10-253-471-53 Sequence 53, Appl
96	29	26.6	21	4	US-10-253-471-16 Sequence 76, Appl
97	29	26.6	21	4	US-10-253-471-510 Sequence 510, Appl
98	29	26.6	21	4	US-10-253-493-53 Sequence 53, Appl
99	29	26.6	21	4	US-10-253-493-76 Sequence 76, Appl
100	29	26.6	21	4	US-10-253-493-510 Sequence 510, Appl

ALIGNMENTS

RESULT 1
US-10-218-743-11

```

: Sequence 11, Application US/10218743
: Publication NO. US20030096779A1
: GENERAL INFORMATION:
: APPLICANT: McCall, Catherine A.
: APPLICANT: Hunter, Shirley Wu
: APPLICANT: Weber, Eric R.
: TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
: TITLE OF INVENTION: AND USES THEREOF
: FILE REFERENCE: AL-2-C3
: CURRENT APPLICATION NUMBER: US/10/218,743
: CURRENT FILING DATE: 2002-08-13
: PRIOR APPLICATION NUMBER: US/09/292,225
: PRIOR FILING DATE: 1999-04-15
: PRIOR APPLICATION NUMBER: 60/098,909
: PRIOR FILING DATE: 1998-09-02
: PRIOR APPLICATION NUMBER: 60/085,295
: PRIOR FILING DATE: 1998-05-13
: PRIOR APPLICATION NUMBER: 60/098,565
: PRIOR FILING DATE: 1998-04-17
: PRIOR APPLICATION NUMBER: 09/062,013
: PRIOR FILING DATE: 1998-04-17
: NUMBER OF SEQ ID NOS: 49
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 11
: LENGTH: 19
: TYPE: PRT
: ORGANISM: Dermatophagoides farinae
: US-10-218-743-11

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Query Match	100.0%;	Score 109;	DB 4;	Length 19;
Best Local Similarity	100.0%;	Pred. No. 1.1e-09;		
Matches 19; Conservative	0;	Mismatches	0;	Gaps 0;

Qy 1 DIPHTNHHKYLVCESVNG 19
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Db 1 DIPHTNHHKYLVCESVNG 19

RESULT 2
US-10-21

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1 Sequence 3 Application US/10218743
2 Publication No. US20030096779A1
3
4 GENERAL INFORMATION:
5
6 APPLICANT: McCall, Catherine A.
7 APPLICANT: Hunter, Shirley W.
8 APPLICANT: Weber, Eric R.
9
10 TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
11 TITLE OF INVENTION: AND USES THEREOF
12
13 FILE REFERENCE: AL-2-C3
14
15 CURRENT APPLICATION NUMBER: US/10/218,743
16
17 CURRENT FILING DATE: 2002-08-13
18
19 PRIOR APPLICATION NUMBER: US/09/292,225
20
21 PRIOR FILING DATE: 1999-04-15
22
23 PRIOR APPLICATION NUMBER: 60/098,909
24
25 PRIOR FILING DATE: 1998-09-02
26
27 PRIOR APPLICATION NUMBER: 60/085,295
28
29 PRIOR FILING DATE: 1998-05-13
30
31 PRIOR APPLICATION NUMBER: 60/098,565
32
33 PRIOR FILING DATE: 1998-04-17
34
35 PRIOR APPLICATION NUMBER: 09/062,013
36
37 PRIOR FILING DATE: 1998-04-17
38
39 NUMBER OF SEQ ID NOS: 49
40
41 SOFTWARE: PatentIn Ver. 2.0
42
43 SEQ ID NO 3
44
45 LENGTH: 20
46
47 TYPE: PRT
48
49
50

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ORGANISM: Dermatophagoides farinae
US-10-218-743-3

Query Match	100.0%;	Score 109;	DB 4;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 1.2e-09;		
Matches 19;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY 1 DIPHPTNIHKYLVCSVNG 19
|||||
Db 1 DIPHPTNIHKYLVCSVNG 19

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RESULT 3
US-09-864-761-38552
/ Sequence 38552, Application US/09864761
/ Patent No. US20020048763A1
GENERAL INFORMATION:
/ APPLICANT: Penn, Sharon G.
/ APPLICANT: Rank, David R.
/ APPLICANT: Hanzel, David K.
/ APPLICANT: Chen, Wensheng
/ TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
/ TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
/ FILE REFERENCE: Aecmics-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
/ SEQ ID NO 38552
/ LENGTH: 20
/ TYPE: prt
/ ORGANISM: Homo sapiens
/ FEATURE:
OTHER INFORMATION: MAP TO AC005099.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7

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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8
OTHER INFORMATION: SWISSPROT HIT: P53820, EVALU8 8.80e+00
US-09-864-761-38552

Query Match 34.4%; Score 37.5; DB 3; Length 20;
Best Local Similarity 42.9%; Pred. No. 1.2e+02;

Matches 6; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 2 IPHPTNIRKYLVC 15
:|:|:|:|:|:|:
Db 8 LPHH-HSHTHLLCQ 20

RESULT 4

US-09-954-385-54
Sequence 54, Application US/09954385
Publication No. US20030100467A1
GENERAL INFORMATION:
APPLICANT: Aehle, Wolfgang
APPLICANT: Baldwin, Toby L.
APPLICANT: Van Gastel, Franciscus J.C.
APPLICANT: Janssen, Giselle G.
APPLICANT: Murray, Christopher J.
APPLICANT: Wang, Huaming
APPLICANT: Minetzky, Deborah S.
TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
FILE REFERENCE: GC690
CURRENT APPLICATION NUMBER: US/09/954,385
CURRENT FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 433
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 54
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: binding peptide
US-09-954-385-54

Query Match 32.1%; Score 35; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PHPTNI 8
:|:|:|:|:|:|:
Db 1 PHPTNL 6

RESULT 5

US-10-912-512-54
Sequence 54, Application US/10912512
Publication No. US20050042684A1
GENERAL INFORMATION:
APPLICANT: Aehle, Wolfgang
APPLICANT: Baldwin, Toby L.
APPLICANT: Van Gastel, Franciscus J.C.
APPLICANT: Janssen, Giselle G.
APPLICANT: Murray, Christopher J.
APPLICANT: Wang, Huaming
APPLICANT: Minetzky, Deborah S.
TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
FILE REFERENCE: GC690
CURRENT APPLICATION NUMBER: US/10/912,512
CURRENT FILING DATE: 2004-08-05
PRIORITY APPLICATION NUMBER: US/09/954,385
PRIORITY FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 433

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 54

LENGTH: 7

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: binding peptide
US-10-912-512-54

Query Match 32.1%; Score 35; DB 5; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PHPTNI 8
:|:|:|:|:|:|:
Db 1 PHPTNL 6

RESULT 6

US-10-235-043-54
Sequence 54, Application US/10235043
Publication No. US20050058956A1
GENERAL INFORMATION:
APPLICANT: Aehle, Wolfgang
APPLICANT: Baldwin, Toby M.
APPLICANT: Van Gastel, Franciscus J.C.
APPLICANT: Janssen, Giselle G.
APPLICANT: Murray, Christopher J.
APPLICANT: Wang, Huaming
APPLICANT: Minetzky, Deborah S.
TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
FILE REFERENCE: GC690-2
CURRENT APPLICATION NUMBER: US/10/235,043
CURRENT FILING DATE: 2002-09-03
NUMBER OF SEQ ID NOS: 446
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 54
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: binding peptide
US-10-235-043-54

Query Match 32.1%; Score 35; DB 5; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PHPTNI 8
:|:|:|:|:|:|:
Db 1 PHPTNL 6

RESULT 7

US-09-964-201A-20
Sequence 20, Application US/09964201A
Publication No. US20030091575A1
GENERAL INFORMATION:
APPLICANT: Kenten, John H.
APPLICANT: Tramontano, Alfonso
APPLICANT: Pilon, April L.
APPLICANT: Lohnas, Gerald L.
APPLICANT: Roberts, Steven F.
TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM
FILE REFERENCE: U.S. Patent Application No. US20030091575A1
CURRENT APPLICATION NUMBER: US/09/964,201A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 20
LENGTH: 20
TYPE: PRT

ORGANISM: Homo sapiens
US-09-964-201A-20

Query Match 32.1%; Score 35; DB 3; Length 20;
Best Local Similarity 36.4%; Pred. No. 2.9e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 4 HPTNHHKYLVC 14
|| : ||:|
Db 7 HPQKVTKEMLC 17

RESULT 8

US-10-681-389-20
Sequence 20, Application US/10681389
Publication No. US20040115218A1
GENERAL INFORMATION:
APPLICANT: Kenten, John H
APPLICANT: Tramonano, Alfonso
APPLICANT: Pilon, April L
APPLICANT: Lohnas, Gerald L
APPLICANT: Roberts, Steven F
TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM
FILE REFERENCE: U.S. Patent Application No. 09/026,276
CURRENT FILING DATE: 2003-10-07
CURRENT APPLICATION NUMBER: US/10/681,389
PRIOR FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US/09/964,201A
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 20
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-681-389-20

Query Match 32.1%; Score 35; DB 4; Length 20;
Best Local Similarity 36.4%; Pred. No. 2.9e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 4 HPTNHHKYLVC 14
|| : ||:|
Db 7 HPQKVTKEMLC 17

RESULT 9

US-10-681-388-20
Sequence 20, Application US/10681388
Publication No. US20040170643A1
GENERAL INFORMATION:
APPLICANT: Kenten, John H
APPLICANT: Tramonano, Alfonso
APPLICANT: Pilon, April L
APPLICANT: Lohnas, Gerald L
APPLICANT: Roberts, Steven F
TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM
FILE REFERENCE: U.S. Patent Application No. 09/026,276
CURRENT FILING DATE: 2003-10-07
CURRENT APPLICATION NUMBER: US/10/681,388
PRIOR FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US/09/964,201
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 20
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-681-388-20

Query Match 32.1%; Score 35; DB 4; Length 20;
Best Local Similarity 36.4%; Pred. No. 2.9e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 4 HPTNHHKYLVC 14
|| : ||:|
Db 7 HPQKVTKEMLC 17

RESULT 10
US-10-062-710-50
Sequence 50, Application US/10062710
Publication No. US20030049253A1
GENERAL INFORMATION:
APPLICANT: Li, Frank Q.
APPLICANT: Chu, Yong-Liang
APPLICANT: Qiu, Jian-Tai
TITLE OF INVENTION: Polymeric Conjugates for Delivery of
TITLE OF INVENTION: MHC-Recognized Epitopes
TITLE OF INVENTION: Via Peptide Vaccines
FILE REFERENCE: 3781-001-27
CURRENT FILING DATE: 2002-02-05
CURRENT APPLICATION NUMBER: US/10/062,710
PRIOR FILING DATE: 2001-08-08
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 50
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HIV Helper-T Cell Epitopes
US-10-062-710-50

Query Match 30.3%; Score 33; DB 4; Length 21;
Best Local Similarity 57.1%; Pred. No. 6.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 PHPTNHH 9
|| : ||:|
Db 1 PHPVSLH 7

RESULT 11
US-10-200-708-47
Sequence 47, Application US/10200708
Publication No. US20030180314A1
GENERAL INFORMATION:
APPLICANT: Degroot, Anne S.
TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
FILE REFERENCE: 17999-001
CURRENT FILING DATE: 2002-07-22
CURRENT APPLICATION NUMBER: US/10/200,708
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: US/09/351,036
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: 60/092,346
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: 60/115,145
PRIOR FILING DATE: 1999-01-08
PRIOR APPLICATION NUMBER: 60/130,677
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 672
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 47
LENGTH: 10
TYPE: PRT
ORGANISM: Human immunodeficiency virus
US-10-200-708-47

Query Match 29.4%; Score 32; DB 4; Length 10;
Best Local Similarity 55.6%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 IPHPTNHHK 10
|| : ||:|
Db 1 IPHPAGLKK 9

RESULT 12
US-10-200-708-95
; Sequence 95, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 95
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-95

Query Match 29.4%; Score 32; DB 4; Length 10;
Best Local Similarity 55.6%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IPHPTNIHK 10
DB 2 IHPHAGLKK 10

RESULT 13
US-10-200-708-117
; Sequence 117, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 117
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-117

Query Match 29.4%; Score 32; DB 4; Length 10;
Best Local Similarity 55.6%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IPHPTNIHK 10
DB 2 IHPHAGLKK 10

RESULT 14

US-10-200-708-119
; Sequence 119, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 119
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-119

Query Match 29.4%; Score 32; DB 4; Length 10;
Best Local Similarity 55.6%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IPHPTNIHK 10
DB 1 IHPHAGLKK 9

RESULT 15
US-10-200-708-671
; Sequence 671, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 671
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-671

Query Match 29.4%; Score 32; DB 4; Length 10;
Best Local Similarity 55.6%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IPHPTNIHK 10
DB 2 IHPHAGLKK 10

RESULT 16
US-10-417-895A-36
; Sequence 36, Application US/10417895A
; Publication No. US20040033569A1

```
GENERAL INFORMATION:
APPLICANT: Crea, Roberto
TITLE OF INVENTION: "DOPING" IN WALK-THROUGH MUTAGENESIS
FILE REFERENCE: 1551.2002-001
CURRENT APPLICATION NUMBER: US/10/417,895A
PRIOR FILING DATE: 2003-04-16
PRIOR APPLICATION NUMBER: 60/373,686
PRIOR FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 36
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: variant peptide for second complementarity
OTHER INFORMATION: determining region of Fv region of an
OTHER INFORMATION: immunoglobulin
US-10-417-895A-36
```

```
Query Match      29.4%; Score 32; DB 4; Length 14;
Best Local Similarity 55.6%; Pred. No. 5.8e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
Oy      4 HPTNIHKL 12
Db      4 HPTIGHDIV 12
```

RESULT 17

```
US-10-808-187-2265
Sequence 2265, Application US/10808187
Publication No. US2005009009A1
```

GENERAL INFORMATION:

```
APPLICANT: PEIRIS, JOSEPH S. M.
APPLICANT: YUEN, KWOK YUNG
APPLICANT: POON, LIT MAN
APPLICANT: GUAN, YI
APPLICANT: CHAN, KWOK HUNG
APPLICANT: NICHOLLS, JOHN
TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
FILE REFERENCE: V9661.0078
CURRENT APPLICATION NUMBER: US/10/808,187
CURRENT FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 60/457,031
PRIOR FILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: 60/457,730
PRIOR FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: 60/459,931
PRIOR FILING DATE: 2003-04-02
PRIOR APPLICATION NUMBER: 60/460,357
PRIOR FILING DATE: 2003-04-03
PRIOR APPLICATION NUMBER: 60/461,265
PRIOR FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: 60/462,805
PRIOR FILING DATE: 2003-04-14
PRIOR APPLICATION NUMBER: 60/468,139
PRIOR FILING DATE: 2003-05-05
PRIOR APPLICATION NUMBER: 60/464,886
PRIOR FILING DATE: 2003-04-23
PRIOR APPLICATION NUMBER: 60/471,200
PRIOR FILING DATE: 2003-05-16
NUMBER OF SEQ ID NOS: 2476
SOFTWARE: PatentIn ver. 3.2
SEQ ID NO 2265
```

```
LENGTH: 14
TYPE: PRT
```

```
ORGANISM: Human severe acute respiratory system virus
US-10-808-187-2265
```

```
Query Match      29.4%; Score 32; DB 5; Length 14;
```

```
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy      4 HPTNIH 9
Db      9 HPTTIH 14
```

RESULT 18

```
US-10-807-807-2265
Sequence 2265, Application US/10807807
Publication No. US20050181357A1
```

GENERAL INFORMATION:

```
APPLICANT: LEUNG, FREDERICK C.
APPLICANT: PEIRIS, JOSEPH S. M.
APPLICANT: YUEN, KWOK YUNG
APPLICANT: POON, LIT MAN
APPLICANT: GUAN, YI
APPLICANT: CHAN, KWOK HUNG
APPLICANT: NICHOLLS, JOHN M.
TITLE OF INVENTION: A HIGH-THROUGHPUT DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS
FILE REFERENCE: V9661.0077
CURRENT APPLICATION NUMBER: US/10/807,807
CURRENT FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 60/457,031
PRIOR FILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: 60/457,730
PRIOR FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: 60/459,931
PRIOR FILING DATE: 2003-04-02
PRIOR APPLICATION NUMBER: 60/460,357
PRIOR FILING DATE: 2003-04-03
PRIOR APPLICATION NUMBER: 60/461,265
PRIOR FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: 60/462,805
PRIOR FILING DATE: 2003-04-14
PRIOR APPLICATION NUMBER: 60/464,886
PRIOR FILING DATE: 2003-04-23
PRIOR APPLICATION NUMBER: 60/465,738
PRIOR FILING DATE: 2003-04-25
PRIOR APPLICATION NUMBER: 60/470,935
PRIOR FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 2487
SOFTWARE: PatentIn ver. 3.2
SEQ ID NO 2265
```

```
LENGTH: 14
TYPE: PRT
```

```
ORGANISM: Human severe acute respiratory system virus
US-10-807-807-2265
```

```
Query Match      29.4%; Score 32; DB 5; Length 14;
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy      4 HPTNIH 9
Db      9 HPTTIH 14
```

RESULT 19

```
US-10-103-395-109
Sequence 109, Application US/10103395
Publication No. US20020160019A1
```

GENERAL INFORMATION:

```
APPLICANT: EPIMUNE, Inc.
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
TITLE OF INVENTION: IDENTIFICATION OF BROADLY REACTIVE DR
FILE REFERENCE: 39963-20016.01
CURRENT APPLICATION NUMBER: US/10/103,395
```

```
Query Match      29.4%; Score 32; DB 5; Length 14;
```

```

; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 09/009,953
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: PCT/US98/01373
; PRIOR FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: US 60/036,713
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 60/037,432
; PRIOR FILING DATE: 1997-02-07
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-103-395-109

Query Match      29.4%; Score 32; DB 4; Length 15;
Best Local Similarity 55.6%; Pred. No. 6.3e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 IPHPTNTHK 10
Db      6 IPHPAGLKK 14

RESULT 20
US-10-062-710-19
; Sequence 19, Application US/10062710
; Publication No. US20030049253A1
; GENERAL INFORMATION:
; APPLICANT: Li, Frank O.
; APPLICANT: Chu, Yong-Liang
; APPLICANT: Qiu, Jian-Tai
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of
; TITLE OF INVENTION: MHC-Recognized Epitopes
; FILE REFERENCE: 3781-001-27
; CURRENT APPLICATION NUMBER: US/10/062,710
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/310,498
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV Helper-T Cell Epitopes
US-10-062-710-19

Query Match      29.4%; Score 32; DB 4; Length 16;
Best Local Similarity 55.6%; Pred. No. 6.7e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 IPHPTNTHK 10
Db      8 IPHPAGLKK 16

RESULT 21
US-10-442-909-32
; Sequence 32, Application US/10442909
; Publication No. US20040001845A1
; GENERAL INFORMATION:
; APPLICANT: Alfeld, Marcus
; APPLICANT: Yu, Xu
; APPLICANT: Walker, Bruce
; APPLICANT: Adoo, Marylyn
; TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of HIV-1 Virus
; FILE REFERENCE: 24028-010
; CURRENT APPLICATION NUMBER: US/10/442,909
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```

; CURRENT FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: 60/382,120
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 32
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-442-909-32

Query Match      29.4%; Score 32; DB 4; Length 17;
Best Local Similarity 55.6%; Pred. No. 7.2e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 IPHPTNTHK 10
Db      8 IPHPAGLKK 16

RESULT 22
US-10-285-649A-9
; Sequence 9, Application US/10285649A
; Publication No. US20030106089A1
; GENERAL INFORMATION:
; APPLICANT: McBride, Kevin
; APPLICANT: Stalker, David M.
; APPLICANT: Pear, Julie
; APPLICANT: Perez-Grau, Luis
; TITLE OF INVENTION: COTTON FIBER TRANSCRIPTIONAL FACTORS
; FILE REFERENCE: 15615/03/US
; CURRENT APPLICATION NUMBER: US/10/285,649A
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 08/984,099
; PRIOR FILING DATE: 1997-12-03
; PRIOR APPLICATION NUMBER: PCT/US96/09897
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,178
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: IBM PC; Windows 2000; Microsoft Word 2000
; SEQ ID NO 9
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Goseyplum Hirsutum
US-10-285-649A-9

Query Match      29.4%; Score 32; DB 4; Length 20;
Best Local Similarity 42.9%; Pred. No. 8.5e+02;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY      2 IPHPTNTHKYLVC 15
Db      6 LPPTTFHKKCTSD 19

RESULT 23
US-11-008-653-128
; Sequence 128, Application US/11008653
; Publication No. US20050175627A1
; GENERAL INFORMATION:
; APPLICANT: Schneider, Joerg
; TITLE OF INVENTION: HIV Pharmacies
; FILE REFERENCE: 3742.1001-000
; CURRENT APPLICATION NUMBER: US/11/008,653
; CURRENT FILING DATE: 2004-12-09
; PRIOR APPLICATION NUMBER: PCT/GB2004/004038
; PRIOR FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: GB 0325011.5
; PRIOR FILING DATE: 2003-10-27
; PRIOR APPLICATION NUMBER: GB 0322637.0
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: GB 0322402.9
```

; PRIOR FILING DATE: 2003-09-24
 ; NUMBER OF SEQ ID NOS: 174
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 128
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: peptide from pol pool 2
 US-11-008-653-128

Query Match 29.4%; Score 32; DB 6; Length 20;
 Best Local Similarity 55.6%; Pred. No. 8.5e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPPTNIHK 10
 Db 5 IHPAGLKK 13

RESULT 24
 US-10-430-685-95
 ; Sequence 95, Application US/10430685
 ; Publication No. US20040039543A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KECK, Peter
 ; TITLE OF INVENTION: COMPUTER METHOD AND APPARATUS FOR CLASSIFYING OBJECTS
 ; FILE REFERENCE: 63040-010210
 ; CURRENT APPLICATION NUMBER: US/10/430,685
 ; PRIOR FILING DATE: 2003-05-06
 ; PRIOR APPLICATION NUMBER: PCT/US01/44000
 ; PRIOR FILING DATE: 2001-11-06
 ; PRIOR APPLICATION NUMBER: 60/246,196
 ; NUMBER OF SEQ ID NOS: 240
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 95
 ; LENGTH: 17
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-430-685-95

Query Match 28.9%; Score 31.5; DB 4; Length 17;
 Best Local Similarity 66.7%; Pred. No. 8.5e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 4 HPTNIHXYL 12
 Db 1 HPTN-HAYI 8

RESULT 25
 US-09-962-756-51
 ; Sequence 51, Application US/09962756
 ; Publication No. US20030195147A1
 ; GENERAL INFORMATION:
 ; APPLICANT: PILUTTLA, RENKA
 ; APPLICANT: BRISSETTE, RENEE
 ; APPLICANT: BLUME, ARTHUR J.
 ; APPLICANT: SCHAFER, LAUGE
 ; APPLICANT: BRANDT, JAKOB
 ; APPLICANT: GOLDSTEIN, NEIL I.
 ; APPLICANT: SPETZLER, JANE
 ; APPLICANT: OSTERGAARD, SOREN
 ; APPLICANT: HANSEN, PER HERTZ
 ; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
 ; FILE REFERENCE: 1878-4051US1
 ; CURRENT APPLICATION NUMBER: US/09/962,756
 ; PRIOR FILING DATE: 2001-09-24
 ; PRIOR APPLICATION NUMBER: 09/538,038
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: 09/146,127
 ; PRIOR FILING DATE: 1998-09-02

; NUMBER OF SEQ ID NOS: 2227
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 51
 ; LENGTH: 21
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-09-962-756-51

Query Match 28.9%; Score 31.5; DB 3; Length 21;
 Best Local Similarity 37.5%; Pred. No. 1.1e+03;
 Matches 6; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

QY 3 PHPTNIHXYLVCEVSN 18
 Db 7 PHGSNFYDFV-EAIN 21

Search completed: January 26, 2006, 08:38:39
 Job time : 63.75 secs

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OM protein - protein search, using sw model

Run on: January 26, 2006, 08:05:12 ; Search time 3.60345 Seconds
(without alignments)
57.099 Million cell updates/sec

Title: US-09-662-293-11

Perfect score: 109
Sequence: 1 DIPHTNHHKLVCEVSNG 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 37628

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

Published Applications AA New:*
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7: /cgn2_6/ptcodata/1/pubppaa/US13_NEW_PUB.pep:*
8: /cgn2_6/ptcodata/1/pubppaa/US14_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	29.4	10	7	US-11-045-024-1294
2	32	29.4	10	7	US-11-045-024-10214
3	32	29.4	10	7	US-11-045-024-12085
4	32	29.4	11	7	US-11-045-024-3376
5	32	29.4	11	7	US-11-045-024-10191
6	32	29.4	11	7	US-11-045-024-10215
7	32	29.4	11	7	US-11-045-024-12063
8	32	29.4	11	7	US-11-045-024-12086
9	32	29.4	11	7	US-11-045-024-13140
10	31	28.4	16	7	US-11-038-980-3
11	31	28.4	17	7	US-11-038-980-4
12	31	28.4	20	7	US-11-038-980-9
13	31	28.4	21	7	US-11-038-980-10
14	29.5	27.1	9	6	US-10-859-643-123
15	29.5	27.1	9	7	US-11-097-864-123
16	29.5	27.1	9	7	US-11-097-912-123
17	29.5	27.1	10	6	US-10-859-643-164
18	29.5	27.1	10	6	US-11-097-864-164
19	29.5	27.1	10	7	US-11-097-912-164
20	29.5	26.6	13	6	US-10-966-483-17
21	29.5	26.6	14	7	US-11-166-412-88
22	29.5	26.6	17	6	US-10-506-443A-18
23	29.5	26.6	20	6	US-10-723-207-71
24	28	25.7	8	7	US-11-045-024-1627
25	28	25.7	8	7	US-11-045-024-4340

26	28	25.7	9	7	US-11-045-024-1222	Sequence 3322, Ap
27	28	25.7	9	7	US-11-045-024-10229	Sequence 10229, A
28	28	25.7	9	7	US-11-045-024-12094	Sequence 12094, A
29	28	25.7	9	7	US-11-045-024-13796	Sequence 13796, A
30	28	25.7	10	7	US-11-045-024-2073	Sequence 2073, Ap
31	28	25.7	10	7	US-11-045-024-4608	Sequence 4608, Ap
32	28	25.7	10	7	US-11-045-024-10231	Sequence 10231, A
33	28	25.7	10	7	US-11-045-024-12095	Sequence 12095, A
34	28	25.7	11	7	US-11-045-024-2288	Sequence 2288, Ap
35	28	25.7	11	7	US-11-045-024-3375	Sequence 3375, Ap
36	28	25.7	11	7	US-11-045-024-10232	Sequence 10232, A
37	28	25.7	11	7	US-11-045-024-12096	Sequence 12096, A
38	28	25.7	15	7	US-11-045-024-13150	Sequence 13150, A
39	28	25.7	16	6	US-10-967-671-10	Sequence 10, Appl
40	27	24.8	13	7	US-11-033-039-792	Sequence 792, App
41	27	24.8	14	7	US-11-152-366-236	Sequence 236, App
42	27	24.8	19	6	US-10-880-238-115	Sequence 115, App
43	27	24.8	19	7	US-11-033-039-794	Sequence 794, App
44	26.5	24.3	18	7	US-11-119-581-113	Sequence 113, App
45	26	23.9	5	6	US-10-986-755A-55	Sequence 55, Appl
46	26	23.9	5	6	US-10-956-755A-73	Sequence 73, Appl
47	26	23.9	5	6	US-10-956-755A-91	Sequence 91, Appl
48	26	23.9	8	7	US-11-045-024-1626	Sequence 1626, Ap
49	26	23.9	8	7	US-11-045-024-10228	Sequence 10228, A
50	26	23.9	9	6	US-10-859-643-17	Sequence 17, Appl
51	26	23.9	9	7	US-11-097-864-17	Sequence 17, Appl
52	26	23.9	9	7	US-11-097-912-17	Sequence 17, Appl
53	26	23.9	9	7	US-11-045-024-1831	Sequence 1831, Appl
54	26	23.9	9	7	US-11-045-024-13806	Sequence 13806, A
55	26	23.9	9	7	US-11-041-893-64	Sequence 64, Appl
56	26	23.9	10	6	US-10-859-643-53	Sequence 53, Appl
57	26	23.9	10	7	US-11-097-912-53	Sequence 53, Appl
58	26	23.9	10	7	US-11-097-912-53	Sequence 53, Appl
59	26	23.9	10	7	US-11-045-024-1072	Sequence 1072, A
60	26	23.9	10	7	US-11-045-024-10220	Sequence 10220, A
61	26	23.9	13	6	US-10-511-559-126	Sequence 126, App
62	26	23.9	13	6	US-10-511-559-127	Sequence 127, App
63	26	23.9	13	6	US-10-511-559-128	Sequence 128, App
64	26	23.9	13	6	US-10-511-559-129	Sequence 129, App
65	26	23.9	13	7	US-11-116-144-64	Sequence 64, Appl
66	26	23.9	15	7	US-11-045-024-13137	Sequence 13137, A
67	26	23.9	20	6	US-10-623-155-247	Sequence 247, App
68	26	23.9	6	7	US-11-084-117-55	Sequence 55, Appl
69	25	22.9	9	7	US-11-010-748A-86	Sequence 86, App
70	25	22.9	9	7	US-11-010-748A-86	Sequence 86, App
71	25	22.9	9	7	US-11-010-748A-86	Sequence 86, App
72	25	22.9	9	7	US-11-010-748A-86	Sequence 86, App
73	25	22.9	9	7	US-11-010-748A-86	Sequence 86, App
74	25	22.9	9	7	US-11-010-748A-86	Sequence 86, App
75	25	22.9	9	7	US-11-010-748A-86	Sequence 86, App
76	25	22.9	9	7	US-11-010-748A-86	Sequence 86, App
77	25	22.9	17	7	US-11-010-748A-85	Sequence 85, App
78	25	22.9	18	7	US-11-033-039-1223	Sequence 1223, App
79	25	22.9	20	6	US-10-485-788A-580	Sequence 580, App
80	25	22.9	20	7	US-11-022-562-141	Sequence 141, App
81	25	22.9	20	7	US-11-022-562-142	Sequence 142, App
82	25	22.9	8	7	US-11-064-416-4	Sequence 4, Appl
83	25	22.9	8	7	US-11-064-416-5	Sequence 5, Appl
84	24	22.0	9	6	US-10-966-483-14	Sequence 14, Appl
85	24	22.0	10	6	US-10-614-599-26	Sequence 26, Appl
86	24	22.0	12	6	US-10-966-371-7	Sequence 7, Appl
87	24	22.0	12	7	US-11-180-897-5	Sequence 5, Appl
88	24	22.0	12	7	US-11-180-997-19	Sequence 19, Appl
89	24	22.0	14	6	US-10-939-890-44	Sequence 44, Appl
90	24	22.0	16	7	US-11-033-039-1428	Sequence 1428, Ap
91	24	22.0	17	7	US-11-033-039-1427	Sequence 1427, Ap
92	24	22.0	17	7	US-11-041-893-132	Sequence 132, App
93	24	22.0	17	7	US-11-033-039-1426	Sequence 1426, Ap
94	24	22.0	19	7	US-11-033-039-1425	Sequence 1425, Ap
95	24	22.0	20	6	US-10-623-155-514	Sequence 514, App
96	24	22.0	20	7	US-11-022-562-173	Sequence 173, App
97	24	22.0	20	7	US-11-033-039-1424	Sequence 1424, Ap
98	24	22.0	21	7	US-11-033-039-1423	Sequence 1423, Ap

99 23 21.1 7 7 US-11-226-701-28 Sequence 28, Appl
100 23 21.1 8 7 US-11-140-417-18 Sequence 18, Appl

ALIGNMENTS

RESULT 1

US-11-045-024-3294
Sequence 3294, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Celis, Esteban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
FILE REFERENCE: 2060.0040007
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US/11/045,024
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3294
LENGTH: 10
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3294

Query Match 29.4%; Score 32; DB 7; Length 10;

Best Local Similarity 55.6%; Pred. No. 11;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IPHPTNIHK 10
Db 2 IPHPAGLKK 10

RESULT 2

US-11-045-024-10214
Sequence 10214, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Celis, Esteban
APPLICANT: Kubo, Ralph

APPLICANT: Grey, Howard M.

APPLICANT: EpiImmune Inc.

TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
FILE REFERENCE: 2060.0040007

TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions

FILE REFERENCE: 2060.0040007

CURRENT FILING DATE: 2005-01-28

PRIOR APPLICATION NUMBER: US/11/045,024

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: US 08/412,863

PRIOR FILING DATE: 1993-03-05

PRIOR APPLICATION NUMBER: US 08/073,205

PRIOR FILING DATE: 1993-06-04

PRIOR APPLICATION NUMBER: US 08/103,396

PRIOR FILING DATE: 1993-08-06

PRIOR APPLICATION NUMBER: US 08/159,184

PRIOR FILING DATE: 1993-11-29

PRIOR APPLICATION NUMBER: US 08/159,339

PRIOR FILING DATE: 1993-11-29

PRIOR APPLICATION NUMBER: US 08/205,713

PRIOR FILING DATE: 1994-03-04

PRIOR APPLICATION NUMBER: US 08/347,610

PRIOR FILING DATE: 1994-12-01

NUMBER OF SEQ ID NOS: 14528

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 10214

LENGTH: 10

TYPE: PRT

ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS

US-11-045-024-10214

Query Match 29.4%; Score 32; DB 7; Length 10;

Best Local Similarity 55.6%; Pred. No. 11;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IPHPTNIHK 10
Db 2 IPHPAGLKK 10

RESULT 3

US-11-045-024-12085
Sequence 12085, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Celis, Esteban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
FILE REFERENCE: 2060.0040007
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US/11/045,024
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713

PRIOR FILING DATE: 1994-03-04
 PRIOR APPLICATION NUMBER: US 08/347,610
 PRIOR FILING DATE: 1994-12-01
 NUMBER OF SEQ ID NOS: 14528
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 12085
 LENGTH: 10
 TYPE: PRT
 ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
 US-11-045-024-12085

Query Match 29.4%; Score 32; DB 7; Length 10;
 Best Local Similarity 55.6%; Pred. No. 11;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 IPHPTNKH 10
 Db 2 IPHPAGLKK 10

RESULT 4
 US-11-045-024-3376
 Sequence 3376, Application US/11045024
 Publication No. US20050271676A1
 GENERAL INFORMATION:
 APPLICANT: Sette, Alessandro
 APPLICANT: Sidney, John
 APPLICANT: Southwood, Scott
 APPLICANT: Livingston, Brian
 APPLICANT: Chesnut, Robert
 APPLICANT: Baker, Denise Marie
 APPLICANT: Celis, Esceban
 APPLICANT: Kubo, Ralph
 APPLICANT: Grey, Howard M.
 APPLICANT: EpiImmune Inc.
 TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
 TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
 FILE REFERENCE: 2060.0040007
 CURRENT APPLICATION NUMBER: US/11/045,024
 CURRENT FILING DATE: 2005-01-28
 PRIOR APPLICATION NUMBER: US 09/412,863
 PRIOR FILING DATE: 1999-10-05
 PRIOR APPLICATION NUMBER: US 08/027,146
 PRIOR FILING DATE: 1993-03-05
 PRIOR APPLICATION NUMBER: US 08/073,205
 PRIOR FILING DATE: 1993-06-04
 PRIOR APPLICATION NUMBER: US 08/103,396
 PRIOR FILING DATE: 1993-08-06
 PRIOR APPLICATION NUMBER: US 08/159,184
 PRIOR FILING DATE: 1993-11-29
 PRIOR APPLICATION NUMBER: US 08/159,339
 PRIOR FILING DATE: 1993-11-29
 PRIOR APPLICATION NUMBER: US 08/205,713
 PRIOR FILING DATE: 1994-03-04
 PRIOR APPLICATION NUMBER: US 08/347,610
 PRIOR FILING DATE: 1994-12-01
 NUMBER OF SEQ ID NOS: 14528
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 3376
 LENGTH: 11
 TYPE: PRT
 ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
 US-11-045-024-3376

Query Match 29.4%; Score 32; DB 7; Length 11;
 Best Local Similarity 55.6%; Pred. No. 13;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 IPHPTNKH 10
 Db 2 IPHPAGLKK 10

RESULT 5
 US-11-045-024-10191
 Sequence 10191, Application US/11045024
 Publication No. US20050271676A1
 GENERAL INFORMATION:
 APPLICANT: Sette, Alessandro
 APPLICANT: Sidney, John
 APPLICANT: Southwood, Scott
 APPLICANT: Livingston, Brian
 APPLICANT: Chesnut, Robert
 APPLICANT: Baker, Denise Marie
 APPLICANT: Celis, Esceban
 APPLICANT: Kubo, Ralph
 APPLICANT: Grey, Howard M.
 APPLICANT: EpiImmune Inc.
 TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
 TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
 FILE REFERENCE: 2060.0040007
 CURRENT APPLICATION NUMBER: US/11/045,024
 CURRENT FILING DATE: 2005-01-28
 PRIOR APPLICATION NUMBER: US 09/412,863
 PRIOR FILING DATE: 1999-10-05
 PRIOR APPLICATION NUMBER: US 08/027,146
 PRIOR FILING DATE: 1993-03-05
 PRIOR APPLICATION NUMBER: US 08/073,205
 PRIOR FILING DATE: 1993-06-04
 PRIOR APPLICATION NUMBER: US 08/103,396
 PRIOR FILING DATE: 1993-08-06
 PRIOR APPLICATION NUMBER: US 08/159,184
 PRIOR FILING DATE: 1993-11-29
 PRIOR APPLICATION NUMBER: US 08/159,339
 PRIOR FILING DATE: 1993-11-29
 PRIOR APPLICATION NUMBER: US 08/205,713
 PRIOR FILING DATE: 1994-03-04
 PRIOR APPLICATION NUMBER: US 08/347,610
 PRIOR FILING DATE: 1994-12-01
 NUMBER OF SEQ ID NOS: 14528
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 10191
 LENGTH: 11
 TYPE: PRT
 ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
 US-11-045-024-10191

Query Match 29.4%; Score 32; DB 7; Length 11;
 Best Local Similarity 55.6%; Pred. No. 13;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 IPHPTNKH 10
 Db 2 IPHPAGLKK 10

RESULT 6
 US-11-045-024-10215
 Sequence 10215, Application US/11045024
 Publication No. US20050271676A1
 GENERAL INFORMATION:
 APPLICANT: Sette, Alessandro
 APPLICANT: Sidney, John
 APPLICANT: Southwood, Scott
 APPLICANT: Livingston, Brian
 APPLICANT: Chesnut, Robert
 APPLICANT: Baker, Denise Marie
 APPLICANT: Celis, Esceban
 APPLICANT: Kubo, Ralph
 APPLICANT: Grey, Howard M.
 APPLICANT: EpiImmune Inc.
 TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
 TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
 FILE REFERENCE: 2060.0040007
 CURRENT APPLICATION NUMBER: US/11/045,024
 CURRENT FILING DATE: 2005-01-28

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; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12063
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10215
; LENGTH: 11
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-10215

Query Match          29.4%; Score 32; DB 7; Length 11;
Best Local Similarity 55.6%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy      2 IPHPTNIHK 10
        ||||| : |
Db      3 IPHPAGLKK 11

RESULT 7
US-11-045-024-12063
; Sequence 12063, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12063
; LENGTH: 11
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; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12063
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12086
; LENGTH: 11
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12086

Query Match          29.4%; Score 32; DB 7; Length 11;
Best Local Similarity 55.6%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy      2 IPHPTNIHK 10
        ||||| : |
Db      3 IPHPAGLKK 11

RESULT 8
US-11-045-024-12086
; Sequence 12086, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12086
; LENGTH: 11
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13140
; Sequence 13140, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
```

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APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Cells, Eteben
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
PRIOR FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13140
LENGTH: 15
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13140

Query Match      29.4%; Score 32; DB 7; Length 15;
Best Local Similarity 55.6%; Pred. No. 17;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      2 IPHPTNIHX 10
Db      6 IPHAGLKK 14

RESULT 10
US-11-038-980-3
Sequence 3, Application US/11038980
Publication No. US2006002893A1
GENERAL INFORMATION:
APPLICANT: Centellon SAS
APPLICANT: Emmanuelle Vigne
APPLICANT: Jean-Francois Dedieu
APPLICANT: Martine Latta
APPLICANT: Patrice Yeh
APPLICANT: Michel Perricaudet
TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
FILE REFERENCE: P26,992-C USA
CURRENT APPLICATION NUMBER: US/11/038,980
PRIOR FILING DATE: 2005-01-20
PRIOR APPLICATION NUMBER: US 09/791,524
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/IB99/01524
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: US 60/098,028
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 16
TYPE: PRT
ORGANISM: Adenovirus
```

```
US-11-038-980-3

Query Match      28.4%; Score 31; DB 7; Length 16;
Best Local Similarity 45.5%; Pred. No. 27;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      2 IPHPTNIHX 12
Db      4 MPHSLNFSQYL 14

RESULT 11
US-11-038-980-4
Sequence 4, Application US/11038980
Publication No. US2006002893A1
GENERAL INFORMATION:
APPLICANT: Centellon SAS
APPLICANT: Emmanuelle Vigne
APPLICANT: Jean-Francois Dedieu
APPLICANT: Martine Latta
APPLICANT: Patrice Yeh
APPLICANT: Michel Perricaudet
TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
FILE REFERENCE: P26,992-C USA
CURRENT APPLICATION NUMBER: US/11/038,980
PRIOR FILING DATE: 2005-01-20
PRIOR APPLICATION NUMBER: US 09/791,524
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/IB99/01524
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: US 60/098,028
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 17
TYPE: PRT
ORGANISM: Adenovirus
US-11-038-980-4

Query Match      28.4%; Score 31; DB 7; Length 17;
Best Local Similarity 45.5%; Pred. No. 29;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      2 IPHPTNIHX 12
Db      4 MPHSLNFSQYL 14

RESULT 12
US-11-038-980-9
Sequence 9, Application US/11038980
Publication No. US2006002893A1
GENERAL INFORMATION:
APPLICANT: Centellon SAS
APPLICANT: Emmanuelle Vigne
APPLICANT: Jean-Francois Dedieu
APPLICANT: Martine Latta
APPLICANT: Patrice Yeh
APPLICANT: Michel Perricaudet
TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
FILE REFERENCE: P26,992-C USA
CURRENT APPLICATION NUMBER: US/11/038,980
PRIOR FILING DATE: 2005-01-20
PRIOR APPLICATION NUMBER: US 09/791,524
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/IB99/01524
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: US 60/098,028
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PatentIn version 3.2
SEQ ID NO 9
```

LENGTH: 20
TYPE: PRT
ORGANISM: Adenovirus
US-11-038-980-9

Query Match 28.4%; Score 31; DB 7; Length 20;
Best Local Similarity 45.5%; Pred. No. 34;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNTHKYL 12
: || | : ||
Db 6 MPHSLNFSQYL 16

RESULT 13
US-11-038-980-10
Sequence 10, Application US/11038980
Publication No. US20060002893A1
GENERAL INFORMATION:
APPLICANT: Centellion SAS
APPLICANT: Emmanuelle Vigne
APPLICANT: Jean-Francois Dedieu
APPLICANT: Martine Latta
APPLICANT: Patrice Yeh
APPLICANT: Michel Perriacaudet
TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
FILE REFERENCE: P26,992-C USA
CURRENT APPLICATION NUMBER: US/11/038,980
PRIOR FILING DATE: 2005-01-20
PRIOR APPLICATION NUMBER: US 09/791,524
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCP/IB99/01524
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: US 60/098,028
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PatentIn version 3.2
SEQ ID NO 10
LENGTH: 21
TYPE: PRT
ORGANISM: Adenovirus
US-11-038-980-10

Query Match 28.4%; Score 31; DB 7; Length 21;
Best Local Similarity 45.5%; Pred. No. 35;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNTHKYL 12
: || | : ||
Db 6 MPHSLNFSQYL 16

RESULT 14
US-10-859-643-123
Sequence 123, Application US/10859643
Publication No. US20060002993A1
GENERAL INFORMATION:
APPLICANT: Chailita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
FILE REFERENCE: 511582006203
CURRENT APPLICATION NUMBER: US/10/859,643
PRIOR FILING DATE: 2004-06-02
PRIOR APPLICATION NUMBER: US 10/005,480
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 765
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 123
LENGTH: 9
TYPE: PRT
ORGANISM: Homo Sapien
US-10-859-643-123

Query Match 27.1%; Score 29.5; DB 6; Length 9;
Best Local Similarity 75.0%; Pred. No. 5.9e+04;
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 2 IPH-PTNI 8
|| | : || :
Db 2 IPHRPTNV 9

RESULT 15
US-11-097-864-123
Sequence 123, Application US/11097864
Publication No. US20050265924A1
GENERAL INFORMATION:
APPLICANT: Chailita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 511582006205
CURRENT APPLICATION NUMBER: US/11/097,864
PRIOR FILING DATE: 2005-04-01
PRIOR APPLICATION NUMBER: US 10/062,109
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 10/005,480
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 765
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 123
LENGTH: 9
TYPE: PRT
ORGANISM: Homo Sapien
US-11-097-864-123

Query Match 27.1%; Score 29.5; DB 7; Length 9;
Best Local Similarity 75.0%; Pred. No. 5.9e+04;
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 2 IPH-PTNI 8
|| | : || :
Db 2 IPHRPTNV 9

RESULT 16
US-11-097-912-123
Sequence 123, Application US/11097912
Publication No. US20050265921A1
GENERAL INFORMATION:
APPLICANT: Chailita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 511582006204
CURRENT APPLICATION NUMBER: US/11/097,912
PRIOR FILING DATE: 2005-04-01
PRIOR APPLICATION NUMBER: US 10/062,109
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 10/005,480
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 765

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 123
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-123
```

```
Query Match      27.1% Score 29.5; DB 7; Length 9;
Best Local Similarity 75.0%; Pred. No. 5.9e+04;
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
```

```
Qy      2 IPR-PTNI 8
        ||| |||:
Db      2 IPRPTNV 9
```

```
RESULT 17
US-10-859-643-164
; Sequence 164, Application US/10859643
; Publication No. US2006002993A1
; GENERAL INFORMATION:
; APPLICANT: Chaillita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 511582006203
; CURRENT APPLICATION NUMBER: US/10/859,643
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-859-643-164
```

```
Query Match      27.1% Score 29.5; DB 6; Length 10;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
```

```
Qy      2 IPR-PTNI 8
        ||| |||:
Db      3 IPRPTNV 10
```

```
RESULT 18
US-11-097-864-164
; Sequence 164, Application US/11097864
; Publication No. US20050265924A1
; GENERAL INFORMATION:
; APPLICANT: Chaillita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-164
```

```
Query Match      27.1% Score 29.5; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
```

```
Qy      2 IPR-PTNI 8
        ||| |||:
Db      3 IPRPTNV 10
```

```
RESULT 19
US-11-097-912-164
; Sequence 164, Application US/11097912
; Publication No. US20050265921A1
; GENERAL INFORMATION:
; APPLICANT: Chaillita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006204
; CURRENT APPLICATION NUMBER: US/11/097,912
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-164
```

```
Query Match      27.1% Score 29.5; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
```

```
Qy      2 IPR-PTNI 8
        ||| |||:
Db      3 IPRPTNV 10
```

```
RESULT 20
US-10-966-483-17
; Sequence 17, Application US/10966483
; Publication No. US20050281783A1
; GENERAL INFORMATION:
; APPLICANT: Kinch, Michael S.
; APPLICANT: Kiener, Peter A.
; APPLICANT: Bruckheimer, Elizabeth
; APPLICANT: Dubensky, Jf. Thomas W.
; APPLICANT: Cook, David N.
; TITLE OF INVENTION: LISTERIA-BASED Epha2 VACCINES
; FILE REFERENCE: 10271-146
; CURRENT APPLICATION NUMBER: US/10/966,483
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: US 60/511,919
; PRIOR FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: US 60/511,719
; PRIOR FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: US 60/532,666
; PRIOR FILING DATE: 2003-12-24
```

PRIOR APPLICATION NUMBER: US 60/556,631
PRIOR FILING DATE: 2004-03-26
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 2004-10-01
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 2004-10-07
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn version 3.2
SEQ ID NO 17
LENGTH: 13
TYPE: PRT
ORGANISM: Homo sapiens
US-10-966-483-17

Query Match 26.6%; Score 29; DB 6; Length 13;
Best Local Similarity 41.7%; Pred. No. 46;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 8 IHXYLVCEVNG 19
| : | | : : |
Db 2 IYMSVCMVMSG 13

RESULT 21
US-11-166-412-88
Sequence 88, Application US/11166412
Publication No. US20060014231A1
GENERAL INFORMATION:
APPLICANT: Van Rompaey, Luc
APPLICANT: Tomme, Peter H. M.
TITLE OF INVENTION: Methods and Compositions To Promote Bone Homeostasis
FILE REFERENCE: P27,927-D USA
CURRENT APPLICATION NUMBER: US/11/166,412
CURRENT FILING DATE: 2005-06-24
PRIOR APPLICATION NUMBER: 60/582,704
PRIOR FILING DATE: 2004-06-24
PRIOR APPLICATION NUMBER: 60/630,449
PRIOR FILING DATE: 2004-11-23
PRIOR APPLICATION NUMBER: 60/673,206
PRIOR FILING DATE: 2005-04-20
NUMBER OF SEQ ID NOS: 231
SOFTWARE: PatentIn version 3.3
SEQ ID NO 88
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Protein domain fragment
US-11-166-412-88

Query Match 26.6%; Score 29; DB 7; Length 14;
Best Local Similarity 36.4%; Pred. No. 50;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 4 HPTNIHKYLV 14
| : | | : : |
Db 4 YSTGVHESLTC 14

RESULT 22
US-10-506-443A-18
Sequence 18, Application US/10506443A
Publication No. US20060013817A1
GENERAL INFORMATION:
APPLICANT: Sahin Dr., Ugur
APPLICANT: Tureci Dr., Ozlem
APPLICANT: Kosciowski Dr., Michael
TITLE OF INVENTION: Genetic Products Differentially Expressed in Tumors and Use There
FILE REFERENCE: 342-3BCT
CURRENT APPLICATION NUMBER: US/10/506,443A
CURRENT FILING DATE: 2004-09-01
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn version 3.1

SEQ ID NO 18
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
US-10-506-443A-18

Query Match 26.6%; Score 29; DB 6; Length 17;
Best Local Similarity 50.0%; Pred. No. 60;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 4 HPTNIHKYLV 13
| : | | : : |
Db 2 HWKNIHKQVI 11

RESULT 23
US-10-723-207-71
Sequence 71, Application US/10723207
Publication No. US20050250934A1
GENERAL INFORMATION:
APPLICANT: Wang, Chang Y1
APPLICANT: Walfield, Alan M.
TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
FILE REFERENCE: 1151-4153US2
CURRENT APPLICATION NUMBER: US/10/723,207
CURRENT FILING DATE: 2003-11-24
PRIOR APPLICATION NUMBER: 09/701,623
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US99/13959
PRIOR FILING DATE: 1999-06-21
PRIOR APPLICATION NUMBER: 09/100,287
PRIOR FILING DATE: 1998-06-20
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 71
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide
OTHER INFORMATION: synthesized from amino acids with no genetic
OTHER INFORMATION: material as source
US-10-723-207-71

Query Match 26.6%; Score 29; DB 6; Length 20;
Best Local Similarity 33.3%; Pred. No. 71;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 3 PHTNIHKYLV 14
| : | | : : |
Db 1 PHTNALQALIC 12

RESULT 24
US-11-045-024-1627
Sequence 1627, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Cells, Esteban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024

```

; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1627
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-1627

Query Match      25.7%; Score 28; DB 7; Length 8;
Best Local Similarity 57.1%; Pred. No. 5.9e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      2 IPHPTNI 8
      |||||
      :
Db      2 IPHPAGL 8

RESULT 25
US-11-045-024-4340
; Sequence 4340, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esceban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045.024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4340

```

```

; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-4340

Query Match      25.7%; Score 28; DB 7; Length 8;
Best Local Similarity 57.1%; Pred. No. 5.9e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      2 IPHPTNI 8
      |||||
      :
Db      2 IPHPAGL 8

Search completed: January 26, 2006, 08:39:07
Job time : 3.60345 secs

```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:48:50 ; Search time 9.5 Seconds

(without alignments)
192,434 Million cell updates/sec

Title: US-09-662-293-11

Perfect score: 109

Sequence: 1 DIPPTNHHKYVCEVNG 19

Scoring table: BLOSUM62

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 4071

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR 80:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the change being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	34.9	15	2	A60929
2	38	34.9	15	2	B60929
3	27	24.8	11	2	S42587
4	27	24.8	18	2	H64711
5	26	23.9	18	2	S65454
6	25.5	23.4	16	2	S55307
7	25	22.9	19	2	PQ0548
8	24	22.9	20	2	D84716
9	24	22.0	9	2	A60108
10	24	22.0	9	2	S10920
11	24	22.0	17	2	S15728
12	24	22.0	18	2	S29264
13	24	22.0	18	2	PN0175
14	24	22.0	19	2	I50153
15	24	22.0	20	2	A45655
16	23	21.1	13	2	S38736
17	23	21.1	16	2	PH1604
18	23	21.1	17	2	S15754
19	23	21.1	17	2	A53503
20	22.5	20.6	18	1	A58589
21	22	20.2	10	2	B59272
22	22	20.2	10	2	B37196
23	22	20.2	11	2	B60409
24	22	20.2	11	2	D60409
25	22	20.2	13	2	B47415
26	22	20.2	15	2	S60007
27	22	20.2	16	2	S00123
28	22	20.2	16	2	A41170
29	22	20.2	16	2	A11488

30	22	20.2	19	2	D44101
31	22	20.2	20	2	A38556
32	21	19.3	12	2	A54315
33	21	19.3	12	2	B47171
34	21	19.3	13	2	A54326
35	21	19.3	14	2	S41601
36	21	19.3	15	2	PQ0232
37	21	19.3	15	2	A56786
38	21	19.3	15	2	PH0136
39	21	19.3	15	2	A08416
40	21	19.3	17	2	C49255
41	21	19.3	17	2	S15064
42	21	19.3	18	2	PQ0680
43	21	19.3	18	2	S20322
44	21	19.3	20	2	A24589
45	21	19.3	20	2	A60100
46	21	19.3	20	2	C56894
47	21	19.3	20	2	B56894
48	21	19.3	20	2	S44465
49	21	19.3	20	2	A60120
50	21	19.3	21	2	PD0015
51	20	18.3	11	2	PA0028
52	20	18.3	11	2	PH1375
53	20	18.3	11	2	PH1376
54	20	18.3	12	1	LPECPB
55	20	18.3	14	2	S48685
56	20	18.3	15	2	B56046
57	20	18.3	15	2	PH1610
58	20	18.3	18	2	PL0025
59	20	18.3	19	2	S29167
60	20	18.3	19	2	PH1352
61	20	18.3	19	2	D49404
62	20	18.3	19	2	PQ0409
63	20	18.3	20	2	PX0042
64	20	18.3	20	2	S68028
65	20	18.3	20	2	B38382
66	20	18.3	21	2	S58431
67	19.5	17.9	14	2	A58963
68	19.5	17.9	19	2	C32735
69	19.5	17.9	19	2	B32735
70	19.5	17.9	19	2	A34233
71	19.5	17.4	9	2	S55696
72	19	17.4	10	2	S77980
73	19	17.4	11	2	A26930
74	19	17.4	13	2	S15755
75	19	17.4	13	2	PT0290
76	19	17.4	13	2	A40207
77	19	17.4	14	2	G61308
78	19	17.4	15	2	PA0024
79	19	17.4	15	2	PC1317
80	19	17.4	15	2	PS0221
81	19	17.4	15	2	PH1619
82	19	17.4	15	4	I38336
83	19	17.4	17	2	A61334
84	19	17.4	17	2	I57941
85	19	17.4	17	2	B25348
86	19	17.4	18	2	S63487
87	19	17.4	18	2	A60118
88	19	17.4	19	2	A31252
89	19	17.4	19	2	C39305
90	19	17.4	20	2	S03335
91	19	17.4	20	2	S66222
92	19	17.4	20	2	C34917
93	19	17.4	20	2	A58569
94	19	17.4	21	2	PC2214
95	19	17.4	21	2	D38837
96	19	17.4	21	2	B41299
97	18.5	17.0	15	2	B41668
98	18.5	17.0	16	2	S30384
99	18.5	17.0	20	2	PQ0537
100	18	16.5	9	2	S26508

calmodulin, vasocac
GTP-binding protei
enactin/nidogen -
chondroitin sulfat
glandular kallikre
interferon alpha r
cystatin Cl-4a - m
pimeloyl-CoA synth
T-cell receptor be
lombiricene kinase
T-cell receptor be
hypothetical prote
photosystem I 5.6K
gluten - wheat
photosystem II chl
limbrial antigen C
intracystalline c
intracystalline c
pyrrocoricin - Py
insertion element
actin-binding prot
protein QA300042 -
T antigen variant
T antigen variant
pyrE leader peptid
extension protein
urinary tract ston
Ig H chain V-D-J r
T-cell surface gly
guinaldine oxidore
Ig heavy chain DJ
T-cell receptor be
RNA-directed RNA p
venomabin B (EC 3.4
iodothronine 5'-mo
15K protein B - ra
phosphatidylinosit
alpha-conotoxin Cn
thyroglobulin - pl
trehalase inhibito
phosphoenolpyruvat
cytochrome-c oxid
emg leader peptid
actin 7 - soybean
Ig heavy chain CRD
cell surface glyco
hemocyanin chain 3
protein QA300050 -
large granule L4-c
gastrin-releasing
Ig H chain V-D-J r
hypothetical TEL/M
trypsin (EC 3.4.21
beta 3 -adrenergic
glycogen(starch) s
fibrinogenolytic p
22K protein - Lyme
metallothionein I
neurotoxin Tx3 - s
photosystem II pho
defensin AMP2 - Da
catechol 1,2-dioxy
hypothetical prote
fibrinogenolytic p
T-cell receptor be
T-cell receptor al
hypothetical prote
hypothetical prote
arylhydroxamic aci
collagen alpha 2(V

ALIGNMENTS

RESULT 1

A60929

diclhomromethane dehalogenase (EC 4.5.1.3) - Hyphomicrobium sp. (ATCC 43129) (fragment)
C:Species: Hyphomicrobium sp.
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004

C:Accession: A60929
R:Kohler-Staub, D.; Hartmann, S.; Gaelli, R.; Suter, F.; Leisinger, T.
J. Gen. Microbiol. 132, 2837-2843, 1986

A:Title: Evidence for identical dichloromethane dehalogenases in different methylotrophic
A:Reference number: A60929

A:Accession: A60929

A:Molecule type: Protein

A:Residues: 1-15 <KOH>

A:Cross-references: UNIPROT:Q7M134; UNIPARC:UPI000017A8F8

C:Keywords: carbon-halide lyase

Query Match 34.9%; Score 38; DB 2; Length 15;
Best Local Similarity 85.7%; Pred. No. 11;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PHPTNIH 9

DB 3 PHPTNIH 9

RESULT 2
B60929
dichloromethane dehalogenase (EC 4.5.1.3) - Pseudomonas sp. (fragment)

C:Species: Pseudomonas sp.
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C:Accession: B60929
R:Kohler-Staub, D.; Hartmann, S.; Gaelli, R.; Suter, F.; Leisinger, T.
J. Gen. Microbiol. 132, 2837-2843, 1986

A:Title: Evidence for identical dichloromethane dehalogenases in different methylotrophic

A:Reference number: A60929

A:Contents: DSM 1565

A:Accession: B60929

A:Molecule type: Protein

A:Residues: 1-15 <KOH>

A:Cross-references: UNIPROT:Q7M126; UNIPARC:UPI000017A8F8

C:Keywords: carbon-halide lyase

Query Match 34.9%; Score 38; DB 2; Length 15;
Best Local Similarity 85.7%; Pred. No. 11;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PHPTNIH 9

DB 3 PHPTNIH 9

RESULT 3
S42587
celF protein - Escherichia coli (fragment)

C:Species: Escherichia coli
C:Date: 25-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995

C:Accession: S42587
R:Guizzo, A.; Dubow, M. S.
Mol. Gen. Genet. 242, 455-460, 1994

A:Title: A luxX transcripctional fusion to the cryptic celF gene of Escherichia coli die

A:Reference number: S42587; MUID:94166755; PMID:8121401

A:Accession: S42587

A:Molecule type: DNA

A:Residues: 1-11 <GUZ>

A:Cross-references: UNIPARC:UPI000017AA33

C:Genetics:

A:Gene: celF

Query Match

24.8%; Score 27; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 4.3e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PHPTN 7

DB 7 PHPTN 11

RESULT 4

H64711

hypothetical protein HP1536 - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004

C:Accession: H64711
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khaliq, H.G.; Glodek, A.; McKenney
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wattey, L.
Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185

A:Accession: H64711

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-18 <TOM>

A:Cross-references: UNIPROT:O26062; UNIPARC:UPI00000C07C3; GB:A600651; GB:A600511; NID

Query Match 24.8%; Score 27; DB 2; Length 18;
Best Local Similarity 55.6%; Pred. No. 7.2e+02;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 HPTNIHXYL 12

DB 10 HPSRNPXYL 18

RESULT 5
S65454
aspergillopepsin I (EC 3.4.23.18) - Aspergillus niger (fragments)

N:Alternate names: aspergillopepsinogen I
C:Species: Aspergillus niger
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C:Accession: S65454
R:Imoue, H.; Hayaishi, T.; Huang, X.P.; Lu, J.F.; Athauda, S.B.P.; Kong, K.H.; Yamagata, I.
Eur. J. Biochem. 237, 719-725, 1996

A:Title: Heterologous expression and site-directed mutagenesis studies on the activation

A:Reference number: S65454; MUID:96235238; PMID:8647118

A:Accession: S65454

A:Molecule type: Protein

A:Residues: 1-5;6-10;11-18 <INO>

A:Cross-references: UNIPARC:UPI000017B3BC; UNIPARC:UPI000017B3BD; UNIPARC:UPI000017B3BE

A:Experimental source: strain var. macrosporus

C:Keywords: aspartic proteinase; hydrolase

Query Match 23.9%; Score 26; DB 2; Length 18;
Best Local Similarity 44.4%; Pred. No. 1e+03;

Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 PHPTNIHXY 11

DB 2 PAPTSLAXF 10

RESULT 6
S55307
glutathione transferase 3-3 - rat (fragments)

C:Species: Rattus norvegicus (Norway rat)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999

C:Accession: S55307

R:Cooke, R.J.; Bjornestedt, R.; Douglas, K.T.; McKie, J.H.; King, M.D.; Colee, B.; Kett

Biochem. J. 302, 383-390, 1994

A:Title: Photoaffinity labelling of the active site of the rat glutathione transferases

A:Reference number: S55307; MUID:9437965; PMID:8092989

A:Accession: S55307

A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-16 <COO>
A:Cross-references: UNIPARC:UPI000017C91E

Query Match 23.4% Score 25.5; DB 2; Length 16;
Best Local Similarity 42.9%; Pred. No. 1.1e+03;
Matches 6; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

QY 2 IPHPTNI--HKYL 12
| | | | |
| | | | |
Db 2 LTHPSQIMRFEKYL 15

RESULT 7
P00548
capsid protein VP26 - human herpesvirus 1 (fragment)
C:Species: human herpesvirus 1
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C:Accession: P00548

R:Davidson, M.D.; Rixon, F.J.; Davison, A.J.

J. Gen. Virol. 73, 2709-2713, 1992

A:Title: Identification of genes encoding two capsid proteins (VP24 and VP26) of herpes

A:Reference number: P00544; PMID:93019027; PMID:1328483

A:Accession: P00548

A:Molecule type: protein

A:Residues: 1-19 <DAV>

A:Cross-references: UNIPROT:Q7LZW5; UNIPARC:UPI000017A7C9

A:Experimental source: strain 17

C:Genetics:

A:Gene: UL35

C:Keywords: capsid protein

Query Match 22.9% Score 25; DB 2; Length 19;
Best Local Similarity 80.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DHPH 5
| | | | |
| | | | |
Db 11 DHPH 15

RESULT 8

D84716

hypothetical protein Atg31090 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: D84716

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Mofeit, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Unayam, L.; Tallon, L.

et al.; Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; PMID:20083487; PMID:10617197

A:Accession: D84716

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-20 <STO>

A:Cross-references: UNIPROT:O82275; UNIPARC:UPI000017A6CB; GB:AE002093; NID:g3746066; PI

C:Genetics:

A:Gene: Atg31090

A:Map position: 2

Query Match 22.9% Score 25; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 12 LVCSVNG 19
| | | | |
| | | | |
Db 7 LVCDCTSG 14

RESULT 9

A60108

exotoxin A - Streptococcus pyogenes (strain C203.S) (fragment)

N:Alternate names: Blactogen A; scarlet fever toxin

C:Species: Streptococcus pyogenes

C>Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 31-Dec-2004

C:Accession: A60108

R:Schlivert, P.M.; Gray, E.D.

Infect. Immun. 57, 1865-1867, 1989

A:Title: Group A streptococcal pyrogenic exotoxin (scarlet fever toxin) type A and blas

A:Reference number: A60108; PMID:89254013; PMID:2498210

A:Accession: A60108

A:Molecule type: protein

A:Residues: 1-9 <SCH>

A:Cross-references: UNIPROT:Q54779; UNIPROT:P97163; UNIPROT:Q9R931; UNIPROT:Q57453; UNI

C:Superfamily: enterotoxin B

C:Keywords: exotoxin

Query Match 22.0% Score 24; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 PHPTNIH 9
| | | | |
| | | | |
Db 3 PDFSQLH 9

RESULT 10

S10920

venom protein HR-3 - oriental hornet (fragment)

C:Species: Vespa orientalis (oriental hornet)

C>Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jul-2004

C:Accession: S10920

R:Tutchbaev, M.U.; Akmedova, N.U.; Kazakov, I.; Korneev, A.S.; Gagel'gans, A.I.

Biochemistry (N.Y.) 53, 183-190, 1988

A:Title: Low-molecular-weight peptides of venom of the giant hornet Vespa orientalis. S

A:Reference number: S06445

A:Accession: S10920

A:Molecule type: protein

A:Residues: 1-9 <TUI>

A:Cross-references: UNIPROT:Q7M471; UNIPARC:UPI000017BF07

C:Keywords: venom

Query Match 22.0% Score 24; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 7 NIHKYLV 13
| | | | |
| | | | |
Db 2 SVHEFLV 8

RESULT 11

S15778

insulin chain B - bovine (fragments)

C:Species: Bos primigenius indicus x Bos primigenius taurus (cattle)

C>Date: 19-Mar-1997 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C:Accession: S15778; S15779

R:Bergerman, T.; Agerberth, B.; Joernvall, H.

FEBS Lett. 283, 100-103, 1991

A:Title: Direct analysis of peptides and amino acids from capillary electrophoresis.

A:Reference number: S15778; PMID:91243852; PMID:2037061

A:Accession: S15778

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <FEB1>

A:Cross-references: UNIPARC:UPI000015BC0B

A:Accession: S15779

A:Status: preliminary

A:Molecule type: protein

A:Residues: 9-17 <FEB2>

A:Cross-references: UNIPARC:UPI000015BC0B

C:Superfamily: insulin

C:Keywords: hormone; pancreas

Query Match 22.0%; Score 24; DB 2; Length 17;
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-19 <CHA>
A:Cross-references: UNIPROT:Q9PSW6; UNIPARC:UPI00000FB20E; GB:X02258; NID:9211084; PIDN:
C:Superfamily: Actin

OY 11 YLVC 14
|||
3 YLVC 6

RESULT 12
S29264
ovoheemerythrin - duck leech (fragment)

N:Alternate names: 14k yolk protein
C:Species: Theromyzon tessulatatum (duck leech)
C:Date: 19-Mar-1997 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: S29264
R:Beert, J.L.; Birtel, M.; Sautiere, P.; Malecha, J.
Eur. J. Biochem. 209, 563-569, 1992
A:Title: Ovoheemerythrin, a major 14-kDa yolk protein distinct from vitellogenin in leech
A:Reference number: S29264; MUID:93049299; PMID:1425663
A:Accession: S29264
A:Molecule type: protein
A:Residues: 1-18 <BA>
A:Cross-references: UNIPROT:P80155; UNIPARC:UPI000012C58F; PIDN:AAB23969.1; PID:G258980
C:Superfamily: hemerythrin
C:Keywords: egg yolk; oxygen carrier

Query Match 22.0%; Score 24; DB 2; Length 18;
Best Local Similarity 80.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DHPH 5
|||
2 DIPEP 6

RESULT 13

PN0175

glutathione transferase (EC 2.5.1.18) 1 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 22-Dec-1995 #sequence_revision 08-Feb-1996 #text_change 23-Mar-2001
C:Accession: PN0175
R:Tangita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.
submitted to JIPID, December 1995
A:Description: Two dimensional electrophoresis of plant proteins and standardization of
A:Reference number: PN0173
A:Accession: PN0175
A:Molecule type: protein
A:Residues: 1-18 <TSU>
A:Cross-references: UNIPARC:UPI000017AF59
A:Experimental source: leaf
C:Keywords: transferase

Query Match 22.0%; Score 24; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 DHPHNT 8
|||
5 DFGHPADI 12

RESULT 14

150153

alpha-actin - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 05-Oct-2004
C:Accession: 150153
R:Chang, K.
Mol. Cell. Biol. 4, 2498-2508, 1984
A:Title: Isolation and characterization of six different chicken actin genes.
A:Reference number: 150153; MUID:85085956; PMID:6513927

A:Accession: 150153
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-19 <CHA>
A:Cross-references: UNIPROT:Q9PSW6; UNIPARC:UPI00000FB20E; GB:X02258; NID:9211084; PIDN:
C:Superfamily: Actin

Query Match 22.0%; Score 24; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 12 LVCEVNG 19
|||
10 LVCDNGSG 17

RESULT 15

A45655

Crotalus atrox serine proteinase (EC 3.4.21.-) - western diamondback rattlesnake (fragment)
N:Alternate names: alpha-fibrinogenase; thrombin-like proteinase
C:Species: Crotalus atrox (western diamondback rattlesnake)
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C:Accession: A45655
R:Chou, S.H.; Hung, C.C.; Lin, C.W.
Biochem. Int. 26, 105-112, 1992
A:Title: Isolation of a crotalase-like protease with alpha-fibrinogenase activity from
A:Reference number: A45655; MUID:92313365; PMID:1616487
A:Accession: A45655
A:Molecule type: protein
A:Residues: 1-20 <CH>
A:Cross-references: UNIPROT:Q9PS55; UNIPARC:UPI00000FB75C
A:Experimental source: venom
A:Note: sequence extracted from NCBI backbone (NCBI:P107297)
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase; venom

Query Match 22.0%; Score 24; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 2.4e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 7 NIKHYLV 13
|||
10 NEHRFLV 16

RESULT 16

S38736

lipid transfer protein a1 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 19-May-1994 #sequence_revision 19-Jan-1996 #text_change 19-Jan-1996
C:Accession: S38736
R:Segura, A.; Moreno, M.; Garcia-Olmedo, F.
FEBS Lett. 332, 243-246, 1993
A:Title: Purification and antipathogenic activity of lipid transfer proteins (LTPs) from
A:Reference number: S38736; MUID:94009709; PMID:8405465
A:Accession: S38736
A:Molecule type: protein
A:Residues: 1-13 <SEG>
A:Cross-references: UNIPARC:UPI000017AFCF

Query Match 21.1%; Score 23; DB 2; Length 13;
Best Local Similarity 71.4%; Pred. No. 2.2e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 12 LVCESVN 18
|||
2 LVCESVN 8

RESULT 17

PH1604

Ig H chain V-D-J region (wild-type clone 327) - mouse (fragment)
C:Species: Mus musculus (house mouse)

C>Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C/Accession: P11604
R/Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A/Title: Molecular characterization of transgene-induced immunodeficiency in B-lees mice
A/Reference number: P11580; MUID:93301609; PMID:8315387
C/Accession: P11604
A/Molecule type: DNA
A/Residues: 1-16 <LEV>
A/Cross-references: UNIPARC:UPI00001766C0
A/Experimental source: bone marrow pre-B lymphocyte
C/Keywords: immunoglobulin

Query Match 21.1%; Score 23; DB 2; Length 16;
Best Local Similarity 44.4%; Pred. No. 2.7e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 PPTNIRKY 11
Db 4 PHRWLHXY 12

RESULT 18
S15754
actin 6 - soybean (fragment)
C/Species: Glycine max (soybean)
C/Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 05-Oct-2004
C/Accession: S15754; S08049
R/Pearson, L.; Meagher, R.B.
Plant Mol. Biol. 14, 513-526, 1990
A/Title: Diverse soybean actin transcripts contain a large intron in the 5' untranslated
A/Reference number: S15754; MUID:91346640; PMID:2102831
C/Accession: S15754
A/Molecule type: DNA
A/Residues: 1-17 <PEA>
A/Cross-references: UNIPROT:P15986; UNIPARC:UPI0000125427; EMBL:X17119; NID:g18525; PIDN
C/Superfamily: Actin
C/Keywords: cytoskeleton

Query Match 21.1%; Score 23; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 2.9e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 12 LVCSNVNG 19
Db 10 LVCDNGTG 17

RESULT 19
S63503
83K proteoln - Eubacterium acidaminophilum (fragment)
C/Species: Eubacterium acidaminophilum
C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C/Accession: S63503
R/Meyer, M.; Granderath, K.; Andreessen, J.R.
Eur. J. Biochem. 234, 184-191, 1995
A/Title: Purification and characterization of protein P(B) of betaine reductase and its
phylum.
A/Reference number: S63502; MUID:96096737; PMID:8529639
A/Accession: S63503
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-17 <MEY>
A/Cross-references: UNIPARC:UPI000017AD3D

Query Match 21.1%; Score 23; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 NIHKYL 12
Db 2 DLHKFL 7

RESULT 20
A58589
alpha-conotoxin EI - cone shell (Conus ermineus)
C/Species: Conus ermineus (ermine cone)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: A58589
R/Martinez, J.S.; Olivera, B.M.; Gray, W.R.; Craig, A.G.; Grebe, D.R.; Abramson, S.N.;
Biochemistry 34, 14519-14526, 1995
A/Title: alpha-Conotoxin EI, a new nicotinic acetylcholine receptor antagonist with nov
A/Reference number: A58589; MUID:96062516; PMID:7578057
C/Accession: A58589
A/Molecule type: protein
A/Residues: 1-18 <MAR>
A/Cross-references: UNIPROT:P50982; UNIPARC:UPI00001287C0
A/Note: sequence confirmed by chemical synthesis
C/Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynaf
C/Superfamily: alpha-conotoxin
C/Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; hydroxyproline; pc
F/3/Modified site: 4-hydroxyproline (Pro) #status experimental
F/4-10-5-18/Disulfide bonds: #status experimental
F/18/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 20.6%; Score 22.5; DB 1; Length 18;
Best Local Similarity 41.7%; Pred. No. 3.7e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 4 HPT-NIHKYLVC 14
Db 7 HPTNMSNPQIC 18

RESULT 21
B59272
peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, small chain
N/Alternate names: peptide N-glycosidase
C/Species: Prunus dulcis var. sativa (sweet almond)
C/Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C/Accession: B59272
R/Altman, F.; Paschinger, K.; Dalik, T.; Vorauer, K.
Eur. J. Biochem. 252, 118-123, 1998
A/Title: Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase
A/Reference number: A59272; MUID:98181894; PMID:9523720
C/Accession: B59272
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-10 <ALT>
A/Cross-references: UNIPROT:P81898; UNIPARC:UPI00000ABBC4
C/Keywords: hydrolase

Query Match 20.2%; Score 22; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 2.4e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 PTNIRKY 11
Db 2 PTPLDHF 8

RESULT 22
B37196
bradykinin-potentiating peptide 2 - island jararaca
C/Species: Bothrops insularis (island jararaca)
C/Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004
C/Accession: B37196
R/Cintre, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A/Title: Primary structure and biological activity of bradykinin potentiating peptides
A/Reference number: A37196; MUID:90351557; PMID:2386615
C/Accession: B37196
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-10 <CIN>

A:Cross-references: UNIPROT:P30422; UNIPARC:UPI0000126A8F
 C:Keywords: pyroglutamic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 20.2%; Score 22; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PHP 5
 |||
 Db 4 PHP 6

RESULT 23

B60409
 kaasinin-like peptide K-1 - frog (Pseudophryne guentheri)

C:Species: Pseudophryne guentheri
 C:Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 16-Aug-2004

C:Accession: B60409

R:Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior
 Peptides 11, 299-304, 1990

A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austro
 A:Reference number: A60409; MUID:90287814; PMID:2356157

A:Accession: B60409
 A:Molecule type: protein

A:Residues: 1-11 <SIM>
 A:Cross-references: UNIPROT:P42986; UNIPARC:UPI0000136FCD

A>Note: this peptide was also found in a deamidated form

C:Keywords: amidated carboxyl end; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:1/Modified site: amidated carboxyl end (Met) (partial) #status experimental

Query Match 20.2%; Score 22; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PHP 5
 |||
 Db 2 PHP 4

RESULT 24

D60409
 kaasinin-like peptide K-III - frog (Pseudophryne guentheri)

C:Species: Pseudophryne guentheri

C:Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 16-Aug-2004

C:Accession: D60409

R:Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior
 Peptides 11, 299-304, 1990

A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austro
 A:Reference number: A60409; MUID:90287814; PMID:2356157

A:Accession: D60409
 A:Molecule type: protein

A:Residues: 1-11 <SIM>
 A:Cross-references: UNIPROT:P42988; UNIPARC:UPI0000136FD7

C:Keywords: amidated carboxyl end; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:1/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 20.2%; Score 22; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PHP 5
 |||
 Db 2 PHP 4

RESULT 25

B47415

mannose-1-phosphate guanylyltransferase (EC 2.7.7.13) 43K alpha chain - pig (fragment)

N:Alternate names: GDP-mannose pyrophosphorylase 43K alpha chain

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 25-Feb-1994 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996
 C:Accession: B47415
 R:Sumiyo, T.; Drake, R.R.; York, J.L.; Elbein, A.D.
 J. Biol. Chem. 268, 17943-17950, 1993

A:Title: GDP-mannose pyrophosphorylase. Purification to homogeneity, properties, and uti

A:Reference number: A47415; MUID:93352609; PMID:7688733

A:Accession: B47415

A:Molecule type: protein
 A:Residues: 1-13 <SZU>

A:Cross-references: UNIPARC:UPI000017C470

A:Experimental source: liver

C:Complex: The enzyme appears to be a heterodimer of alpha and beta chains.

C:Function:
 A:Description: generates GDP-mannose and pyrophosphate from mannose-1-phosphate and GTP

A>Note: also catalyzes synthesis of GDP-glucose from glucose-1-phosphate (EC 2.7.7.34 ac

C:Keywords: blocked amino end; nucleotidyltransferase

Query Match 20.2%; Score 22; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PHP 5
 |||
 Db 8 PHP 10

Search completed: January 26, 2006, 08:05:05
 Job time : 11.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:47:56 : Search time 56.5086 Seconds
(without alignments)
237.221 Million cell updates/sec

Title: US-09-662-293-11
Perfect score: 109
Sequence: 1 DIHPHTIHKKLVCESVNG 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 70528306 residues

Total number of hits satisfying chosen parameters: 15779

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	34.9	15	2	Q7M126 PSESP
2	38	34.9	15	2	Q7M134 BRHIZ
3	37	33.9	13	2	Q00789 SDELA
4	37	33.9	13	2	Q76R60 SDELA
5	37	33.9	21	2	O82439 SDELA
6	33	30.3	19	2	O5C123 SCHUA
7	32	29.4	13	2	O7S901 NEUCR
8	30	27.5	10	2	Q4X4H2 PLACH
9	30	27.5	18	2	Q16244 HUMAN
10	29	26.6	6	1	TMOF_SARBU
11	29	26.6	19	2	O5EX89 PLAMI
12	29	26.6	21	2	Q4YCP3 PLABZ
13	28	25.7	19	2	O5EX77 PLAMI
14	28	25.7	19	2	O5EX78 PLAMI
15	28	25.7	19	2	O5EX88 PLAMI
16	28	25.7	19	2	O5EX90 PLAMI
17	28	25.7	19	2	O5EX91 PLAMI
18	28	25.7	19	2	O5EX92 PLAMI
19	28	25.7	19	2	O5EX94 PLAMI
20	28	25.7	19	2	O5EX95 PLAMI
21	28	25.7	19	2	O5EX96 PLAMI
22	28	25.7	19	2	O5EX97 PLAMI
23	28	25.7	19	2	O5EX98 PLAMI
24	28	25.7	19	2	O5EX99 PLAMI
25	28	25.7	19	2	O5EXA2 PLAMI
26	28	25.7	19	2	O5EXA3 PLAMI
27	28	25.7	19	2	O5EXA4 PLAMI
28	28	25.7	19	2	O5EXA5 PLAMI
29	28	25.7	19	2	O5EXA6 PLAMI
30	28	25.7	19	2	O5EXA7 PLAMI
31	28	25.7	19	2	O5EXA7 PLAMI

32	28	25.7	19	2	O5EXA8 PLAMI	O5EXA8 streptocarp
33	28	25.7	19	2	O5EXA9 PLAMI	O5EXA9 saintpaulia
34	28	25.7	19	2	O5EXB0 PLAMI	O5EXB0 saintpaulia
35	28	25.7	19	2	O5EXB1 PLAMI	O5EXB1 saintpaulia
36	28	25.7	20	2	O4YMN1 PLABZ	O4YMN1 plasmodium
37	28	25.7	21	2	O712N7 HUMAN	O712N7 homo sapien
38	27	24.8	18	2	O26062 HELPY	O26062 heliobacte
39	27	24.8	19	2	O4X138 PLACH	O4X138 plasmodium
40	27	24.8	19	2	O4YK87 PLABZ	O4YK87 plasmodium
41	27	24.8	20	2	O7RR59 PLAVO	O7RR59 plasmodium
42	26	23.9	12	2	O9UMR0 HUMAN	O9UMR0 homo sapien
43	26	23.9	17	2	O410W0 BACTK	O410W0 bacillus th
44	26	23.9	19	2	O9XN07 BOOMI	O9XN07 boophilus m
45	26	23.9	19	2	O5EX86 PLAMI	O5EX86 streptocarp
46	26	23.9	20	1	PHYI4 PHYOR	PHYI4 phyliomedus
47	26	23.9	20	2	O7RS12 PLAVO	O7RS12 plasmodium
48	26	23.9	20	2	O5K4V0 BOVIN	O5K4V0 bos taurus
49	26	23.9	20	2	O90X94 CHICK	O90X94 gallus gall
50	25	22.9	11	2	O8MM58 GNEOP	O8MM58 heliconius
51	25	22.9	12	2	O8MUN4 GNEOP	O8MUN4 heliconius
52	25	22.9	12	2	O8MUN9 GNEOP	O8MUN9 heliconius
53	25	22.9	13	2	O8MM57 GNEOP	O8MM57 heliconius
54	25	22.9	14	2	O8MUN8 GNEOP	O8MUN8 heliconius
55	25	22.9	14	2	O8MUN0 GNEOP	O8MUN0 heliconius
56	25	22.9	15	2	O9BZNO HUMAN	O9BZNO homo sapien
57	25	22.9	15	2	O8MUP2 GNEOP	O8MUP2 heliconius
58	25	22.9	16	2	O8MM83 GNEOP	O8MM83 heliconius
59	25	22.9	16	2	O8MM84 GNEOP	O8MM84 heliconius
60	25	22.9	16	2	O8MM85 GNEOP	O8MM85 heliconius
61	25	22.9	16	2	O8MUN3 GNEOP	O8MUN3 heliconius
62	25	22.9	16	2	O8MUN5 GNEOP	O8MUN5 heliconius
63	25	22.9	18	1	O9TWR4 PLICD	O9TWR4 dictyosteli
64	25	22.9	18	1	PHYI2 PHYRX	PHYI2 phyliomedus
65	25	22.9	18	2	O6VYB3 GNEOP	O6VYB3 heliconius
66	25	22.9	18	2	O6VYD9 GNEOP	O6VYD9 heliconius
67	25	22.9	18	2	O6VYE7 GNEOP	O6VYE7 heliconius
68	25	22.9	18	2	O4YEL0 PLABZ	O4YEL0 plasmodium
69	25	22.9	18	2	O28069 BOVIN	O28069 bos taurus
70	25	22.9	19	2	O6VYD8 GNEOP	O6VYD8 heliconius
71	25	22.9	19	2	O6VYE1 GNEOP	O6VYE1 heliconius
72	25	22.9	19	2	O7RG13 PLAVO	O7RG13 plasmodium
73	25	22.9	19	2	O7YK42 PFABA	O7YK42 desmanthus
74	25	22.9	19	2	O8CJ05 MESNU	O8CJ05 mesocricetu
75	25	22.9	19	2	O7LZM5 HHVI	O7LZM5 human herpe
76	25	22.9	20	1	APY3 PLECI	APY3 pleurotus c
77	25	22.9	20	1	APY3 PLECI	APY3 pleurotus c
78	25	22.9	21	2	O6LD41 HUMAN	O6LD41 homo sapien
79	25	22.9	21	2	O6VYA6 GNEOP	O6VYA6 heliconius
80	25	22.9	21	2	O4YEA9 PLABZ	O4YEA9 plasmodium
81	24	22.0	9	2	O7M471 VESOR	O7M471 vespa osten
82	24	22.0	15	2	O9UC17 HUMAN	O9UC17 homo sapien
83	24	22.0	17	2	O6R909 HUMAN	O6R909 homo sapien
84	24	22.0	17	2	O6R9P0 TRABH	O6R9P0 crachypithe
85	24	22.0	17	2	O6R9P1 TRABH	O6R9P1 crachypithe
86	24	22.0	17	2	O6R9P2 PYGNE	O6R9P2 pygathrix n
87	24	22.0	17	2	O6R9P3 PYGNI	O6R9P3 pygathrix b
88	24	22.0	17	2	O6R9P4 MACCU	O6R9P4 macaca mula
89	24	22.0	17	2	O6R9Q1 PONYR	O6R9Q1 pongo pygma
90	24	22.0	17	2	O6R9Q5 PPRIM	O6R9Q5 gorilla gor
91	24	22.0	17	2	O6R9R4 PANTR	O6R9R4 pan troglod
92	24	22.0	18	1	HEMT0 THERS	HEMT0 theromyzon
93	24	22.0	18	2	O9ZYV5 GHYME	O9ZYV5 opus kraus
94	24	22.0	18	2	O4XS69 PLACH	O4XS69 plasmodium
95	24	22.0	19	2	O5CS58 SCHUA	O5CS58 schistosoma
96	24	22.0	19	2	O9ZYW3 GHYME	O9ZYW3 gnampitodon
97	24	22.0	19	2	O9ZYX2 GHYME	O9ZYX2 centistes s
98	24	22.0	19	2	O4Y3P1 PLACH	O4Y3P1 plasmodium
99	24	22.0	19	2	O6R9P5 PHYLE	O6R9P5 hyllobates 1
100	24	22.0	19	2	O6R9P6 PPRIM	O6R9P6 bunopithec

ALIGNMENTS

```

RESULT 1
OQ7M126_PSESP PRELIMINARY; PRT; 15 AA.
ID Q7M126;
AC Q7M126;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Dichloromethane dehalogenase (EC 4.5.1.3) (Fragment).
OS Pseudomonas sp.
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=306;
RN [1]
RP PROTEIN SEQUENCE.
RA Kohler-Staub D., Hartmans S., Gaeili R., Suter F., Leisinger T.;
RT "Evidence for identical dichloromethane dehalogenases in different
methylophilic bacteria."
RL J. Gen. Microbiol. 132:2837-2843(1986).
DR PIR; B60929; B60929.
DR GO; GO:0018834; F:dichloromethane dehalogenase activity; IEA.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1667 MW; 05B170EF8B3721D9 CRC64;

Query Match 34.9%; Score 38; DB 2; Length 15;
Best Local Similarity 85.7%; Pred. No. 57;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 PHPTNIH 9
Db 3 PNPTNIH 9

RESULT 2
OQ7M134_9RHIZ PRELIMINARY; PRT; 15 AA.
ID Q7M134;
AC Q7M134;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Dichloromethane dehalogenase (EC 4.5.1.3) (Fragment).
OS Hypomicrobium sp.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Hypomicrobiaceae; Hyphomicrobium.
OX NCBI_TaxID=82;
RN [1]
RP PROTEIN SEQUENCE.
RA Kohler-Staub D., Hartmans S., Gaeili R., Suter F., Leisinger T.;
RT "Evidence for identical dichloromethane dehalogenases in different
methylophilic bacteria."
RL J. Gen. Microbiol. 132:2837-2843(1986).
DR PIR; A60929; A60929.
DR GO; GO:0018834; F:dichloromethane dehalogenase activity; IEA.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1667 MW; 05B170EF8B3721D9 CRC64;

Query Match 34.9%; Score 38; DB 2; Length 15;
Best Local Similarity 85.7%; Pred. No. 57;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 PHPTNIH 9
Db 3 PNPTNIH 9

RESULT 3
OQ00789_9DELA PRELIMINARY; PRT; 13 AA.
ID Q00789;
AC Q00789;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Gag protein (Fragment).
GN Name=gag;

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OS Human T-lymphotropic virus 1.
OC Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
OX NCBI_TaxID=11908;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87111460; Pubmed=3027244;
RA Hirataetsu K., Nishida J., Naito A., Yoshikawa H.;
RT "Molecular cloning of the closed circular provirus of human T cell
leukaemia virus type I: A new open reading frame in the gag-pol
region."
RL J. Gen. Virol. 68:213-218(1987).
DR EMBL; D10033; BAA00925.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1363 MW; 408035320911B443 CRC64;

Query Match 33.9%; Score 37; DB 2; Length 13;
Best Local Similarity 85.7%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DIPHPN 7
Db 1 DIPHPN 7

RESULT 4
OQ76R60_9DELA PRELIMINARY; PRT; 13 AA.
ID Q76R60;
AC Q76R60;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Gag protein (Fragment).
OS Human T-lymphotropic virus 1.
OC Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
OX NCBI_TaxID=11908;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87111460; Pubmed=3027244;
RA Hirataetsu K., Nishida J., Naito A., Yoshikawa H.;
RT "Molecular cloning of the closed circular provirus of human T cell
leukaemia virus type I: A new open reading frame in the gag-pol
region."
RL J. Gen. Virol. 68:213-218(1987).
DR EMBL; X04800; CAA28492.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1363 MW; 408035320911B443 CRC64;

Query Match 33.9%; Score 37; DB 2; Length 13;
Best Local Similarity 85.7%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DIPHPN 7
Db 1 DIPHPN 7

RESULT 5
OQ82439_9DELA PRELIMINARY; PRT; 21 AA.
ID Q82439;
AC Q82439;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Gag protein (Fragment).
GN Name=gag;
OS Human T-lymphotropic virus 1.
OC Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
OX NCBI_TaxID=11908;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=85211032; Pubmed=2987530;
RA Ratner L., Josephs S.F., Starcich B., Hahn B.H., Shaw G.M.,
Gallo R.C., Wong-Staal F.;

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RT "Nucleotide sequence analysis of a variant human T-cell leukemia virus (HTLV-Ib) provirus with a deletion in pX-I.";

RL J. Virol. 54:781-790(1985).

DR EMBL; M10977; AAA46203.1; -; Genomic DNA.

FT NON_TER

SO SEQUENCE 21 AA; 2169 MW; 7B0EB0675406840D CRC64;

Query Match 33.9%; Score 37; DB 2; Length 21;

Best Local Similarity 85.7%; Pred. No. 1.2e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DIPPTN 7

Db 9 DIPPTN 15

RESULT 6

Q5C123 SCHJA PRELIMINARY; PRT; 19 AA.

AC Q5C123

DT 10-MAY-2005 (TrEMBLrel. 30, Created)

DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)

DE Hypothetical protein.

OS Schistosoma japonicum (Blood fluke).

OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;

OC Schistosomacidae; Schistosomatidae; Schistosoma.

OX NCBI_TaxID=6182;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Han Z.;

RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY610763; AAX26552.1; -; mRNA.

KW Hypothetical protein.

SO SEQUENCE 19 AA; 2259 MW; FE2492F8464550 CRC64;

Qy Query Match 30.3%; Score 33; DB 2; Length 19;

Best Local Similarity 66.7%; Pred. No. 4.8e+02;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PTNIRKLV 13

Db 8 PMKIHNYLV 16

RESULT 7

Q7S901 NEUCR PRELIMINARY; PRT; 13 AA.

ID Q7S901

DT 01-MAR-2004 (TrEMBLrel. 26, Created)

DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)

DE Predicted protein.

GN Name=NCU05297.1;

OS Neurospora crassa.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

OX NCBI_TaxID=5141;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=OR74A.

RA Galagan J.E., Calvo S.E., Borkovich K.A., Selzer E.U., Read N.D.,

RA Ulje D., Fitzgerald W., Ma L.-J., Smirnov S., Purcell S., Renman B.,

RA Ekfeldt T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,

RA Qui D., Iankilev P., Pedersen D., Nelson M., Washburne M.,

RA Selitrenikoff C.P., Kinsey J.A., Braun E.L., Zeller A., Schulte U.,

RA Koche G.O., Jedd G., Mewes W., Scaben C., Marotte E., Greenberg D.,

RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,

RA Kamal M., Kamyshelev M., Mauceli E., Bielke C., Rudd S., Fishman D.,

RA Kryzhefova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,

RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,

RA Desouza C.C., Glaes L., Orbach M.J., Berglund J., Voelker R.,

RA Varden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,

RA Natvig D.O., Alex L.A., Mannheim G., Ebbola D.J., Preitag M.,

RA Paulsen I., Sachs M.S., Lander E.S., Nebaum C., Birren B.,

RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";

RL Nature 0:0-0(2003).

CC -i CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

DR EMBL; AABX01000220; EAA32832.1; -; Genomic DNA.

SO SEQUENCE 13 AA; 1543 MW; 09180701868D404B CRC64;

Query Match 29.4%; Score 32; DB 2; Length 13;

Best Local Similarity 36.4%; Pred. No. 4.6e+02;

Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 8 IHKYLVCESV 18

Db 3 VHTYINCTALN 13

RESULT 8

Q4X4H2 PLACH PRELIMINARY; PRT; 10 AA.

ID Q4X4H2

DT 13-SEP-2005 (TrEMBLrel. 31, Created)

DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DE Hypothetical protein (fragment).

GN ORFNames=PC400586.00.0;

OS Plasmodium chabaudi.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.

OX NCBI_TaxID=5825;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Hall N., Karras M., Raine J.D., Carlton J.M., Kocif T.W.A.,

RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,

RA James K., Rutherford K., Harris B., Harris D., Churcher C.,

RA Quail M.A., Ormond D., Doggett J., Truman H.E., Mendoza J.,

RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,

RA Jansz C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.,

RT "A comprehensive survey of the Plasmodium life cycle by genomic,

RL transcriptomic, and proteomic analyses.";

RL Science 307:82-86(2005).

CC -i CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

DR EMBL; CAAG01010050; CAH88321.1; -; Genomic DNA.

KW Hypothetical protein.

FT NON_TER

SO SEQUENCE 10 AA; 1230 MW; 4C729FD7205059C3 CRC64;

Qy Query Match 27.5%; Score 30; DB 2; Length 10;

Best Local Similarity 30.0%; Pred. No. 7.3e+02;

Matches 3; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 8 IHKYLVCESV 17

Db 1 MHKFTLIQST 10

RESULT 9

Q16244 HUMAN PRELIMINARY; PRT; 18 AA.

ID Q16244

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DE SRS protein (fragment).

GN Name=STS;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

```
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95038775; PubMed=7951263;
RA Yen P.H., Ferrero G.B., Chinault A.C., Mohandas T., Ballabio A.;
RT "Characterization of the deletion breakpoints in a patient with
  steroid sulfatase deficiency."
RL Hum. Mutat. 4:76-78(1994).
DR EMBL; S74383; AAD14153.1; -; Genomic_DNA.
RT NON_TER
FT 18
SQ SEQUENCE 18 AA; 1958 MW; 3B3072711330CCRA CRC64;

Query Match 27.5%; Score 30; DB 2; Length 18;
Best Local Similarity 41.7%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 3 PHPNTHKYLVC 14
DB 7 PCEVNSHSYOLC 18

RESULT 10
TMOF_SARBU STANDARD; PRT; 6 AA.
AC P41495;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Trypsin-modulating oostatic factor (TMOF).
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga; Neobellieria.
OX NCBI_TaxID=7385;
RN [1]
RP PROTEIN SEQUENCE, AND SYNTHESIS.
RX TISSUE-Ovary;
RX MEDLINE=94211930; PubMed=8159807; DOI=10.1016/0167-0115(94)90192-9;
RA Bylemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,
RA de Loof A.;
RT "Sequencing and characterization of trypsin modulating oostatic factor
  (TMOF) from the ovaries of the grey fleshfly, Neobellieria
  (Sarcophaga) bullata."
RL Regul. Pept. 50:61-72(1994).
CC -!- FUNCTION: Has an oostatic activity. Inhibits trypsin biosynthesis
  in the midgut which indirectly reduces the vitellogenin
  concentration in the hemolymph resulting in inhibition of oocyte
  development.
CC -!- DEVELOPMENTAL STAGE: Synthesized and released from follicular
  epithelium after a blood meal.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use as long as its content is in no way modified and this statement is not
  removed.
CC -----
CC Direct protein sequencing; Hormone.
KW SEQUENCE 6 AA; 695 MW; 61E72451B7642000 CRC64;

Query Match 26.6%; Score 29; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 HPTNTH 9
DB 1 NPTNTH 6

RESULT 11
O5EX89_9LAMI PRELIMINARY; PRT; 19 AA.
AC O5EX89;
DT 10-MAY-2005 (TREMBLrel. 30, Created)
```

```
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DE STM2 protein (Fragment).
OS Streptocarpus venosus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroidae; Didymocarpeae;
OC Streptocarpus.
OX NCBI_TaxID=301922;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B;
RX PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
  Streptocarpus."
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662115; AAW33769.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER
FT 19
SQ SEQUENCE 19 AA; 2057 MW; 1069FC9782AFD64A CRC64;

Query Match 26.6%; Score 29; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 2.1e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 3 PHPNTHKYLVCES 16
DB 1 PYPSEXOKTALAES 14

RESULT 12
O4YCP3_PLABE PRELIMINARY; PRT; 21 AA.
AC O4YCP3;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB100163.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandrem M.A., Carnucci D.J., Yates J.R., Kafatos F.C.,
RA Jansz C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
  transcriptomic, and proteomic analyses."
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
  EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
  preliminary data.
CC EMBL; CA01006597; CA104242.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER
FT 1
SQ SEQUENCE 21 AA; 2405 MW; E307CB4E71595CA4 CRC64;

Query Match 26.6%; Score 29; DB 2; Length 21;
Best Local Similarity 35.7%; Pred. No. 2.4e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 6 TTHKYLVCESVNG 19
DB 8 TNESEVAISQDFNG 21
```

RESULT 13

Q5EX77_9LAMI PRELIMINARY; PRT; 19 AA.
ID Q5EX77_9LAMI PRELIMINARY; PRT; 19 AA.
AC Q5EX77_9LAMI PRELIMINARY; PRT; 19 AA.
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE STM1 protein (Fragment).
OS Streptococcus thermophilus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroideae; Didymocarpeae;
OC Streptocarpus.
NCBI_TaxID=167308;
RX PubMed=15659624; DOI=10.1105/lpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk O., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
Streptocarpus";
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662127; AAW33745.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 25.7%; Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.1e+03;

Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 PHPTNIHKYLVCS 16
Db 1 PYPSQSOKLALAS 14

RESULT 14

Q5EX78_9LAMI PRELIMINARY; PRT; 19 AA.
ID Q5EX78_9LAMI PRELIMINARY; PRT; 19 AA.
AC Q5EX78_9LAMI PRELIMINARY; PRT; 19 AA.
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE STM1 protein (Fragment).
OS Streptocarpus glandulosissimus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroideae; Didymocarpeae;
OC Streptocarpus.
NCBI_TaxID=167270;
RX PubMed=15659624; DOI=10.1105/lpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk O., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
Streptocarpus";
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662126; AAW33744.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 25.7%; Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.1e+03;

Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 PHPTNIHKYLVCS 16
Db 1 PYPSQSOKLALAS 14

RESULT 15

Q5EX88_9LAMI PRELIMINARY; PRT; 19 AA.
ID Q5EX88_9LAMI PRELIMINARY; PRT; 19 AA.
AC Q5EX88_9LAMI PRELIMINARY; PRT; 19 AA.
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE STM2 protein (Fragment).
OS Streptocarpus beampingsarattensis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroideae; Didymocarpeae;
OC Streptocarpus.
NCBI_TaxID=167246;
RX PubMed=15659624; DOI=10.1105/lpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk O., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
Streptocarpus";
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662116; AAW33770.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 25.7%; Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.1e+03;

Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 PHPTNIHKYLVCS 16
Db 1 PYPSQSOKLALAS 14

RESULT 16

Q5EX90_9LAMI PRELIMINARY; PRT; 19 AA.
ID Q5EX90_9LAMI PRELIMINARY; PRT; 19 AA.
AC Q5EX90_9LAMI PRELIMINARY; PRT; 19 AA.
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE STM2 protein (Fragment).
OS Streptocarpus venosus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroideae; Didymocarpeae;
OC Streptocarpus.
NCBI_TaxID=301922;
RX PubMed=15659624; DOI=10.1105/lpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk O., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
Streptocarpus";
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662114; AAW33768.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 25.7%; Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.1e+03;

Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 PHPTNIHKYLVCS 16
Db 1 PYPSQSOKLALAS 14

Db 1 PYPSQSOKLALAES 14

RESULT 17

Q5EX91_9LAMI PRELIMINARY; PRT; 19 AA.
AC Q5EX91;
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DE STM2 protein (Fragment).
OS Streptocarpus thompsonii.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Gentianaceae; Cyrtandroidae; Didymocarpaceae;
OC Streptocarpus.
OX NCBI_TaxID=167307;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/lpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
Streptocarpus."
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662113; AAW33767.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR Prodom; PD000010; Homeobox; 1.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 25.7%; Score 28; DB 2; Length 19;

Best Local Similarity 35.7%; Pred. No. 3.1e+03;

Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 PHPTNIHKYLVCS 16

1 PYPSQSOKLALAES 14

RESULT 18

Q5EX92_9LAMI PRELIMINARY; PRT; 19 AA.
AC Q5EX92;
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DE STM2 protein (Fragment).
OS Streptocarpus primulifolius.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Gentianaceae; Cyrtandroidae; Didymocarpaceae;
OC Streptocarpus.
OX NCBI_TaxID=64018;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/lpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
Streptocarpus."
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662112; AAW33766.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR Prodom; PD000010; Homeobox; 1.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 25.7%; Score 28; DB 2; Length 19;

Best Local Similarity 35.7%; Pred. No. 3.1e+03;

Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 PHPTNIHKYLVCS 16

Db 1 PYPSQSOKLALAES 14

RESULT 19
Q5EX94_9LAMI PRELIMINARY; PRT; 19 AA.
AC Q5EX94;
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DE STM2 protein (Fragment).
OS Streptocarpus modestus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Gentianaceae; Cyrtandroidae; Didymocarpaceae;
OC Streptocarpus.
OX NCBI_TaxID=167287;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=A, and B;
RA PubMed=15659624; DOI=10.1105/lpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
Streptocarpus."
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662111; AAW33765.1; -; Genomic_DNA.
DR EMBL; AY662110; AAW33764.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR Prodom; PD000010; Homeobox; 1.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 25.7%; Score 28; DB 2; Length 19;

Best Local Similarity 35.7%; Pred. No. 3.1e+03;

Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 PHPTNIHKYLVCS 16

1 PYPSQSOKLALAES 14

RESULT 20

Q5EX95_9LAMI PRELIMINARY; PRT; 19 AA.
AC Q5EX95;
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DE STM2 protein (STM1 protein) (Fragment).
OS Streptocarpus hirticarpa.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Gentianaceae; Cyrtandroidae; Didymocarpaceae;
OC Streptocarpus.
OX NCBI_TaxID=167276;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/lpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
Streptocarpus."
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662109; AAW33763.1; -; Genomic_DNA.
DR EMBL; AY662122; AAW33740.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR Prodom; PD000010; Homeobox; 1.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 25.7%; Score 28; DB 2; Length 19;

Best Local Similarity 35.7%; Pred. No. 3.1e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 PHPTNHYLVCS 16
|:|:|:|:|
Db 1 PYPESQKLALES 14

RESULT 21

QSEX96_9LAMI PRELIMINARY; PRT; 19 AA.
AC QSEX96;
DT 10-MAY-2005 (TReMBLrel. 30, Created)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DE STW2 protein (STW1 protein) (Fragment).
OS Streptococcus burundianus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroideae; Didymocarpeae;
OC Streptocarpus.
OX NCBI_TaxId=167253;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/lpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
RT Streptocarpus."
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662108; AAW33762.1; -; Genomic_DNA.
DR EMBL; AY662123; AAW33741.1; -; Genomic_DNA.
DR InterPro: IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1
FT NON_TER 19
SO SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 25.7%; Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.1e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 PHPTNHYLVCS 16
|:|:|:|:|
Db 1 PYPESQKLALES 14

RESULT 22

QSEX97_9LAMI PRELIMINARY; PRT; 19 AA.
AC QSEX97;
DT 10-MAY-2005 (TReMBLrel. 30, Created)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
DE STW2 protein (Fragment).
OS Streptocarpus willetii.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroideae; Didymocarpeae;
OC Streptocarpus.
OX NCBI_TaxId=167311;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/lpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
RT Streptocarpus."
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662107; AAW33761.1; -; Genomic_DNA.
DR InterPro: IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1
FT NON_TER 19
SO SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 25.7%; Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.1e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 PHPTNHYLVCS 16
|:|:|:|:|
Db 1 PYPESQKLALES 14

RESULT 23

QSEX98_9LAMI PRELIMINARY; PRT; 19 AA.
AC QSEX98;
DT 10-MAY-2005 (TReMBLrel. 30, Created)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
DE STW2 protein (Fragment).
OS Streptocarpus rexii.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroideae; Didymocarpeae;
OC Streptocarpus.
OX NCBI_TaxId=121488;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/lpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
RT Streptocarpus."
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662106; AAW33760.1; -; Genomic_DNA.
DR InterPro: IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1
FT NON_TER 19
SO SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 25.7%; Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.1e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 PHPTNHYLVCS 16
|:|:~:~:~:~:~
Db 1 PYPESQKLALES 14

RESULT 24

QSEX99_9LAMI PRELIMINARY; PRT; 19 AA.
AC QSEX99;
DT 10-MAY-2005 (TReMBLrel. 30, Created)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
DE STW2 protein (Fragment).
OS Streptocarpus wendlandii.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroideae; Didymocarpeae;
OC Streptocarpus.
OX NCBI_TaxId=167310;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/lpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
RT Streptocarpus."
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662105; AAW33759.1; -; Genomic_DNA.
DR InterPro: IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1
FT NON_TER 19
SO SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

SEQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query March 25.7%; Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.1e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 3 PHPTNHKYLVCES 16
|:|:|:|:
Db 1 PYPSBSQKLALES 14

RESULT 25

OSEXAL_9LAMI PRELIMINARY; PRT; 19 AA.
ID OSEXAL_9LAMI
AC OSEXAL_10-MAY-2005 (TREMBlrel. 30. Created)
DT 10-MAY-2005 (TREMBlrel. 30. Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30. Last annotation update)
DE STM2 protein (Fragment).
OS Streptococcus dunnii.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Gentianales; Gentianaceae; Cyrtandroidae; Didymocarpaceae;
OC Streptocarpus.
OC NCBI_TaxID=121487;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RP PubMed:15659624; DOI=10.1105/lpc.104.028936;
RX Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
RT Streptocarpus."
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662103; AAW33757.1; -, Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query March 25.7%; Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.1e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 3 PHPTNHKYLVCES 16
|:|:|:|:
Db 1 PYPSBSQKLALES 14

Search completed: January 26, 2006, 08:04:02
Job time : 58.5086 secs

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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:47:09 : Search time 67.911 Seconds
(without alignments)
129.360 Million cell updates/sec

Title: US-09-662-293-13

Perfect score: 105
Sequence: 1 DPAKGMSPPGFIVGEEGVLS 20

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 897420

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

A_GeneSeq_21: *
1: geneeqp1980s: *
2: geneeqp1990s: *
3: geneeqp2000s: *
4: geneeqp2001s: *
5: geneeqp2002s: *
6: geneeqp2003as: *
7: geneeqp2003bs: *
8: geneeqp2004s: *
9: geneeqp2005s: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	100.0	20	3	AAV52513 House dus
2	105	100.0	20	3	AAV52522 House dus
3	105	100.0	20	5	AAU96317 Der HMW-m
4	105	100.0	20	5	AAU96326 Der HMW-m
5	37	35.2	21	8	ADR50710 Mouse/r
6	36	34.3	16	8	ADR67576 Nitrilase
7	35	33.3	9	5	AAE28728 Human CAS
8	35	33.3	10	5	AAE28775 Human CAS
9	35	33.3	20	7	AAE28775 Human CAS
10	34	32.4	8	4	AAE09067 Cancer-re
11	34	32.4	8	4	AAE09067 Peptide #
12	34	32.4	8	4	AAE09067 Human aut
13	34	32.4	8	6	ABU07632 Epelein-B
14	34	32.4	11	8	ADR43749 Maximakin
15	34	32.4	12	8	ADR43750 Maximakin
16	34	32.4	13	8	ADR43752 Maximakin
17	34	32.4	18	5	ABP48137 GHR blind
18	34	32.4	18	8	ADR43748 Maximakin
19	34	32.4	19	8	ADN17072 Second ge
20	34	32.4	19	8	ADR43747 Maximakin
21	33	31.4	15	2	AAW18175 Immunodom
22	33	31.4	15	2	AAW75617 M. tuberc
23	33	31.4	15	6	ABU56381 Mycobacte
24	33	31.4	15	7	AAE39326 M. tuberc

25	33	31.4	15	7	ADP45168	Adf45168 M. tuberc
26	33	31.4	15	8	AD036853	Ad036853 Majorly a
27	33	31.4	15	8	ADU64228	ADU64228 30 KD pro
28	33	31.4	16	4	AAU07809	AAU07809 Peptide e
29	33	31.4	20	5	ABP30905	ABP30905 OEB antilb
30	33	31.4	20	7	ADAB08550	ADAB08550 Human OEB
31	33	31.4	20	7	ADFO9099	ADFO9099 Secreted
32	33	31.4	20	7	ADFO8893	ADFO8893 Secreted
33	33	31.4	20	7	ADG46180	ADG46180 OEB antilb
34	33	31.4	20	7	ADK40495	ADK40495 KDR & VEG
35	33	31.4	20	8	ADRA40713	ADRA40713 KDR/ VEGF
36	33	31.4	20	9	ADXL17766	ADXL17766 Human ova
37	33	31.4	20	9	ADXL17982	ADXL17982 Human ova
38	33	31.4	21	8	ADRS0711	ADRS0711 Rat sheat
39	32	30.5	10	5	AAO14949	AAO14949 Surivivin-
40	32	30.5	10	8	ADSS92606	ADSS92606 Platelet
41	32	30.5	15	7	ADBA92200	ADBA92200 Biotinyla
42	32	30.5	16	5	AAU10333	AAU10333 Human PRO
43	32	30.5	16	9	AECL13757	AECL13757 Staphyloc
44	32	30.5	18	6	ABP57840	ABP57840 A. margin
45	32	30.5	20	5	AAU71011	AAU71011 M. tuberc
46	32	30.5	20	7	ADK40519	ADK40519 KDR & VEG
47	32	30.5	20	8	ADRA40737	ADRA40737 KDR/ VEGF
48	31	29.5	9	2	AAW49486	AAW49486 Human leu
49	31	29.5	9	8	AD068173	AD068173 Human 213
50	31	29.5	9	8	AD068472	AD068472 Human 213
51	31	29.5	9	8	AD069312	AD069312 Human 213
52	31	29.5	9	8	AD069700	AD069700 Human 213
53	31	29.5	9	8	AD071975	AD071975 Human 213
54	31	29.5	9	8	AD068215	AD068215 Human 213
55	31	29.5	9	8	AD068624	AD068624 Human 213
56	31	29.5	9	8	AD072059	AD072059 Human 213
57	31	29.5	9	8	AD068890	AD068890 Human 213
58	31	29.5	9	8	AD068347	AD068347 Human 213
59	31	29.5	9	8	AD068354	AD068354 Human 213
60	31	29.5	9	8	AD068030	AD068030 Human 213
61	31	29.5	9	8	AD068858	AD068858 Human 213
62	31	29.5	9	8	AD069100	AD069100 Human 213
63	31	29.5	9	8	AD067954	AD067954 Human 213
64	31	29.5	9	8	AD066277	AD066277 Human 213
65	31	29.5	9	8	AD068944	AD068944 Human 213
66	31	29.5	9	8	AD069211	AD069211 Human 213
67	31	29.5	9	8	AD068650	AD068650 Human 213
68	31	29.5	9	8	AD069433	AD069433 Human 213
69	31	29.5	9	8	AD069643	AD069643 Human 213
70	31	29.5	9	8	AD071860	AD071860 Human 213
71	31	29.5	9	8	AD072141	AD072141 Human 213
72	31	29.5	10	8	AD074908	AD074908 Human 213
73	31	29.5	10	8	AD067058	AD067058 Human 213
74	31	29.5	10	8	AD074471	AD074471 Human 213
75	31	29.5	10	8	AD074828	AD074828 Human 213
76	31	29.5	10	8	AD066467	AD066467 Human 213
77	31	29.5	10	8	AD075227	AD075227 Human 213
78	31	29.5	10	8	AD074526	AD074526 Human 213
79	31	29.5	10	8	AD075022	AD075022 Human 213
80	31	29.5	10	8	AD065940	AD065940 Human 213
81	31	29.5	10	8	AD074212	AD074212 Human 213
82	31	29.5	10	8	AD075255	AD075255 Human 213
83	31	29.5	10	8	AD067592	AD067592 Human 213
84	31	29.5	10	8	AD074085	AD074085 Human 213
85	31	29.5	10	8	AD074939	AD074939 Human 213
86	31	29.5	10	8	AD075094	AD075094 Human 213
87	31	29.5	10	8	AD075374	AD075374 Human 213
88	31	29.5	10	8	AD074213	AD074213 Human 213
89	31	29.5	10	8	AD075134	AD075134 Human 213
90	31	29.5	10	8	AD074599	AD074599 Human 213
91	31	29.5	11	5	ABP62415	ABP62415 Human imm
92	31	29.5	13	2	AAK13452	AAK13452 Residues
93	31	29.5	13	2	AAK13455	AAK13455 Residues
94	31	29.5	14	4	AAAB83040	AAAB83040 Human Sma
95	31	29.5	14	7	ADCC22507	ADCC22507 Protein b
96	31	29.5	15	7	ADP89482	ADP89482 Human E2F
97	31	29.5	15	8	ADK48864	ADK48864 C-termina

AC AAU96317;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Der HMW-map polypeptide #4.
 XX
 XX Der HMW-map; American house dust mite; antiallergic; mite; IgE;
 KM mite allergenic protein; immunoglobulin E; hypersensitivity;
 KM immunocomplex formation.
 XX
 OS Dermatophagoides farinae.
 XX
 PN WO200222807-A2.
 XX
 PD 21-MAR-2002.
 XX
 PF 14-SEP-2001; 2001WO-US028730.
 XX
 PR 14-SEP-2000; 2000US-00662293.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PI Mccall CA, Hunter SW, Weber ER;
 DR WPI; 2002-351888/38.
 XX
 PT New mite allergenic protein isolated from Dermatophagoides, designated
 PS Der HMW-map protein, useful as a vaccine for treating mite allergy.
 XX
 PS Claim 12; Page 70; 161pp; English.
 XX
 CC The invention relates to an isolated mite allergenic protein of
 CC Dermatophagoides, designated Der HMW-map protein, and its related nucleic
 CC acid. The Der HMW-map protein is useful for eliciting an immune response
 CC against Der HMW-map protein. The protein or a reagent comprising a non-
 CC proteinaceous epitope is useful for identifying an animal (e.g., dog,
 CC cat) susceptible to or having an allergic response to a mite. A
 CC therapeutic composition is useful for desensitizing a host animal to an
 CC allergic response to a mite. The DNA and protein can be used in the
 CC detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
 CC of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a
 CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting
 CC binding of proteins to IgE, to prevent immunocomplex formation, thus
 CC reducing hypersensitivity responses to mite allergens, and as vaccines
 CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
 CC represent Der HMW-map polypeptides of the invention
 XX
 SO Sequence 20 AA;
 Query Match 100.0%; Score 105; DB 5; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.7e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DPAKMSPPGFIVGEGVLS 20
 DB 1 DPAKMSPPGFIVGEGVLS 20
 XX
 RESULT 4
 ID AAU96326 standard; peptide: 20 AA.
 XX
 AC AAU96326;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Der HMW-map polypeptide #13.
 XX
 KM Der HMW-map; American house dust mite; antiallergic; mite; IgE;
 KM mite allergenic protein; immunoglobulin E; hypersensitivity;
 KM immunocomplex formation.
 XX
 OS Dermatophagoides farinae.
 XX

XX
 PN WO200222807-A2.
 XX
 PD 21-MAR-2002.
 XX
 PF 14-SEP-2001; 2001WO-US028730.
 XX
 PR 14-SEP-2000; 2000US-00662293.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PI Mccall CA, Hunter SW, Weber ER;
 DR WPI; 2002-351888/38.
 XX
 PT New mite allergenic protein isolated from Dermatophagoides, designated
 PS Der HMW-map protein, useful as a vaccine for treating mite allergy.
 XX
 PS Claim 12; Page 71; 161pp; English.
 XX
 CC The invention relates to an isolated mite allergenic protein of
 CC Dermatophagoides, designated Der HMW-map protein, and its related nucleic
 CC acid. The Der HMW-map protein is useful for eliciting an immune response
 CC against Der HMW-map protein. The protein or a reagent comprising a non-
 CC proteinaceous epitope is useful for identifying an animal (e.g., dog,
 CC cat) susceptible to or having an allergic response to a mite. A
 CC therapeutic composition is useful for desensitizing a host animal to an
 CC allergic response to a mite. The DNA and protein can be used in the
 CC detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
 CC of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a
 CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting
 CC binding of proteins to IgE, to prevent immunocomplex formation, thus
 CC reducing hypersensitivity responses to mite allergens, and as vaccines
 CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
 CC represent Der HMW-map polypeptides of the invention
 XX
 SO Sequence 20 AA;
 Query Match 100.0%; Score 105; DB 5; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.7e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DPAKMSPPGFIVGEGVLS 20
 DB 1 DPAKMSPPGFIVGEGVLS 20
 XX
 RESULT 5
 ID ADR50710 standard; peptide: 21 AA.
 XX
 AC ADR50710;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Mouse/ rat sheathlin peptide SegID 6.
 XX
 KM sheathlin; ameljin; ameloblactin; enamel matrix protein;
 KM proliferation promoter; differentiation promoter; periodontitis;
 KM fracture; bone defect; osteoporosis; osteoarthritis; bone grafting;
 KM bone fenestration; bone cartilage transplantation; bone supplementation;
 KM antiinflammatory; osteopathic.
 XX
 OS Murinae.
 XX
 PN WO2004074319-A1.
 XX
 PD 02-SEP-2004.
 XX
 PF 20-FEB-2004; 2004WO-JP002009.
 XX
 PR 21-FEB-2003; 2003JP-00045166.
 XX
 PR 21-MAY-2003; 2003JP-00142845.

OY 5 GMSPPG 10
 DB 1 GMSPPG 6

RESULT 9
 ID AAE28775 standard; peptide; 10 AA.
 AC AAE28775;
 DT 27-DEC-2002 (first entry)
 DE Human CASB88 antigenic epitope #66.
 XX CASB88 protein; Crohn's disease; Colitis ulcerosa; preneoplastic lesion;
 KM colorectal cancer; Wilm's tumour; retinoblastoma; cancer; gene therapy;
 KM rhabdomyosarcoma; leiomyosarcoma; synovial sarcoma; vaccine; human;
 KM epitope.
 OS Homo sapiens.
 XX WO200250103-A2.
 PN 27-JUN-2002.
 PD 18-SEP-2001; 2001WO-EP010980.
 PF 20-DEC-2000; 2000GB-00031095.
 PR 27-MAR-2001; 2001GB-00007632.
 PR 02-AUG-2001; 2001GB-00018926.
 XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 PA Casb88 J, Coche T, Gaulis SRJ, Orncoft T, Vinals Y De Bassolac;
 PI WPI; 2002-691493/74.
 DR Novel CASB88 polypeptide and polynucleotide useful for treating cancer,
 PT Crohn's disease, colitis ulcerosa, colorectal cancer, lung cancer and
 PT preneoplastic lesions, Wilm's tumor, retinoblastoma and rhabdomyosarcoma.
 XX Claim 6; Page 81; 122pp; English.
 PS The invention relates to novel CASB88 polypeptides and polynucleotides.
 CC Sequences of the invention are used for the treatment of diseases e.g.
 CC Crohn's disease, Colitis ulcerosa, colorectal cancer, lung cancer and
 CC preneoplastic lesions, breast, brain, uterus, muscle, eye and germ cell
 CC cancers, Wilm's tumour, retinoblastoma, rhabdomyosarcoma, leiomyosarcoma
 CC and synovial sarcoma. They are useful in gene therapy and as vaccines.
 CC The present sequence is human CASB88 antigenic epitope
 XX
 SQ Sequence 10 AA;

Query Match 33.3%; Score 35; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 GMSPPG 10
 DB 3 GMSPPG 8

RESULT 9
 ID ADC99464 standard; peptide; 20 AA.
 AC ADC99464;
 DT 01-JAN-2004 (first entry)
 DE Cancer-related DGI-5-binder peptide - SEQ ID 302.

XX cyrostatic; cancer; gene therapy; DGI-2; DGI-5; DGI-7; DGI-9; Hras;
 KM Leptin; VEGF; vascular endothelial growth factor receptor; VEGF-R1;
 KM VEGF-R2; VEGF-R3; FLT1; FMS-related tyrosine kinase 1; FLK1; KDR;
 KM kinase insert domain protein receptor; EGFR; epidermal growth factor;
 KM FGFR1; fibroblast growth factor; Tie-1.
 XX Unidentified.
 OS WO2003035839-A2.
 PN 01-MAY-2003.
 PD 24-OCT-2002; 2002WO-US034021.
 PF 24-OCT-2001; 2001US-0345471P.
 PR (DGI-5) DGI BIOTECHNOLOGIES INC.
 PA Piliulita RC, Brissette R, Spruyt M, Dedova O, Blume A;
 PI Prendergast J, Goldstein N;
 PI WPI; 2003-457332/43.
 DR Selecting target and target binder pairs for preparing a composition for
 XX treating cancer by mixing in a reaction vessel phage expressing
 PT biological targets and phage expressing target binders.
 PT Claim 26; SEQ ID NO 302; 172pp; English.
 PS The invention relates to a novel method of selecting target and target
 CC binder pairs comprising mixing in a reaction vessel phage expressing
 CC biological targets and phage expressing target binders, each having
 CC distinguishable selection markers and selecting target and target binder
 CC pairs based on the selection markers. The molecules of the invention
 CC demonstrate cyrostatic activity whilst the method may be useful for
 CC selecting target and target binder pairs for preparing a composition for
 CC treating cancer. Furthermore, the method may be utilised during gene
 CC therapy procedures. The current sequence is that of the cancer-related
 CC DGI-5-binder peptide of the invention.
 XX
 SQ Sequence 20 AA;

Query Match 33.3%; Score 35; DB 7; Length 20;
 Best Local Similarity 53.3%; Pred. No. 3.4e+02;
 Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 5 GMSPPGRIVEGVL 19
 DB 2 GRUPEMGLVGERGL 16

RESULT 10
 ID AAM65590 standard; peptide; 8 AA.
 AC AAM65590;
 DT 15-OCT-1998 (first entry)
 DE Peptide #6.
 XX Epstein-Barr virus; diagnostic test; autoimmune disease; vaccine;
 KM infection; antibody; screening; genetic marker.
 XX Synthetic.
 OS WO9830586-A2.
 PN 16-JUL-1998.
 PD 13-JAN-1998; 98WO-US000342.

PR 13-JAN-1997; 97US-00781296.
 XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.
 PA
 PI Harley JB, James JA;
 XX WPI; 1998-399062/34.
 DR
 XX Use of Epstein-Barr virus or component(s) - for developing product(s)
 PT which can be used for preventing, diagnosing, treating or determining
 PT risk of developing autoimmune disease.
 PS
 XX Disclosure; Page 54; 81pp; English.
 XX The invention relates to a vaccine for alleviating or preventing
 CC autoimmune disorders induced by infection with Epstein-Barr virus (EBV).
 CC It comprises EBV or a component in a carrier for administration of the
 CC virus or viral component to alleviate or prevent the autoimmune disorder.
 CC Also claimed are: (1) a diagnostic test kit comprising: (a) reagents
 CC which can be used to detect levels of antibodies to EBV, indicators of
 CC EBV infection of cells, or levels of EBV DNA or protein in a patient; (b)
 CC control samples from individuals not at risk of developing an autoimmune
 CC disease; and (c) a device for determining the differences in levels of a
 CC patient and control samples to distinguish individuals at higher risk of
 CC developing an autoimmune disease from those at lower risk of developing
 CC an autoimmune disease; and (2) a method for screening for genetic markers
 CC or risk factors for development of autoimmune disorders induced by
 CC infection with EBV comprising comparing the responses of different
 CC strains of the same species of an animal vaccinated with EBV or a
 CC component to induce an autoimmune response in at least one of the strains
 CC and comparing the differences in the genetics of the different strains to
 CC identify potential genetic markers or risk factors. The methods can be
 CC used for the prevention, diagnosis, and treatment of autoimmune diseases
 CC having EBV as an etiological agent. The autoimmune diseases may be e.g.
 CC systemic lupus erythematosus, Sjogren's syndrome, rheumatoid arthritis,
 CC juvenile onset diabetes mellitus, Wegener's granulomatosis, etc. The
 CC present sequence is shown in the specification
 CC
 XX Sequence 8 AA:
 SQ
 Query Match 32.4%; Score 34; DB 2; Length 8;
 Best Local Similarity 75.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

KM renal cell carcinoma; eosinophilia; immunosuppressive; ophthalmological;
 KM thymimetic; neuroprotective; cyostatic; nephrotropic; antiallergic;
 KM dengue; antitumor; vasotropic; antipruritic; hepatotropic; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200158481-A2.
 XX
 PD 16-AUG-2001.
 XX
 PP 09-FEB-2001; 2001WO-US004191.
 XX
 PR 09-FEB-2000; 2000US-00500904.
 XX
 PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
 XX
 PI Harley JB, James JA, Kaufman KM;
 XX WPI; 2001-522437/57.
 DR
 XX Novel vaccine for alleviating or preventing autoimmune disorders induced
 PT Epstein-Barr virus (EBV) infection e.g. systemic lupus erythematosus,
 PT juvenile onset diabetes mellitus, comprises EBV virus or its component.
 XX
 XX Example 1; Fig 3; 114pp; English.
 XX The present invention relates to a vaccine for alleviating or preventing
 CC autoimmune disorders induced by infection with Epstein-Barr virus (EBV),
 CC comprising EBV or its component in a carrier. The vaccine is useful for
 CC preventing or alleviating autoimmune disorders induced by EBV, e.g.
 CC systemic lupus erythematosus (SLE), Sjogren's syndrome, juvenile onset
 CC diabetes mellitus, rheumatoid arthritis, Wegener's granulomatosis,
 CC inflammatory bowel disease, polymyositis, dermatomyositis, multiple
 CC endocrine failure, Schmidt's syndrome, autoimmune uveitis, Addison's
 CC disease, adrenalitis, primary biliary cirrhosis, Graves' disease,
 CC perniosis, Hashimoto's thyroiditis, autoimmune thyroid disease,
 CC dermatitis and haemolytic anaemia, lupoid hepatitis, demyelinating
 CC disease, multiple sclerosis, subacute cutaneous lupus erythematosus,
 CC hypoparathyroidism, Dressler's syndrome, myasthenia gravis, autoimmune
 CC idiopathic thrombocytopenic purpura, autoimmune pemphigus vulgaris,
 CC pemphigus, bullous pemphigoid, dermatitis herpetiformis, alopecia areata,
 CC autoimmune cystitis, pemphigoid, scleroderma, progressive systemic
 CC sclerosis, CREST syndrome (calcinosis, Raynaud's oesophageal dysmotility,
 CC sclerodactyly and telangiectasia), adult onset diabetes mellitus (Type II
 CC diabetes), male or female autoimmune infertility, ankylosing spondylitis,
 CC ulcerative colitis, Crohn's disease, mixed connective tissue disease,
 CC polyarteritis nodosa, systemic necrotizing vasculitis,
 CC glomerulonephritis, atopic dermatitis, atopic rhinitis, Goodpasture's
 CC syndrome, Chagas' disease, sarcoidosis, rheumatic fever, asthma,
 CC recurrent abortion, anti-phospholipid syndrome, Farmer's lung, erythema
 CC multiforme, postcardiotomy syndrome, Cushing's syndrome, autoimmune
 CC chronic active hepatitis, bird-fancier's lung, allergic
 CC encephalomyelitis, toxic necrodermal lysis, alopecia, Alport's syndrome,
 CC allergic alveolitis, fibrosing alveolitis, interstitial lung disease,
 CC erythema nodosum, pyoderma gangrenosum, transfusion reaction, chronic
 CC fatigue syndrome, fibromyalgia, Takayasu's arteritis, Kawasaki's disease,
 CC polymyalgia rheumatica, temporal arteritis, giant cell arteritis, dengue,
 CC Sampter's syndrome (triaditis, nasal polyps, eosinophilia) and Behcet's
 CC disease, Caplan's syndrome, encephalomyositis, erythema elevatum et
 CC ditinum, psoriasis, erythroblastosis foetalis, Shulman's syndrome, IGA
 CC nephropathy, Felty's syndrome, fascitis with eosinophilia, filariasis,
 CC chronic cystitis, heterochromic cystitis, Fuchs's cystitis, Hodgkin's and
 CC non-Hodgkin's lymphoma, cardiomyopathy, Henoch-Schönlein purpura, post
 CC vaccination syndromes, renal cell carcinoma, Eaton-Lambert syndrome or
 CC relapsing polychondritis. The present sequence is human autoantigen Sm
 CC B/B octapeptide used in the invention
 XX
 SQ Sequence 8 AA:
 Query Match 32.4%; Score 34; DB 4; Length 8;
 Best Local Similarity 75.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKMSPP 9
DB 1 PAPGMRPP 8

RESULT 12
AAB97330
ID AAB97330 standard; peptide; 8 AA.

XX AAB97330;

AC 13-AUG-2001 (first entry)

DE UI RNP with A and C proteins epitope peptide.

XX B cell; toxin; antigen specific; antibody mediated disease; virucide;
KM immunosuppressive; antitubercular; antidiabetic;
KM thyromimetic; antihypertensive; vasodilator; antidiabetic;
KM neuroprotective; antineoplastic; antidiabetic; dermatological;
KM ophthalmological; nephrotoxic; allergy; autoimmune disorder;
KM skin diseases; autoimmune endocrinopathy; vasculitic syndrome;
KM cardiovascular disease; immunohaematologic disorder; neurological disease;
KM gastrointestinal disease; collagen vascular disease; renal diseases;
KM pulmonary disease; infertility disorder; UI-U6 RNP;
KM systemic lupus erythematosus.

XX Unidentified.

XX WO200132853-A1.

XX 10-MAY-2001.

XX 12-OCT-2000; 2000WO-US028157.

XX 29-OCT-1999; 99US-0162464P..

XX (BIOM-) INST APPLIED BIOMEDICINE.

XX Chaplin JM;

XX WPI; 2001-316435/33.

XX B cell clonal toxin useful for treating autoimmune disorders such as
PT Grave's disease, myocardial infarction, Crohn's disease, multiple
PT sclerosis, comprises a group that causes toxin to be internalized by B
PT cell.

XX Disclosure; Page 33; 46pp; English.

XX This invention relates to a B cell clonal toxin. The toxin is made from
CC two moieties, the first causes the toxin to be internalized by a B cell,
CC and the second is a biologically acceptable toxin. The invention includes
CC a method for inactivating/killing an antigen specific B cell. A target B
CC cell is contacted with an effective amount of a B cell clonal toxin. The
CC method is useful for selective immunosuppression in conditions
CC characterized by the presence of an unwanted or deleterious immune
CC response, e.g. in the treatment of antigen specific antibody mediated
CC disease conditions. Use of the B cell clonal toxin can result in
CC immunosuppressive; antitubercular; antidiabetic; virucide; antidiabetic
CC ; thyromimetic; antihypertensive; vasodilator; antidiabetic;
CC neuroprotective; antineoplastic; antidiabetic; dermatological;
CC ophthalmological; and nephrotoxic activity. The toxin is particularly
CC useful for treating a host suffering from an antigen specific antibody
CC mediated disease condition, where the antigen specific antibody is
CC produced by an antigen-reactive B cell population present in a host. The
CC toxin is useful for treating allergies, viral disease conditions, and
CC autoimmune disorders. Also treated are skin diseases; autoimmune
CC endocrinopathies; vasculitic syndromes; cardiovascular disease;
CC immunohaematologic disorders; gastrointestinal diseases; neurologic
CC diseases; collagen vascular diseases; renal diseases; pulmonary diseases;
CC and infertility disorders. The present sequence represents a UI RNP with
CC A and C protein epitope. An antibody response to this antigen is
CC implicated in systemic lupus erythematosus, a disorder which may be

CC created using the toxin of the invention
XX
SQ Sequence 8 AA;

Query Match 32.4%; Score 34; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKMSPP 9
DB 1 PAPGMRPP 8

RESULT 13
ABU07632
ID ABU07632 standard; peptide; 8 AA.

XX ABU07632;

AC 23-OCT-2003 (revised)

DT 10-MAY-2003 (first entry)

DE Epstein-Barr virus nuclear antigen peptide #6.

XX EBV; viral; Epstein-Barr virus nuclear antigen; vaccine;
KM autoimmune disorder; Epstein-Barr virus infection; diabetes mellitus;
KM arthritis; multiple sclerosis; dermatitis; psoriasis; asthma; anaemia;
KM allergy.

XX Human herpesvirus 4.

XX US2002164355-A1.

XX 07-NOV-2002.

XX 24-OCT-2001; 2001US-00012756.

XX 30-NOV-1993; 93US-00160604.

XX 16-MAY-1996; 96US-0019053P.

XX 13-JAN-1997; 97US-00781296.

XX (HARL/) HARLEY J B.

XX (JAME/) JAMES J A.

XX Harley JB, James JA;

XX WPI; 2003-298686/29.

XX Example 1; Fig 3; 41pp; English.

XX The invention relates to a vaccine for alleviating or preventing
CC autoimmune disorders induced by infection with Epstein-Barr virus,
CC comprising an Epstein-Barr virus or a component in a carrier for
CC administration to alleviate or prevent the autoimmune disorders. The
CC methods and compositions of the present invention are useful for
CC diagnosing, preventing, treating and/or alleviating autoimmune disorders,
CC such as diabetes mellitus, rheumatoid arthritis, juvenile rheumatoid
CC arthritis, osteoarthritis, psoriatic arthritis, multiple sclerosis,
CC encephalomyelitis, myasthenia gravis, systemic lupus erythematosus,
CC autoimmune thyroiditis, atopic dermatitis, eczematous dermatitis,
CC psoriasis, Sjogren's Syndrome, Crohn's disease, aphthous ulcer, iritis,
CC conjunctivitis, keratoconjunctivitis, ulcerative colitis, asthma,
CC allergic asthma, cutaneous lupus erythematosus, scleroderma, vaginitis,
CC proctitis, drug eruptions, leprosy reversal reactions, erythema
CC nodosum/erythema, autoimmune uveitis, allergic encephalomyelitis, acute
CC necrotizing haemorrhagic encephalopathy, idiopathic bilateral progressive
CC sensorineural hearing loss, aplastic anaemia, pure red cell anaemia,
CC idiopathic thrombocytopenia, polychondritis, Wegener's granulomatosis,

CC chronic active hepatitis, Stevens-Johnson syndrome, idiopathic sprue,
CC lichen planus, Graves' disease, sarcoidosis, primary biliary cirrhosis,
CC uveitis posterior, interstitial lung fibrosis, graft-versus-host disease,
CC and allergy. The present sequence represents an Epstein-Barr virus
CC nuclear antigen peptide used in the method of the invention. (updated on
CC 23-OCT-2003 to standardise OS field)

XX
SQ Sequence 8 AA:

Query Match 32.4%; Score 34; DB 6; Length 8;
Best Local Similarity 75.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PAKGSP 9
Db 1 PAKGMRP 8

RESULT 14

ID ADR43749 standard; peptide; 11 AA.

XX ADR43749;

DT 04-NOV-2004 (first entry)

DE Maximakinin 8-18 as a bradykinin agonist.

XX bradykinin; Cardiovascular; Vasotropic; Hypotensive; Cytostatic;

KW vascular stenosis; hypertension; tumour; cancer; Maximakinin.

XX Unidentified.

PN WO2004069857-A2.

XX 19-AUG-2004.

PF 06-FEB-2004; 2004WO-GB000470.

PR 06-FEB-2003; 2003GB-00002623.

PR 06-JUN-2003; 2003GB-00012992.

PA (UUTE-) UUTECH LTD.

PI Shaw C, Hirst D, Chen T, O'Rourke M, Rao P;

XX WPI; 2004-604409/58.

Bradykinin agonists comprising maximakinin and its fragments, useful for
PT selectively stimulating arterial smooth muscle bradykinin receptors and
PT for treating cardiovascular disease e.g. ischemic heart disease.

PS Claim 7; SEQ ID NO 3; 67bp; English.

The present invention relates to a bradykinin agonist, useful in the
CC selective stimulation of arterial smooth muscle bradykinin receptors or
CC treatment of cardiovascular disease comprises maximakinin, its analogue
CC or fragment or their encoding nucleic acids. Maximakinin derivatives are
CC used in the preparation of a medicament for selectively stimulating
CC arterial smooth muscle bradykinin receptors; for treating cardiovascular
CC disease (claimed) e.g. ischemic heart disease, occlusion to peripheral
CC organs or organ systems, vascular stenosis, occlusion to peripheral
CC vessels (such as limb), hypertension; and on the treatment of a condition
CC or disorder that can be ameliorated with the selective bradykinin
CC receptor agonist. Also useful for treatment of a condition for which
CC dilation of vessels is required e.g. treatment of tumours and cancers,
CC and for gene therapy. Maximakinin is a selective bradykinin receptor
CC agonist and exhibits both tissue and receptor specific targeting. This
CC tissue selectivity enables the use of the peptides in the treatment of
CC diseases of the cardiovascular system while minimizing the side effects
CC associated with the use of less selective agents. The present sequence
CC represents a maximakinin derivative as a bradykinin agonist

SQ Sequence 11 AA:

Query Match 32.4%; Score 34; DB 8; Length 11;
Best Local Similarity 75.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 KGMSPPGF 11
Db 1 KGPRPPGF 8

RESULT 15

ID ADR43750 standard; peptide; 12 AA.

XX ADR43750;

DT 04-NOV-2004 (first entry)

DE Maximakinin 8-19 as a bradykinin agonist.

XX bradykinin; Cardiovascular; Vasotropic; Hypotensive; Cytostatic;

KW vascular stenosis; hypertension; tumour; cancer; Maximakinin.

XX Unidentified.

PN WO2004069857-A2.

XX 19-AUG-2004.

PF 06-FEB-2004; 2004WO-GB000470.

PR 06-FEB-2003; 2003GB-00002623.

PR 06-JUN-2003; 2003GB-00012992.

PA (UUTE-) UUTECH LTD.

PI Shaw C, Hirst D, Chen T, O'Rourke M, Rao P;

XX WPI; 2004-604409/58.

Bradykinin agonists comprising maximakinin and its fragments, useful for
PT selectively stimulating arterial smooth muscle bradykinin receptors and
PT for treating cardiovascular disease e.g. ischemic heart disease.

PS Claim 7; SEQ ID NO 4; 67bp; English.

The present invention relates to a bradykinin agonist, useful in the
CC selective stimulation of arterial smooth muscle bradykinin receptors or
CC treatment of cardiovascular disease comprises maximakinin, its analogue
CC or fragment or their encoding nucleic acids. Maximakinin derivatives are
CC used in the preparation of a medicament for selectively stimulating
CC arterial smooth muscle bradykinin receptors; for treating cardiovascular
CC disease (claimed) e.g. ischemic heart disease, occlusion to peripheral
CC organs or organ systems, vascular stenosis, occlusion to peripheral
CC vessels (such as limb), hypertension; and on the treatment of a condition
CC or disorder that can be ameliorated with the selective bradykinin
CC receptor agonist. Also useful for treatment of a condition for which
CC dilation of vessels is required e.g. treatment of tumours and cancers,
CC and for gene therapy. Maximakinin is a selective bradykinin receptor
CC agonist and exhibits both tissue and receptor specific targeting. This
CC tissue selectivity enables the use of the peptides in the treatment of
CC diseases of the cardiovascular system while minimizing the side effects
CC associated with the use of less selective agents. The present sequence
CC represents a maximakinin derivative as a bradykinin agonist

SQ Sequence 12 AA;

Query Match 32.4%; Score 34; DB 8; Length 12;
Best Local Similarity 75.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 KGMSPPGF 11

Db 1 KGRPPPGF 8

RESULT 16

ADRA3752 ID ADRA3752 standard; peptide: 13 AA.

AC ADRA3752;

DT 04-NOV-2004 (first entry)

DE Maximakinin 7-19 as a bradykinin agonist.

KM bradykinin; Cardiovascular; Vasotropic; Hypotensive; Cytostatic;

KW vascular stenosis; hypertension; tumour; cancer; Maximakinin.

OS Unidentified.

PN WO2004069857-A2.

PD 19-AUG-2004.

PF 06-FEB-2004; 2004WO-GB000470.

PR 06-FEB-2003; 2003GB-00002623.

PR 06-JUN-2003; 2003GB-00012992.

PA (UUTE-) UUTECH LTD.

PI Shaw C, Hirst D, Chen T, O'Rourke M, Rao P;

DR WPI; 2004-604409/58.

PT Bradykinin agonists comprising maximakinin and its fragments, useful for selectively stimulating arterial smooth muscle bradykinin receptors and for treating cardiovascular disease e.g. ischemic heart disease.

PS Claim 7; SEQ ID NO 6; 67pp; English.

CC The present invention relates to a bradykinin agonist, useful in the CC selective stimulation of arterial smooth muscle bradykinin receptors or CC treatment of cardiovascular disease comprises maximakinin, its analogue CC or fragment or their encoding nucleic acids. Maximakinin derivatives are CC used in the preparation of a medicament for selectively stimulating CC arterial smooth muscle bradykinin receptors; for treating cardiovascular CC disease (claimed) e.g. ischemic heart disease, ischemic disease of other CC organs or organ systems, vascular stenosis, occlusion to peripheral CC vessels (such as limb), hypertension; and on the treatment of a condition CC or disorder that can be ameliorated with the selective bradykinin CC receptor agonist. Also useful for treatment of a condition for which CC dilation of vessels is required e.g. treatment of tumours and cancers, CC and for gene therapy. Maximakinin is a selective bradykinin receptor CC agonist and exhibits both tissue and receptor specific targeting. This CC tissue selectivity enables the use of the peptides in the treatment of CC diseases of the cardiovascular system while minimizing the side effects CC associated with the use of less selective agents. The present sequence CC represents a maximakinin derivative as a bradykinin agonist

SQ Sequence 13 AA;

Query Match 32.4%; Score 34; DB 8; Length 13;

Best Local Similarity 75.0%; Pred. No. 3.1e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 KGMSPPGF 11

DB 2 KGRPPPGF 9

RESULT 17

ABPA8137 ID ABPA8137 standard; peptide: 18 AA.

XX AC ABPA8137;

XX DT 23-AUG-2002 (first entry)

DE GHR binding H5 peptide secondary library sequence #13.

KW Growth hormone; receptor; osteopathic; endocrine; hormonal; dwarfism;

KW acromegaly; animal husbandry; milk production; GHR.

OS Synthetic.

PN US6387879-B1.

PD 14-MAY-2002.

PF 15-DEC-1997; 97US-00990888.

PR 15-DEC-1997; 97US-00990888.

PA (DGIB-) DGI BIOTECHNOLOGIES INC.

PI Blume AJ, Bissette R, Carcamo J, Manddecki WS, Tang PM;

DR WPI; 2002-478462/51.

PT New amino acid sequences fully defined in the specification mimic growth PT hormones and are useful to treat conditions such as dwarfism and PT acromegaly, and to promote growth and milk production in cows.

PS Claim 1; Fig 15A; 46pp; English.

CC The invention relates to novel amino acid sequences which bind CC specifically to growth hormone receptor (GHR). The peptides of the CC invention have osteopathic, endocrine; and hormonal activity. The amino CC acid sequences are useful to treat dwarfism and acromegaly, and in animal CC husbandry to promote growth and milk production in cows. The sequence CC represents a growth hormone receptor binding peptide of the invention

SQ Sequence 18 AA;

Query Match 32.4%; Score 34; DB 5; Length 18;

Best Local Similarity 60.0%; Pred. No. 4.4e+02;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 5 GMSPPGFIVG 14

DB 6 GVSYPGWLVG 15

RESULT 18

ADRA3748 ID ADRA3748 standard; peptide: 18 AA.

AC ADRA3748;

DT 04-NOV-2004 (first entry)

DE Maximakinin 1-18 as a bradykinin agonist.

KM bradykinin; Cardiovascular; Vasotropic; Hypotensive; Cytostatic;

KW vascular stenosis; hypertension; tumour; cancer; Maximakinin.

OS Unidentified.

PN WO2004069857-A2.

PD 19-AUG-2004.

PF 06-FEB-2004; 2004WO-GB000470.

PR 06-FEB-2003; 2003GB-00002623.

PR 06-JUN-2003; 2003GB-00012992.

XX (UUTE-) UUTECH LTD.
XX
XX Shaw C, Hirst D, Chen T, O'Rourke M, Rao P;
XX WPI; 2004-604409/58.
XX
XX Bradykinin agonists comprising maximakinin and its fragments, useful for
PT selectively stimulating arterial smooth muscle bradykinin receptors and
PT for treating cardiovascular disease e.g. ischemic heart disease.
XX
XX Claim 7; SEQ ID NO 2; 67pp; English.
XX
XX The present invention relates to a bradykinin agonist, useful in the
CC selective stimulation of arterial smooth muscle bradykinin receptors or
CC treatment of cardiovascular disease comprises maximakinin, its analogue
CC or fragment or their encoding nucleic acids. Maximakinin derivatives are
CC used in the preparation of a medicament for selectively stimulating
CC arterial smooth muscle bradykinin receptors, for treating cardiovascular
CC disease (claimed) e.g. ischemic heart disease, ischemic disease of other
CC organs or organ systems, vascular stenosis, occlusion to peripheral
CC vessels (such as limb), hypertension; and on the treatment of a condition
CC or disorder that can be ameliorated with the selective bradykinin
CC receptor agonist. Also useful for treatment of a condition for which
CC dilation of vessels is required e.g. treatment of tumours and cancers,
CC and for gene therapy. Maximakinin is a selective bradykinin receptor
CC agonist and exhibits both tissue and receptor specific targeting. This
CC tissue selectivity enables the use of the peptides in the treatment of
CC diseases of the cardiovascular system while minimizing the side effects
CC associated with the use of less selective agents. The present sequence
CC represents a maximakinin derivative as a bradykinin agonist
XX
XX Sequence 18 AA;
SQ

Query Match 32.4%; Score 34; DB 8; Length 18;
Best Local Similarity 75.0%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 KGMSPPGF 11
|||
|||
Db 8 KQPRPPGF 15

RESULT 19
ADN17072
ID ADN17072 standard; peptide; 19 AA.
XX
XX ADN17072;
AC
XX
XX 15-JUL-2004 (first entry)
DT
XX
XX Second generation G protein library g-alpha peptide, SEQ ID No 81.
DE
XX G alpha subunit; G protein; G protein coupled receptor; GPCR;
KW allosteric modulator; g-alpha.
XX
XX Unidentified.
OS
XX WO2004035614-A1.
PN
XX
XX 29-APR-2004.
PD
XX
XX 15-JAN-2003; 2003WO-EP000352.
PF
XX
XX 18-OCT-2002; 2002US-0419143P.
PR
XX
XX (KARO-) KARO BIO AB.
PA
XX
XX Fowles DM, Christensen DJ, Hamilton PT, Blasius R, Ramer JK;
PI Hyde-Derzytscher R, Duffin D, Fredericks Z,
XX WPI; 2004-365151/34.
DR
XX

PT New synthetic or partially purified peptides that can bind to specific
PT subunits of G proteins, useful for detecting the activation or
PT deactivation of a G protein-coupled receptor (GPCR) or for identifying
PT allosteric modulators of GPCR.
XX
XX Example 300d; SEQ ID NO 81; 242pp; English.
XX

XX The invention relates to a novel non-naturally occurring and/or at least
CC partially purified peptide, which does not comprise a V-H or V-L homology
CC unit of an antibody and specifically binds to an activated G alpha
CC subunit of a G protein. The invention further comprises: an assay kit for
CC the identification of the activation state of a G protein coupled
CC receptor (GPCR), the kit comprising a first peptide cited above labeled
CC with a first label; methods of identifying the activation state of a GPCR
CC; a method of identifying a modulator of a GPCR; a method of determining
CC the presence or amount of a modulator of a GPCR in a sample; methods of
CC identifying a substance as an agonist or antagonist of GPCR; and a method
CC of identifying a G-alpha subunit which interacts with a GPCR. The
CC composition and methods are useful in detecting the activation or
CC deactivation of a G protein-coupled receptor or in monitoring the
CC activation state of a GPCR within a cell. These may also be used for
CC identifying allosteric modulators of GPCRs. This sequence represents a G
CC protein library g-alpha peptide oligo of the invention.
XX
XX Sequence 19 AA;
SQ

Query Match 32.4%; Score 34; DB 8; Length 19;
Best Local Similarity 72.7%; Pred. No. 4.6e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 GFIVGEGVLS 20
|
|
|
|
|
Db 8 GIWVGEGRLS 18

RESULT 20
ADR43747
ID ADR43747 standard; peptide; 19 AA.
XX

AC ADR43747;
XX

DT 04-NOV-2004 (first entry)
XX

DE Maximakinin 1-19 as a bradykinin agonist.
XX

KW bradykinin; Cardiovascular; Vasotropic; Hypotensive; Cytostatic;
XX

KW vascular stenosis; hypertension; tumour; cancer; Maximakinin.
XX

XX Unidentified.
OS

PN WO2004069857-A2.
XX

PD 19-AUG-2004.
XX

DE 06-FEB-2004; 2004WO-GB000470.
XX

PF 06-FEB-2003; 2003GB-00002623.
XX

PR 06-JUN-2003; 2003GB-00012992.
XX

PA (UUTE-) UUTECH LTD.
XX

PI Shaw C, Hirst D, Chen T, O'Rourke M, Rao P;
XX

DR WPI; 2004-604409/58.
XX

XX Bradykinin agonists comprising maximakinin and its fragments, useful for
PT selectively stimulating arterial smooth muscle bradykinin receptors and
PT for treating cardiovascular disease e.g. ischemic heart disease.
XX

PS Disclosure; SEQ ID NO 1; 67pp; English.
XX

XX The present invention relates to a bradykinin agonist, useful in the
CC selective stimulation of arterial smooth muscle bradykinin receptors or

CC treatment of cardiovascular disease comprises maximakinin, its analogue
 CC or fragment or their encoding nucleic acids. Maximakinin derivatives are
 CC used in the preparation of a medicament for selectively stimulating
 CC arterial smooth muscle bradykinin receptors, for treating cardiovascular
 CC disease (claimed) e.g. ischemic heart disease, ischemic disease of other
 CC organs or organ systems, vascular stenosis, occlusion to peripheral
 CC vessels (such as limb), hypertension; and on the treatment of a condition
 CC or disorder that can be ameliorated with the selective bradykinin
 CC receptor agonist. Also useful for treatment of a condition for which
 CC dilation of vessels is required e.g. treatment of tumours and cancers,
 CC and for gene therapy. Maximakinin is a selective bradykinin receptor
 CC agonist and exhibits both tissue and receptor specific targeting. This
 CC tissue selectivity enables the use of the peptides in the treatment of
 CC diseases of the cardiovascular system while minimizing the side effects
 CC associated with the use of less selective agents. The present sequence
 CC represents maximakinin 1-19 as a bradykinin agonist
 XX

SQ Sequence 19 AA;
 Query Match 33.4%; Score 34; DB 8; Length 19;
 Best Local Similarity 75.0%; Pred. No. 4.6e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 KGMSPGPF 11
 |||||
 Db 8 KGRPRPGF 15

RESULT 21
 AAW18175
 ID AAW18175 standard; peptide: 15 AA.
 XX
 AC AAW18175;
 DT 13-AUG-1997 (first entry)
 XX
 DE Immunodominant epitope from Mycobacterium tuberculosis 30KD protein.
 XX
 KM Vaccine; vaccinating agent; M. tuberculosis; pathogen; bacteria; virus;
 KM fungus; protozoan; HIV.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN M09637219-A1.
 XX
 PD 28-NOV-1996.
 XX
 PF 23-MAY-1996; 96WO-US007781.
 XX
 PR 23-MAY-1995; 95US-00447398.
 PR 20-OCT-1995; 95US-00545926.
 PR 31-OCT-1995; 95US-00551149.
 PR 06-DEC-1995; 95US-00568357.
 XX
 PA (REGC) UNIV CALIFORNIA.
 PI Horwitz MA, Harth G;
 DR WPI; 1997-020936/02.
 XX
 PT Vaccines derived from M. tuberculosis major abundant extracellular
 PT proteins - are easy to prepare and less toxic than conventional Killed or
 PT attenuated vaccines, useful for protecting against or treating
 PT Mycobacterial infections.
 XX
 PS Claim 49; Page 162; 193pp; English.
 XX
 CC A vaccinating agent for promoting an immune response in a mammal against
 CC Mycobacterium pathogen comprises at least one immunodominant epitope of
 CC at least one majorly abundant extracellular protein, i.e. the
 CC M. tuberculosis 110, 80, 71, 58, 45, 32A, 32B, 30, 24, 23.5, 23, 16, 14 or
 CC 12 kD proteins, or their analogues, homologues and subunits. The present
 CC sequence represents an immunodominant epitope from the major abundant

CC extracellular product 30 kD protein. The vaccinating agents are used to
 CC protect against (or to treat existing) infections by Mycobacterium
 CC (especially M. tuberculosis) while the epitopes can also be used to
 CC detect presence of an immune response to a Mycobacterium pathogen. The
 CC vectors, containing the DNA for the extracellular proteins, are used to
 CC transform cells for production of recombinant DNA molecules. More
 CC generally the DNA from other pathogens can be used in vaccines, e.g.
 CC against other bacteria, viruses, fungi and protozoa. Since different
 CC combinations of DNA can be used, a wide range of effective compositions
 CC can be produced. They generate a response against the antigens most often
 CC found on infected cells during the infection, regardless of the strength
 CC or specificity of the immune response. The vaccines are easy to produce
 CC and less toxic than known killed or attenuated vaccines, so can be given
 CC to immunocompromised subjects, e.g. those with HIV infection
 XX

SQ Sequence 15 AA;
 Query Match 31.4%; Score 33; DB 2; Length 15;
 Best Local Similarity 62.5%; Pred. No. 5.1e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKMGSP 8
 ||::|||
 Db 4 DPSQGMGP 11

RESULT 22
 AAW75617
 ID AAW75617 standard; peptide: 15 AA.
 XX
 AC AAW75617;
 DT 23-OCT-1998 (first entry)
 XX
 DE M. tuberculosis 30 kD protein derived peptide 31 (residues 151-165).
 XX
 KM Mycobacterium tuberculosis; vaccination; extracellular product;
 KM immunodominant epitope; interleukin-12; M559; immune response;
 KM opsonising humoral response; intracellular pathogen.
 XX
 OS Synthetic.
 XX
 PN Mycobacterium tuberculosis.
 XX
 PD M09831388-A1.
 XX
 PF 23-JUL-1998.
 XX
 PR 15-JAN-1998; 98WO-US000942.
 XX
 PR 21-JAN-1997; 97US-00786533.
 XX
 PA (REGC) UNIV CALIFORNIA.
 PI Horwitz MA, Harth G, Lee B;
 DR WPI; 1998-413815/35.
 XX
 PT Vaccines against Mycobacterium containing major extracellular proteins -
 PT used to, e.g. induce protective and therapeutic immune responses, and for
 PT detecting an immune response.
 XX
 PS Example 28; Page 96; 236pp; English.
 XX
 CC Sequences shown in AAW75587 to AAW75641 represent synthetic peptides
 CC derived from the native 30kD major secretory protein of M. tuberculosis.
 CC These peptides are used for splenic lymphocyte proliferation assays to
 CC identify the immunodominant T-cell epitope of the 30kD protein. The
 CC invention provides an agent for vaccinating mammals against
 CC Mycobacterium. The agent comprises at least one of the major abundant
 CC extracellular 110, 80, 71, 58, 45, 32A, 32B, 30, 24, 23.5, 23, 16, 14 or
 CC 12 kD proteins of M. tuberculosis, or at least 1 of their immunodominant
 CC epitopes and interleukin-12 (IL-12) or M559 as adjuvants. The agent
 CC containing the nucleic acid encoding the extracellular products are used

CC to raise a protective or therapeutic immune response against
CC Mycobacterium, specifically M. tuberculosis. The immunodominant epitopes
CC can also be used (typically in a cutaneous hypersensitivity test) to
CC detect an immune response to vaccination. Preparation of the agent does
CC not require selection of the most immunogenic products, so large scale
CC production and purification are easy, resulting in a consistent,
CC standardised formulation, having lower toxicity than killed or attenuated
CC vaccines. The agents provide a rapid and effective response (including a
CC strong cell-mediated component) and are safe even in immunocompromised
CC subjects. They prevent development of an opsonising humoral response that
CC might spread intracellular pathogens

XX
SQ Sequence 15 AA;

Query Match 31.4%; Score 33; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 5.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKGMSP 8
||:|:|
Db 4 DPSQGMGP 11

RESULT 23
ABUS6381
ID ABUS6381 standard; peptide; 15 AA.
XX
AC ABUS6381;
XX
DT 31-MAR-2003 (first entry)
XX
DE Mycobacterium tuberculosis 30kDa protein fragment #31.
XX
KW Antibacterial; tuberculosis; vaccine; gene therapy; 30kda protein.
XX
OS Synthetic.
XX
PN US2002131975-A1.
XX
PD 19-SEP-2002.
XX
PF 14-SEP-2001; 2001US-00953510.
XX
PR 23-NOV-1993; 93US-00156358.
PR 12-AUG-1994; 94US-00289667.
PR 23-MAY-1995; 95US-00447398.
PR 31-OCT-1995; 95US-00551149.
PR 06-DEC-1995; 95US-00568357.
PR 23-MAY-1996; 96US-00652842.
PR 21-SEP-1998; 98US-00157689.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Horwitz MA, Harch G;
XX
DR WPI; 2003-174073/17.
XX
PT New vaccine, useful for promoting an immune response against infectious
PT pathogens of the genus Mycobacterium in a mammalian host.
XX
PS Claim 3; Page 66; 82pp; English.
XX
CC The invention describes a vaccine for promoting an immune response, in a
CC mammalian host, against infectious pathogens of the genus Mycobacterium,
CC comprising at least 1 immunodominant epitope of at least one majority
CC abundant extracellular product comprising Mycobacterium tuberculosis 110,
CC 80, 71, 58, 45, 32A, 32B, 30, 24, 23.5, 23, 16, 14, 12 KD protein or
CC their analogues, homologues or subunits. The proteins and polypeptides of
CC the invention are useful in gene therapy and treatment of diseases caused
CC by Mycobacterium such as tuberculosis. This sequence represents a
CC fragment of the Mycobacterium tuberculosis 30kDa protein

XX
SO Sequence 15 AA;

Query Match 31.4%; Score 33; DB 6; Length 15;
Best Local Similarity 62.5%; Pred. No. 5.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKGMSP 8
||:|:|
Db 4 DPSQGMGP 11

RESULT 24
AAE39326
ID AAE39326 standard; peptide; 15 AA.
XX
AC AAE39326;
XX
DT 18-DEC-2003 (first entry)
XX
DE M. tuberculosis 30 KD protein immunodominant T-cell epitope peptide #31.
XX
KW Vaccine; antibacterial; fungicide; protozoacide; immunostimulant;
KW virucide; therapy.
XX
OS Mycobacterium tuberculosis.
XX
PN US6599510-B1.
XX
PD 29-JUL-2003.
XX
PF 21-SEP-1998; 98US-00157689.
XX
PR 23-NOV-1993; 93US-00156358.
PR 12-AUG-1994; 94US-00289667.
PR 23-MAY-1995; 95US-00447398.
PR 31-OCT-1995; 95US-00551149.
PR 06-DEC-1995; 95US-00568357.
PR 23-MAY-1996; 96US-00652842.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Horwitz MA, Harch G;
XX
DR WPI; 2003-669607/63.
XX
PT A nucleic acid encoding an abundant extracellular protein of
PT Mycobacterium tuberculosis useful as vaccines for generating protective
PT or therapeutic immune response against viral, bacterial, fungal or
PT protozoal infections.
XX
PS Example 25; Col 64; 82pp; English.
XX
CC The invention relates to a novel nucleic acid encoding an abundant
CC extracellular protein of Mycobacterium tuberculosis useful as vaccines
CC for generating protective or therapeutic immune response against viral,
CC bacterial, fungal and protozoal infections. They are also used as
CC immunotherapeutic agents. The present sequence is M. tuberculosis strain
CC Erdman 30 KD major secretory protein immunodominant T-cell epitope
CC peptide

XX
SQ Sequence 15 AA;

Query Match 31.4%; Score 33; DB 7; Length 15;
Best Local Similarity 62.5%; Pred. No. 5.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKGMSP 8
||:|:|
Db 4 DPSQGMGP 11

RESULT 25
ADP45168
ID ADP45168 standard; peptide; 15 AA.

Search completed: January 26, 2006, 07:58:12
Job time : 70.931 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:50:06 ; Search time 18.7931 Seconds
(without alignments)
87.985 Million cell updates/sec

Title: US-09-662-293-13

Perfect score: 105

Sequence: 1 DPAKMSPPGRTVCEGVLS 20

Scoring table: BLOSUM62

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 229350

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5-COMB pep: *
2: /cgn2_6/ptodata/1/1aa/6-COMB pep: *
3: /cgn2_6/ptodata/1/1aa/H-COMB pep: *
4: /cgn2_6/ptodata/1/1aa/PTUS-COMB pep: *
5: /cgn2_6/ptodata/1/1aa/RE-COMB pep: *
6: /cgn2_6/ptodata/1/1aa/Backfile1 pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	100.0	20	2	US-09-293-225-4
2	105	100.0	20	2	US-09-293-225-13
3	35	33.3	21	2	US-09-270-767-58368
4	34	32.4	8	2	US-08-475-955-116
5	34	32.4	8	2	US-07-867-819D-116
6	34	32.4	9	2	US-08-475-955-100
7	34	32.4	9	2	US-07-867-819D-100
8	34	32.4	18	2	US-08-990-888-28
9	33	31.4	15	2	US-09-157-689-67
10	33	31.4	15	2	US-09-953-510-67
11	33	31.4	20	2	US-09-667-857-397
12	33	31.4	20	2	US-10-198-053-397
13	33	31.4	20	2	US-10-198-053-603
14	33	31.4	16	1	US-08-483-142-137
15	33	29.5	16	1	US-08-478-572-185
16	31	29.5	16	1	US-08-484-286-185
17	31	29.5	18	2	US-08-990-888-36
18	31	29.5	18	2	US-09-570-022-13
19	31	29.5	18	2	US-09-635-501-29
20	31	29.5	20	2	US-10-007-700-463
21	31	29.5	8	2	US-08-475-955-12
22	30	28.6	8	2	US-08-475-955-205
23	30	28.6	8	2	US-08-475-955-206
24	30	28.6	8	2	US-07-867-819D-112
25	30	28.6	8	2	US-07-867-819D-113
26	30	28.6	8	2	US-07-867-819D-113
27	30	28.6	8	2	US-07-867-819D-113

28	30	28.6	10	2	US-08-476-509B-32	Sequence 32, App1
29	30	28.6	10	2	US-08-476-509B-35	Sequence 35, App1
30	30	28.6	10	2	US-08-988-242-11	Sequence 11, App1
31	30	28.6	11	1	US-08-526-764-1	Sequence 1, App1
32	30	28.6	12	2	US-08-988-242-10	Sequence 10, App1
33	30	28.6	12	2	US-07-867-819D-14	Sequence 14, App1
34	30	28.6	14	2	US-08-630-916A-53	Sequence 53, App1
35	30	28.6	14	2	US-08-630-916A-54	Sequence 54, App1
36	30	28.6	14	2	US-09-509-325B-20	Sequence 20, App1
37	30	28.6	18	2	US-08-990-888-25	Sequence 25, App1
38	30	28.6	18	2	US-08-990-888-55	Sequence 65, App1
39	30	28.6	19	2	US-09-010-999-9	Sequence 9, App1
40	30	28.6	19	2	US-09-470-830A-27	Sequence 27, App1
41	30	28.6	20	2	US-08-928-213B-128	Sequence 128, App
42	30	28.6	20	2	US-08-928-213B-129	Sequence 129, App
43	30	28.6	21	1	US-08-325-071-16	Sequence 16, App1
44	30	28.6	21	1	US-08-325-071-32	Sequence 32, App1
45	30	28.6	21	2	US-08-461-004A-16	Sequence 16, App1
46	30	28.6	21	2	US-08-461-004A-32	Sequence 32, App1
47	29.5	28.1	14	1	US-07-721-761A-17	Sequence 17, App1
48	29.5	28.1	14	1	US-07-978-687-17	Sequence 17, App1
49	29.5	28.1	14	4	PCT-US91-05801-17	Sequence 17, App1
50	29.5	28.1	17	1	US-07-721-761A-10	Sequence 10, App1
51	29.5	28.1	17	1	US-07-978-687-10	Sequence 10, App1
52	29.5	28.1	17	4	PCT-US91-05801-10	Sequence 10, App1
53	29	27.6	8	2	US-08-160-604-1	Sequence 1, App1
54	29	27.6	8	2	US-08-475-955-123	Sequence 123, App
55	29	27.6	8	2	US-09-718-693A-3	Sequence 3, App1
56	29	27.6	8	2	US-07-867-819D-147	Sequence 147, App
57	29	27.6	8	2	US-07-867-819D-149	Sequence 149, App
58	29	27.6	8	2	US-07-867-819D-157	Sequence 157, App
59	29	27.6	11	2	US-08-475-955-10	Sequence 10, App1
60	29	27.6	11	2	US-07-867-819D-10	Sequence 10, App1
61	29	27.6	12	2	US-08-475-955-14	Sequence 14, App1
62	29	27.6	16	1	US-07-994-469A-21	Sequence 21, App1
63	29	27.6	16	1	US-08-482-142-186	Sequence 186, App
64	29	27.6	16	1	US-08-478-572-186	Sequence 186, App
65	29	27.6	16	2	US-08-484-286-186	Sequence 186, App
66	29	27.6	18	2	US-08-990-888-46	Sequence 46, App1
67	29	27.6	18	2	US-08-990-888-62	Sequence 62, App1
68	29	27.6	18	2	US-09-010-999-8	Sequence 8, App1
69	29	27.6	20	2	US-09-980-177A-77	Sequence 77, App1
70	29	27.6	20	2	US-10-007-700-413	Sequence 413, App
71	29	27.6	21	1	US-08-325-071-31	Sequence 31, App1
72	29	27.6	21	1	US-08-461-004A-31	Sequence 31, App1
73	29	27.6	21	2	US-10-394-880-149	Sequence 149, App
74	28.5	27.1	5	1	US-08-488-470A-7	Sequence 7, App1
75	28	26.7	5	1	US-07-946-239-15	Sequence 15, App1
76	28	26.7	5	1	US-08-484-205A-7	Sequence 7, App1
77	28	26.7	5	1	US-08-383-766-3	Sequence 3, App1
78	28	26.7	5	2	US-09-151-467-15	Sequence 15, App1
79	28	26.7	5	2	US-09-078-403A-7	Sequence 7, App1
80	28	26.7	5	2	US-09-256-838-15	Sequence 15, App1
81	28	26.7	5	2	US-09-261-718-3	Sequence 3, App1
82	28	26.7	5	4	PCT-US92-07815-15	Sequence 15, App1
83	28	26.7	8	2	US-08-475-955-117	Sequence 117, App
84	28	26.7	8	2	US-07-867-819D-117	Sequence 117, App
85	28	26.7	9	2	US-09-769-180-11	Sequence 11, App1
86	28	26.7	13	2	US-08-630-916A-85	Sequence 85, App1
87	28	26.7	14	2	US-08-630-916A-141	Sequence 141, App
88	28	26.7	14	2	US-09-879-957-141	Sequence 141, App
89	28	26.7	15	6	5187078-4	Patent No. 5187078
90	28	26.7	18	2	US-08-630-916A-9	Sequence 9, App1
91	28	26.7	18	2	US-08-990-888-30	Sequence 30, App1
92	28	26.7	18	2	US-08-990-888-69	Sequence 69, App1
93	28	26.7	18	2	US-09-292-225-12	Sequence 12, App1
94	28	26.7	19	2	US-09-570-022-12	Sequence 12, App1
95	28	26.7	19	2	US-09-068-624-2	Sequence 2, App1
96	28	26.7	19	2		
97	28	26.7	19	2		
98	28	26.7	19	2		
99	28	26.7	19	2		
100	28	26.7	19	2		

ALIGNMENTS

RESULT 1

US-09-292-225-4
; Sequence 4, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; EARLIER FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 4
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-4

Query Match 100.0%; Score 105; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DPAKMSPPGFIVEGVLS 20
Db 1 DPAKMSPPGFIVEGVLS 20

RESULT 2

US-09-292-225-13
; Sequence 13, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; EARLIER FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 13
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-13

Query Match 100.0%; Score 105; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DPAKMSPPGFIVEGVLS 20
Db 1 DPAKMSPPGFIVEGVLS 20

RESULT 3

US-09-270-767-58368
; Sequence 58368, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; EARLIER FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 58368
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-58368

Query Match 33.3%; Score 35; DB 2; Length 21;
Best Local Similarity 54.5%; Pred. No. 49;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 6 MSPPGFIVEG 16
Db 11 IAPGGRIDGE 21

RESULT 4

US-08-475-955-116
; Sequence 116, Application US/08475955
; Patent No. 6641813
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1250 West Peachtree Street
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,955
; FILING DATE: June 7, 1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/867,819
; FILING DATE: April 13, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/648,205
; FILING DATE: January 31, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/472,947
; FILING DATE: January 31, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284

REFERENCE/DOCKET NUMBER: OMRf114CIP(2)DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-475-955-116

Query Match 32.4%; Score 34; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGMSP 9
Db 1 PAKGMRP 8

RESULT 5
US-07-867-819D-116
Sequence 116, Application US/07867819D
Patent No. 6897287
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies
FILE REFERENCE: OMRf 114 CIP (2)
CURRENT APPLICATION NUMBER: US/07/867,819D
CURRENT FILING DATE: 1992-04-13
PRIOR APPLICATION NUMBER: 07/472,947
PRIOR FILING DATE: 1990-01-31
PRIOR APPLICATION NUMBER: 07/648,205
PRIOR FILING DATE: 1991-01-31
NUMBER OF SEQ ID NOS: 161
SOFTWARE: PatentIn version 3.1
SEQ ID NO 116
LENGTH: 8
TYPE: PRT
ORGANISM: homo sapien
US-07-867-819D-116

Query Match 32.4%; Score 34; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGMSP 9
Db 1 PAKGMRP 8

RESULT 6
US-08-475-955-100
Sequence 100, Application US/08475955
Patent No. 6641813
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
TITLE OF INVENTION: AUTOANTIBODIES
NUMBER OF SEQUENCES: 218
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patricia L. Pabst
STREET: 2800 One Atlantic Center, 1250 West Peachtree Street
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,955
FILING DATE: June 7, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patricia L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRf114CIP(2)DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Binding-site
LOCATION: 1..8
US-08-475-955-100

Query Match 32.4%; Score 34; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGMSP 9
Db 2 PAKGMRP 9

RESULT 7
US-07-867-819D-100
Sequence 100, Application US/07867819D
Patent No. 6897287
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies
FILE REFERENCE: OMRf 114 CIP (2)
CURRENT APPLICATION NUMBER: US/07/867,819D
CURRENT FILING DATE: 1992-04-13
PRIOR APPLICATION NUMBER: 07/472,947
PRIOR FILING DATE: 1990-01-31
PRIOR APPLICATION NUMBER: 07/648,205
PRIOR FILING DATE: 1991-01-31
NUMBER OF SEQ ID NOS: 161
SOFTWARE: PatentIn version 3.1
SEQ ID NO 100
LENGTH: 9
TYPE: PRT
ORGANISM: homo sapien
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)-(8)
OTHER INFORMATION: Binding site
US-07-867-819D-100

Query Match 32.4%; Score 34; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PAKGMSP 9
Db 2 PAKGMSP 9

RESULT 8

US-08-990-888-28
Sequence 28, Application US/08990888B
Patent No. 6387879
GENERAL INFORMATION:
APPLICANT: Blume, Arthur J.
APPLICANT: Brissette, Renee
APPLICANT: Carcamo, Juan
APPLICANT: Mandeck, Wlodek S.
APPLICANT: Tang, Pauline M.
TITLE OF INVENTION: Assays For Compounds Which Bind Growth Hormone Receptor
FILE REFERENCE: 2598-4002
CURRENT APPLICATION NUMBER: US/08/990,888B
CURRENT FILING DATE: 1997-12-15
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: H5 peptide secondary library sequence
US-08-990-888-28

Query Match 32.4%; Score 34; DB 2; Length 18;
Best Local Similarity 60.0%; Pred. No. 60;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 5 GMSPPGTVG 14
Db 6 GVSYPGWLVG 15

RESULT 9

US-09-157-689-67
Sequence 67, Application US/09157689
Patent No. 6599510
GENERAL INFORMATION:
APPLICANT: Horwitz, Marcus A.
APPLICANT: Harth, Gunter
TITLE OF INVENTION: Abundant Extracellular Products and
TITLE OF INVENTION: Methods for Their Production and Use
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kurt A. Maclean
STREET: 2029 Century Park East, Suite 3800
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/157,689
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/568,357
FILING DATE: 06-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/551,149
FILING DATE: 31-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/447,398
FILING DATE: 23-MAY-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,667
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/156,358
FILING DATE: 23-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Maclean, Kurt A.
REGISTRATION NUMBER: 31,118
REFERENCE/DOCKET NUMBER: 118-119
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 788-5000
TELEFAX: (310) 277-1297
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:
MOLECULE TYPE: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Mycobacterium tuberculosis
STRAIN: Erdman
US-09-157-689-67

Query Match 31.4%; Score 33; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 71;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 DPAKMSP 8
Db 4 DPSQMGSP 11

RESULT 10

US-09-953-510-67
Sequence 67, Application US/09953510
Patent No. 6818223
GENERAL INFORMATION:
APPLICANT: Horwitz, Marcus A.
TITLE OF INVENTION: Abundant Extracellular
TITLE OF INVENTION: Products and Methods for Their Production and Use
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kurt A. Maclean
STREET: 2029 Century Park East, Suite 3800
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/953,510
FILING DATE: 14-SEP-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/447,398
FILING DATE: 23-MAY-1995
APPLICATION NUMBER: US 08/289,667
FILING DATE: 12-AUG-1994
APPLICATION NUMBER: US 08/156,358
FILING DATE: 23-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Maclean, Kurt A.
REGISTRATION NUMBER: 31,118


```
REFERENCE/DOCKET NUMBER: 112-272
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 788-5000
TELEFAX: (310) 277-1297
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEetical: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Mycobacterium tuberculosis
STRAIN: Erdman
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-353-510-67

Query Match      31.4% Score 33; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 71;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy      1 DPAKMSP 8
Db      4 DPGQMGP 11

RESULT 11
US-09-667-857-397
Sequence 397, Application US/09667857
Patent No. 6699664
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C5
CURRENT APPLICATION NUMBER: US/09/667,857
CURRENT FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 397
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-09-667-857-397

Query Match      31.4% Score 33; DB 2; Length 20;
Best Local Similarity 62.5%; Pred. No. 99;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy      13 VGEQGVLS 20
Db      3 IGEDGILS 10

RESULT 12
US-10-198-053-397
Sequence 397, Application US/10198053
Patent No. 6858710
GENERAL INFORMATION:
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
```

```
APPLICANT: Hill, Paul
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C9
CURRENT APPLICATION NUMBER: US/10/198,053
CURRENT FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 624
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 397
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-198-053-397

Query Match      31.4% Score 33; DB 2; Length 20;
Best Local Similarity 62.5%; Pred. No. 99;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy      13 VGEQGVLS 20
Db      3 IGEDGILS 10

RESULT 13
US-10-198-053-603
Sequence 603, Application US/10198053
Patent No. 6858710
GENERAL INFORMATION:
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
APPLICANT: Hill, Paul
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C9
CURRENT APPLICATION NUMBER: US/10/198,053
CURRENT FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 624
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 603
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-198-053-603

Query Match      31.4% Score 33; DB 2; Length 20;
Best Local Similarity 62.5%; Pred. No. 99;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy      13 VGEQGVLS 20
Db      3 IGEDGILS 10

RESULT 14
US-09-827-271-397
Sequence 397, Application US/09827271
Patent No. 6962980
GENERAL INFORMATION:
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C6
CURRENT APPLICATION NUMBER: US/09/827,271
CURRENT FILING DATE: 2001-04-04
NUMBER OF SEQ ID NOS: 461
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 397
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-09-827-271-397
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Query Match 31.4%; Score 33; DB 2; Length 20;
Best Local Similarity 62.5%; Pred. No. 99;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 13 VGEBCVLS 20
:|:|:|:
Db 3 IGEDGILS 10

RESULT 15
US-08-482-142-185
; Sequence 185, Application US/08482142
; Patent No. 5820862
; GENERAL INFORMATION:
; APPLICANT: Garman, Richard
; APPLICANT: Greenstein, Julia
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Rogers, Bruce
; APPLICANT: Franzen, Henry
; APPLICANT: Chen, Xian
; APPLICANT: Evans, Sean
; APPLICANT: Shaked, Ze'ev
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
; TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: MA
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,142
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,307
; FILING DATE: 07 June 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAIG, ANNE I.
; REGISTRATION NUMBER: 32,976
; REFERENCE/DOCKET NUMBER: 017.6US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 185:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-482-142-185

Query Match 29.5%; Score 31; DB 1; Length 16;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 12 IVGEGVLS 20
:|:|:|:
Db 6 LVGDDGVLA 14

RESULT 16
US-08-478-572-185
; Sequence 185, Application US/08478572

; Patent No. 5968526
; GENERAL INFORMATION:
; APPLICANT: Garman, Richard
; APPLICANT: Greenstein, Julia
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Rogers, Bruce
; APPLICANT: Franzen, Henry
; APPLICANT: Chen, Xian
; APPLICANT: Evans, Sean
; APPLICANT: Shaked, Ze'ev
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
; TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: MA
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,572
; FILING DATE: 07-June-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/445,307
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAIG, ANNE I.
; REGISTRATION NUMBER: 32,976
; REFERENCE/DOCKET NUMBER: 017.6US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 185:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-478-572-185

Query Match 29.5%; Score 31; DB 1; Length 16;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 12 IVGEGVLS 20
:|:|:|:
Db 6 LVGDDGVLA 14

RESULT 17
US-08-484-296-185
; Sequence 185, Application US/08484296
; Patent No. 6268491
; GENERAL INFORMATION:
; APPLICANT: Garman, Richard
; APPLICANT: Greenstein, Julia
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Rogers, Bruce
; APPLICANT: Franzen, Henry
; APPLICANT: Chen, Xian
; APPLICANT: Evans, Sean
; APPLICANT: Shaked, Ze'ev
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
; TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
; NUMBER OF SEQUENCES: 207

CORRESPONDENCE ADDRESS:
 ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
 STREET: 610 LINCOLN STREET
 CITY: WALTHAM
 STATE: MA
 COUNTRY: USA
 ZIP: 02154
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII TEXT
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/484,296
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/445,307
 FILING DATE: 07 June 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: CRAIG, ANNE I.
 REGISTRATION NUMBER: 32,976
 REFERENCE/DOCKET NUMBER: 017.6US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 466-6000
 TELEFAX: (617) 466-6040
 INFORMATION FOR SEQ ID NO: 185:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal
 US-08-484-296-185

Query Match 29.5%; Score 31; DB 2; Length 16;
 Best Local Similarity 55.6%; Pred. No. 1.9e+02;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 12 IVEEGVLS 20
 DB 6 LVGDGVLA 14

RESULT 18
 US-08-990-888-36
 Sequence 36, Application US/08990888B
 Patent No. 6387879
 GENERAL INFORMATION:
 APPLICANT: Blume, Arthur J.
 APPLICANT: Brissette, Renee
 APPLICANT: Carcamo, Juan
 APPLICANT: Mandeckl, Wlodeck S.
 APPLICANT: Tang, Pauline M.
 TITLE OF INVENTION: Assays For Compounds Which Bind Growth Hormone Receptor
 FILE REFERENCE: 2598-4002
 CURRENT APPLICATION NUMBER: US/08/990,888B
 CURRENT FILING DATE: 1997-12-15
 NUMBER OF SEQ ID NOS: 81
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 36
 LENGTH: 18
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: H5 peptide secondary library sequence
 US-08-990-888-36

Query Match 29.5%; Score 31; DB 2; Length 18;
 Best Local Similarity 50.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 GMSPPGIVG 14

DB 6 GVTYFGWLVG 15

RESULT 19
 US-09-570-022-13
 Sequence 13, Application US/09570022
 Patent No. 6573244
 GENERAL INFORMATION:
 APPLICANT: GORDON, RICHARD K.
 APPLICANT: MOORAD, DEBORAH R.
 APPLICANT: DOCTOR, BHUPENDRA P.
 APPLICANT: GARCIA, GREGORY E.
 TITLE OF INVENTION: PREVINS AS SPECIFIC INHIBITORS AND THERAPEUTIC AGENTS
 FILE REFERENCE: 36644-170531
 CURRENT APPLICATION NUMBER: US/09/570,022
 CURRENT FILING DATE: 2000-05-12
 PRIOR APPLICATION NUMBER: 60/134,446
 PRIOR FILING DATE: 1999-05-17
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 13
 LENGTH: 18
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-09-570-022-13

Query Match 29.5%; Score 31; DB 2; Length 18;
 Best Local Similarity 54.5%; Pred. No. 1.9e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 AKGMSPPGIV 13
 DB 5 AKGLQFGLMV 15

RESULT 20
 US-09-635-501-29
 Sequence 29, Application US/09635501
 Patent No. 6884771
 GENERAL INFORMATION:
 APPLICANT: Accon, Susan L. et al.
 TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
 FILE REFERENCE: MNI-132CP3
 CURRENT APPLICATION NUMBER: US/09/635,501
 CURRENT FILING DATE: 2000-08-09
 PRIOR APPLICATION NUMBER: 09/407,427
 PRIOR FILING DATE: 1999-09-29
 PRIOR APPLICATION NUMBER: 09/163,648
 PRIOR FILING DATE: 1998-09-30
 PRIOR APPLICATION NUMBER: 08/989,299
 PRIOR FILING DATE: 1997-12-11
 NUMBER OF SEQ ID NOS: 107
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 29
 LENGTH: 18
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: motifs
 US-09-635-501-29

Query Match 29.5%; Score 31; DB 2; Length 18;
 Best Local Similarity 54.5%; Pred. No. 1.9e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DPAKMSPPGF 11

Db 1 DISKENNPGF 11

RESULT 21

US-10-007-700-463

Sequence 463, Application US/10007700
Patent No. 6960570

GENERAL INFORMATION:

APPLICANT: Wang, Tongrong

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Li, Samuel X.

APPLICANT: Kalos, Michael D.

APPLICANT: Henderson, Robert A.

APPLICANT: McNeill, Patricia D.

APPLICANT: Fanger, Neil

APPLICANT: Recter, Marc W.

APPLICANT: Durham, Margalita

APPLICANT: Fanger, Gary R.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Carter, Darick

APPLICANT: Matanabe, Yoshihiro

APPLICANT: Peckman, David W.

APPLICANT: Cai, Feng

APPLICANT: Foy, Teresa M.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

FILE REFERENCE: 210121.455C17

CURRENT APPLICATION NUMBER: US/10/007,700

CURRENT FILING DATE: 2001-11-30

NUMBER OF SEQ ID NOS: 469

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 463

LENGTH: 20

TYPE: PRT

ORGANISM: Homo sapiens

US-10-007-700-463

Query Match Best Local Similarity 29.5%; Score 31; DB 2; Length 20;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9

Db 9 PTSGMPP 16

RESULT 22

US-08-475-955-12

Sequence 12, Application US/08475955

GENERAL INFORMATION:

APPLICANT: Harley, John

TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF

NUMBER OF SEQUENCES: 218

CORRESPONDENCE ADDRESS:

ADDRESSEE: Patrea L. Pabst

STREET: 2800 One Atlantic Center, 1250 West Peachtree Street

CITY: Atlanta

STATE: GA

COUNTRY: USA

ZIP: 30309-3450

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/475,955

FILING DATE: June 7, 1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/867,819

FILING DATE: April 13, 1992

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/648,205

FILING DATE: January 31, 1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/472,947

FILING DATE: January 31, 1990

ATTORNEY/AGENT INFORMATION:

NAME: Pabst, Patrea L.

REGISTRATION NUMBER: 31,284

REFERENCE/DOCKET NUMBER: OMR114CIP(2)DIV

TELECOMMUNICATION INFORMATION:

TELEPHONE: (404)-873-8794

TELEFAX: (404)-873-8795

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Binding-site

LOCATION: 1..8

US-08-475-955-12

Query Match Best Local Similarity 28.6%; Score 30; DB 2; Length 8;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GMSPPG 10

Db 3 GMPPPG 8

RESULT 23

US-08-475-955-205

Sequence 205, Application US/08475955

GENERAL INFORMATION:

APPLICANT: Harley, John

TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF

NUMBER OF SEQUENCES: 218

CORRESPONDENCE ADDRESS:

ADDRESSEE: Patrea L. Pabst

STREET: 2800 One Atlantic Center, 1250 West Peachtree Street

CITY: Atlanta

STATE: GA

COUNTRY: USA

ZIP: 30309-3450

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/475,955

FILING DATE: June 7, 1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/867,819

FILING DATE: April 13, 1992

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/648,205

FILING DATE: January 31, 1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/472,947

FILING DATE: January 31, 1990

ATTORNEY/AGENT INFORMATION:

NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRP114CIP(2)DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 205:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-475-955-205

Query Match 28.6%; Score 30; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 GMSPPG 10
DB 2 GMPPEPG 7

RESULT 24
US-08-475-955-206
Sequence 206, Application US/08475955
Patent No. 6641813
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 218
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1250 West Peachtree Street
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,955
FILING DATE: June 7, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRP114CIP(2)DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 206:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-475-955-206

Query Match 28.6%; Score 30; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GMSPPG 10
DB 1 GMPPEPG 6

RESULT 25
US-07-867-819D-12
Sequence 12, Application US/07867819D
Patent No. 6897287
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies
FILE REFERENCE: OMRP 114 CIP (2)
CURRENT APPLICATION NUMBER: US/07/867,819D
CURRENT FILING DATE: 1992-04-13
PRIOR APPLICATION NUMBER: 07/472,947
PRIOR FILING DATE: 1990-01-31
PRIOR APPLICATION NUMBER: 07/648,205
PRIOR FILING DATE: 1991-01-31
NUMBER OF SEQ ID NOS: 161
SOFTWARE: Patentin Version 3.1
SEQ ID NO 12
LENGTH: 8
TYPE: PRT
ORGANISM: homo sapien
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)..(8)
OTHER INFORMATION: Binding site
US-07-867-819D-12

Query Match 28.6%; Score 30; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GMSPPG 10
DB 3 GMPPEPG 8

Search completed: January 26, 2006, 08:07:04
Job time : 19.9598 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 08:04:12 : Search time 65 Seconds
(without alignments)
128.563 Million cell updates/sec

Title: US-09-662-293-13
Perfect score: 105
Sequence: 1 DPAKMSPPGFVCEGVLS 20

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 389445

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/ptodata/1/pubppaa/US08_PUBSCOMB.pep:*
3: /cgn2_6/ptodata/1/pubppaa/US09_PUBSCOMB.pep:*
4: /cgn2_6/ptodata/1/pubppaa/US10A_PUBSCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubppaa/US11_PUBSCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	105	100.0	20	4	US-10-218-743-4
2	105	100.0	20	4	US-10-218-743-13
3	35	33.3	20	4	US-10-280-066-302
4	34	32.4	8	4	US-10-012-756-6
5	34	32.4	8	4	US-10-376-121A-116
6	34	32.4	9	4	US-10-376-121A-116
7	33	31.4	15	3	US-09-953-510-67
8	33	31.4	15	3	US-09-953-413-67
9	33	31.4	15	4	US-10-147-355-67
10	33	31.4	15	5	US-10-655-155-67
11	33	31.4	20	3	US-09-884-441-397
12	33	31.4	20	3	US-09-907-969-397
13	33	31.4	20	3	US-09-827-271-397
14	33	31.4	20	4	US-10-198-053-397
15	33	31.4	20	4	US-10-198-053-603
16	33	31.4	20	5	US-10-860-790-297
17	33	31.4	20	5	US-10-860-790-603
18	33	31.4	20	5	US-10-661-156-146
19	32	30.5	15	4	US-10-328-916-58
20	32	30.5	16	3	US-09-838-785-26
21	32	30.5	16	5	US-10-953-901-593
22	32	30.5	20	5	US-10-661-156-170
23	31	29.5	14	4	US-10-307-956-25
24	31	29.5	15	4	US-10-211-088-356
25	31	29.5	17	5	US-10-950-163-8
26	31	29.5	18	3	US-09-999-781-10
27	31	29.5	18	5	US-10-854-646-13

28	31	29.5	18	6	US-11-059-218-29	Sequence 29, Appl
29	31	29.5	20	3	US-09-897-778-463	Sequence 463, Appl
30	31	29.5	20	4	US-10-007-700-463	Sequence 463, Appl
31	31	29.5	20	4	US-10-117-982-463	Sequence 463, Appl
32	31	29.5	20	4	US-10-313-986-463	Sequence 463, Appl
33	31	29.5	20	4	US-10-313-986-463	Sequence 541, Appl
34	31	29.5	20	5	US-10-775-972-463	Sequence 463, Appl
35	31	29.5	20	5	US-10-775-972-463	Sequence 541, Appl
36	31	29.5	20	5	US-10-922-124-463	Sequence 463, Appl
37	31	29.5	20	5	US-10-922-124-463	Sequence 541, Appl
38	31	29.5	21	3	US-09-945-825-13	Sequence 13, Appl
39	31	29.5	21	5	US-10-319-315-45	Sequence 45, Appl
40	31	29.5	21	5	US-10-895-359-13	Sequence 13, Appl
41	30	28.6	8	4	US-10-376-121A-123	Sequence 123, Appl
42	30	28.6	8	4	US-10-376-121A-123	Sequence 205, Appl
43	30	28.6	8	4	US-10-376-121A-205	Sequence 206, Appl
44	30	28.6	8	4	US-10-376-121A-206	Sequence 272, Appl
45	30	28.6	10	3	US-09-572-404B-272	Sequence 274, Appl
46	30	28.6	12	4	US-09-572-404B-274	Sequence 14, Appl
47	30	28.6	12	4	US-10-376-121A-14	Sequence 27, Appl
48	30	28.6	13	5	US-10-972-236A-27	Sequence 53, Appl
49	30	28.6	14	4	US-10-185-050-53	Sequence 54, Appl
50	30	28.6	14	4	US-10-185-050-53	Sequence 3, Appl
51	30	28.6	15	5	US-10-434-906-3	Sequence 28, Appl
52	30	28.6	15	5	US-10-972-236A-28	Sequence 376, Appl
53	30	28.6	16	4	US-10-285-194-376	Sequence 32096, Appl
54	30	28.6	18	4	US-10-029-186-22096	Sequence 907, Appl
55	30	28.6	18	5	US-10-862-195-307	Sequence 27, Appl
56	30	28.6	19	4	US-10-714-212-27	Sequence 24, Appl
57	29.5	28.1	7	3	US-09-990-332C-57	Sequence 57, Appl
58	29	27.6	8	4	US-10-012-756-4	Sequence 4, Appl
59	29	27.6	8	5	US-10-646-132-3	Sequence 3, Appl
60	29	27.6	9	4	US-10-224-999A-2893	Sequence 2893, Appl
61	29	27.6	10	3	US-09-572-404B-1350	Sequence 1352, Appl
62	29	27.6	10	3	US-09-572-404B-1352	Sequence 684, Appl
63	29	27.6	10	3	US-09-573-822C-684	Sequence 2899, Appl
64	29	27.6	10	4	US-10-224-999A-2899	Sequence 2900, Appl
65	29	27.6	10	4	US-10-224-999A-2900	Sequence 2907, Appl
66	29	27.6	11	4	US-10-224-999A-2906	Sequence 2908, Appl
67	29	27.6	11	4	US-10-224-999A-2908	Sequence 10, Appl
68	29	27.6	11	4	US-10-376-121A-110	Sequence 140, Appl
69	29	27.6	11	4	US-10-285-194-140	Sequence 50, Appl
70	29	27.6	12	4	US-10-286-457-50	Sequence 2914, Appl
71	29	27.6	12	4	US-10-224-999A-2914	Sequence 2915, Appl
72	29	27.6	12	4	US-10-224-999A-2915	Sequence 2916, Appl
73	29	27.6	12	4	US-10-224-999A-2916	Sequence 2917, Appl
74	29	27.6	12	4	US-10-224-999A-2917	Sequence 2923, Appl
75	29	27.6	13	4	US-10-224-999A-2923	Sequence 2924, Appl
76	29	27.6	13	4	US-10-224-999A-2924	Sequence 2925, Appl
77	29	27.6	13	4	US-10-224-999A-2925	Sequence 2926, Appl
78	29	27.6	13	4	US-10-224-999A-2926	Sequence 2927, Appl
79	29	27.6	13	4	US-10-224-999A-2927	Sequence 1350, Appl
80	29	27.6	13	5	US-10-948-707-1350	Sequence 2933, Appl
81	29	27.6	14	4	US-10-224-999A-2933	Sequence 2934, Appl
82	29	27.6	14	4	US-10-224-999A-2934	Sequence 2935, Appl
83	29	27.6	14	4	US-10-224-999A-2935	Sequence 2936, Appl
84	29	27.6	14	4	US-10-224-999A-2936	Sequence 2937, Appl
85	29	27.6	14	4	US-10-224-999A-2937	Sequence 2938, Appl
86	29	27.6	14	4	US-10-224-999A-2938	Sequence 12, Appl
87	29	27.6	15	4	US-10-224-999A-2945	Sequence 2944, Appl
88	29	27.6	15	4	US-10-224-999A-2945	Sequence 2946, Appl
89	29	27.6	15	4	US-10-224-999A-2946	Sequence 2947, Appl
90	29	27.6	15	4	US-10-224-999A-2947	Sequence 2948, Appl
91	29	27.6	15	4	US-10-224-999A-2948	Sequence 2949, Appl
92	29	27.6	15	4	US-10-224-999A-2949	Sequence 2950, Appl
93	29	27.6	15	4	US-10-224-999A-2950	Sequence 1513, Appl
94	29	27.6	16	4	US-10-128-520-38	Sequence 2956, Appl
95	29	27.6	16	4	US-10-225-567A-1513	Sequence 2957, Appl
96	29	27.6	16	4	US-10-224-999A-2956	
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99	29	27.6	16	4	US-10-224-999A-2956	
100	29	27.6	16	4	US-10-224-999A-2957	

ALIGNMENTS

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RESULT 1
US-10-218-743-4
; Sequence 4, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-4

Query Match          100.0%; Score 105; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1,1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DPAKMSPPGFIVGEGVLS 20
DB      1 DPAKMSPPGFIVGEGVLS 20

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US-10-218-743-13
; Sequence 13, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 20
; TYPE: PRT
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; ORGANISM: Dermatophagoides farinae
US-10-218-743-13

Query Match          100.0%; Score 105; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1,1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DPAKMSPPGFIVGEGVLS 20
DB      1 DPAKMSPPGFIVGEGVLS 20

RESULT 3
US-10-280-066-302
; Sequence 302, Application US/10280066
; Publication No. US20030180718A1
; GENERAL INFORMATION:
; APPLICANT: Pillutia, Renuka C.
; APPLICANT: Brissette, Renee
; APPLICANT: Spruyt, Michael
; APPLICANT: Dedova, Olga
; APPLICANT: Blume, Arthur J.
; APPLICANT: Prendergast, John
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING TARGET BIND
; FILE REFERENCE: 2598-4009US1
; CURRENT APPLICATION NUMBER: US/10/280,066
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,471
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 537
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 302
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Eschericia coli
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: DGIS-20M-4-E4
US-10-280-066-302

Query Match          33.3%; Score 35; DB 4; Length 20;
Best Local Similarity 53.3%; Pred. No. 3,7e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      5 GMSPPGFIVGEGVL 19
DB      2 GRPPMGIVGERGGL 16

RESULT 4
US-10-012-756-6
; Sequence 6, Application US/10012756
; Publication No. US20020164355A1
; GENERAL INFORMATION:
; APPLICANT: John B. Harley and Judith A. James
; TITLE OF INVENTION: Diagnostics And Therapy Of Epstein-Barr
; VIRUS IN Autoimmune Disorders
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30306-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/10/012,756
FILING DATE: 24-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/781,296
FILING DATE: 13-JAN-1997
APPLICATION NUMBER: 60/019,053
FILING DATE: 16-MAY-1996
APPLICATION NUMBER: 08/160,604
FILING DATE: 30-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF161
TELEPHONE: (404)873-8794
TELEFAX: (404)873-8795
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-012-756-6

Query Match 32.4%; Score 34; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PAKMSPP 9
Db 1 PAKMSPP 8

RESULT 5
US-10-376-121A-116
Sequence 116, Application US/10376121A
Publication No. US20030216544A1
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
AUTOANTIBODIES
NUMBER OF SEQUENCES: 218
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: Suite 2000, 1201 West Peachtree Street, N.E.
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/376,121A
FILING DATE: 27-Mar-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284

REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV(2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-817-8473
TELEFAX: (404)-817-8588
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 116:
US-10-376-121A-116

Query Match 32.4%; Score 34; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PAKMSPP 9
Db 1 PAKMSPP 8

RESULT 6
US-10-376-121A-100
Sequence 100, Application US/10376121A
Publication No. US20030216544A1
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
AUTOANTIBODIES
NUMBER OF SEQUENCES: 218
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: Suite 2000, 1201 West Peachtree Street, N.E.
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/376,121A
FILING DATE: 27-Mar-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV(2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-817-8473
TELEFAX: (404)-817-8588
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Binding-site
LOCATION: 1..8
SEQUENCE DESCRIPTION: SEQ ID NO: 100:

US-10-376-121A-100

Query Match 32.4%; Score 34; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGMSP 9
2 PAKGMSP 9

DB 2 PAKGMSP 9

RESULT 7

US-09-953-510-67
Sequence 67, Application US/09953510
Patent No. US20020131975A1

GENERAL INFORMATION:

APPLICANT: Horwitz, Marcus A.

TITLE OF INVENTION: Abundant Extracellular
Products and Methods for Their Production and Use

NUMBER OF SEQUENCES: 91

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kurt A. Maclean

STREET: 2029 Century Park East, Suite 3800

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90067

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0,
Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/953,510

FILING DATE: 14-Sep-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/447,398

FILING DATE: 23-MAY-1995

APPLICATION NUMBER: US 08/289,667

FILING DATE: 12-AUG-1994

APPLICATION NUMBER: US 08/156,358

FILING DATE: 23-NOV-1993

ATTORNEY/AGENT INFORMATION:
NAME: Maclean, Kurt A.

REGISTRATION NUMBER: 31,118

REFERENCE/DOCKET NUMBER: 112-272

TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 788-5000

TELEFAX: (310) 277-1297

INFORMATION FOR SEQ ID NO: 67:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: linear

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

ORIGINAL SOURCE:

ORGANISM: Mycobacterium tuberculosis

STRAIN: Erdman

SEQUENCE DESCRIPTION: SEQ ID NO: 67:

US-09-953-510-67

Query Match 31.4%; Score 33; DB 3; Length 15;
Best Local Similarity 62.5%; Pred. No. 5.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKMSP 8
1 DPAKMSP 8

DB 4 DPSCGMSP 11

RESULT 8
US-09-953-413-67
Sequence 67, Application US/09953413
Publication No. US20040018209A1

GENERAL INFORMATION:

APPLICANT: Horwitz, Marcus A.

TITLE OF INVENTION: Abundant Extracellular
Products and Methods for Their Production and Use

NUMBER OF SEQUENCES: 91

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kurt A. Maclean

STREET: 2029 Century Park East, Suite 3800

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90067

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0,
Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/953,413

FILING DATE: 14-Sep-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/447,398

FILING DATE: 23-MAY-1995

APPLICATION NUMBER: US 08/289,667

FILING DATE: 12-AUG-1994

APPLICATION NUMBER: US 08/156,358

FILING DATE: 23-NOV-1993

ATTORNEY/AGENT INFORMATION:
NAME: Maclean, Kurt A.

REGISTRATION NUMBER: 31,118

REFERENCE/DOCKET NUMBER: 112-272

TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 788-5000

TELEFAX: (310) 277-1297

INFORMATION FOR SEQ ID NO: 67:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: linear

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

ORIGINAL SOURCE:

ORGANISM: Mycobacterium tuberculosis

STRAIN: Erdman

SEQUENCE DESCRIPTION: SEQ ID NO: 67:

US-09-953-413-67

Query Match 31.4%; Score 33; DB 3; Length 15;
Best Local Similarity 62.5%; Pred. No. 5.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKMSP 8
1 DPAKMSP 8

DB 4 DPSCGMSP 11

RESULT 9
US-10-147-255-67
Sequence 67, Application US/10147255
Publication No. US20030152584A1

GENERAL INFORMATION:

```

; APPLICANT: Horwitz, Marcue A.
; TITLE OF INVENTION: Abundant Extracellular
; Products and Methods for Their Production and Use
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kurt A. Maclean
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0,
; Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/147,255
; FILING DATE: 15-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/226,539A
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/447,398
; FILING DATE: 23-MAY-1995
; APPLICATION NUMBER: US 08/289,667
; FILING DATE: 12-AUG-1994
; APPLICATION NUMBER: US 08/156,358
; FILING DATE: 23-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Maclean, Kurt A.
; REGISTRATION NUMBER: 31,118
; REFERENCE/DOCKET NUMBER: 112-272
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 788-5000
; TELEFAX: (310) 277-1297
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: Internal
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
; STRAIN: Erdman
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-10-147-255-67

Query Match          31.4% Score 33; DB 4; Length 15;
Best Local Similarity 62.5%; Pred. No. 5.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 DPAKGMSP 8
      ||::|||
Db      4 DPGQGMGP 11

RESULT 10
US-10-695-155-67
; Sequence 67, Application US/10695155
; Publication No. US20040228873A1
; GENERAL INFORMATION:
; APPLICANT: HORWITZ, MARCUS A.
; APPLICANT: HARTH, GUNTER
; APPLICANT: LEE, BAI-YU
; TITLE OF INVENTION: ABUNDANT EXTRACELLULAR PRODUCTS AND METHODS FOR THEIR PRODUCTION
; TITLE OF INVENTION: AND USE
; FILE REFERENCE: 51326-00004
```

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; CURRENT APPLICATION NUMBER: US/10/695,155
; CURRENT FILING DATE: 2003-10-27
; PRIOR APPLICATION NUMBER: 08/652,842
; PRIOR FILING DATE: 1996-03-23
; PRIOR APPLICATION NUMBER: 08/568,357
; PRIOR FILING DATE: 1995-12-06
; PRIOR APPLICATION NUMBER: 08/551,149
; PRIOR FILING DATE: 1995-10-31
; PRIOR APPLICATION NUMBER: 08/447,398
; PRIOR FILING DATE: 1995-05-23
; PRIOR APPLICATION NUMBER: 08/289,667
; PRIOR FILING DATE: 1994-08-12
; PRIOR APPLICATION NUMBER: 08/156,358
; PRIOR FILING DATE: 1993-11-23
; PRIOR APPLICATION NUMBER: 08/545,926
; PRIOR FILING DATE: 1995-10-20
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: Patent version 3.2
; SEQ ID NO: 67
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-695-155-67

Query Match          31.4% Score 33; DB 5; Length 15;
Best Local Similarity 62.5%; Pred. No. 5.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 DPAKGMSP 8
      ||::|||
Db      4 DPGQGMGP 11

RESULT 11
US-09-884-441-397
; Sequence 397, Application US/09884441
; Patent No. US20020119158A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Carter, Darick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C7
; CURRENT APPLICATION NUMBER: US/09/884,441
; CURRENT FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 397
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-884-441-397

Query Match          31.4% Score 33; DB 3; Length 20;
Best Local Similarity 62.5%; Pred. No. 7.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      13 VGEKGVLS 20
      :||:|:|
Db      3 IGEDGILS 10

RESULT 12
US-09-907-969-397
; Sequence 397, Application US/09907969
; Publication No. US20030091580A1
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Flinn, Steven P.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary Richard
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: APPLICANT: Reed, Steven G.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Hill, Paul
: APPLICANT: Albone, Earl
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.462C8
: CURRENT APPLICATION NUMBER: US/09/997,969
: CURRENT FILING DATE: 2001-07-17
: NUMBER OF SEQ ID NOS: 596
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 397
: LENGTH: 20
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-907-969-397

Query Match      31.4%: Score 33; DB 3; Length 20;
Best Local Similarity 62.5%; Pred No. 7.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0

QY      13 VGEBCVLS 20
: ||: ||: ||
Db      3 IGEBCILS 10

RESULT 13
US-09-827-271-397
: Sequence 397, Application US/09827271
: Publication No. US20030165504A1
: GENERAL INFORMATION:
: APPLICANT: Retter, Marc W.
: APPLICANT: Fanger, Gary R.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.462C6
: CURRENT APPLICATION NUMBER: US/09/827,271
: CURRENT FILING DATE: 2001-04-04
: NUMBER OF SEQ ID NOS: 461
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 397
: LENGTH: 20
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-827-271-397

Query Match      31.4%: Score 33; DB 3; Length 20;
Best Local Similarity 62.5%; Pred No. 7.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0

QY      13 VGEBCVLS 20
: ||: ||: ||
Db      3 IGEBCILS 10

RESULT 14
US-10-198-053-397
: Sequence 397, Application US/10198053
: Publication No. US20030124140A1
: GENERAL INFORMATION:
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Retter, Marc W.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Hill, Paul
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.462C9
: CURRENT APPLICATION NUMBER: US/10/198,053
: CURRENT FILING DATE: 2002-07-17
: NUMBER OF SEQ ID NOS: 624
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 397

```

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/      LENGTH: 20
/      TYPE: PRT
/      ORGANISM: Homo sapiens
US-10-198-053-397

Query Match      31.4%; Score 33; DB 4; Length 20;
Best Local Similarity 62.5%; Pred. No. 7.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      13 VGEBCVLS 20
      :|:|:|
Db      3 IGEDGILS 10

RESULT 15
US-10-198-053-603
/ Sequence 603, Application US/10198053
/ Publication No. US20030124140A1
/ GENERAL INFORMATION:
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Hill, Paul
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
/ FILE REFERENCE: 210121.462C9
/ CURRENT FILING DATE: 2002-07-17
/ CURRENT APPLICATION NUMBER: US/10/198,053
/ NUMBER OF SEQ ID NOS: 624
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 603
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-198-053-603

Query Match      31.4%; Score 33; DB 4; Length 20;
Best Local Similarity 62.5%; Pred. No. 7.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      13 VGEBCVLS 20
      :|:|:|
Db      3 IGEDGILS 10

RESULT 16
US-10-860-790-397
/ Sequence 397, Application US/10860790
/ Publication No. US20050031634A1
/ GENERAL INFORMATION:
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Hill, Paul
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
/ FILE REFERENCE: 210121.462C11
/ CURRENT APPLICATION NUMBER: US/10/860,790
/ CURRENT FILING DATE: 2004-06-02
/ NUMBER OF SEQ ID NOS: 624
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 397
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-860-790-397

Query Match      31.4%; Score 33; DB 5; Length 20;
Best Local Similarity 62.5%; Pred. No. 7.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      13 VGEBCVLS 20
      :|:|:|

```

Db 3 IGEDGILS 10

RESULT 17
US-10-860-790-603

Sequence 603, Application US/10860790
Publication No. US20050031634A1

GENERAL INFORMATION:

APPLICANT: Bangur, Chaitanya S.

APPLICANT: Reiter, Marc W.

APPLICANT: Panger, Gary R.

APPLICANT: Hill, Paul

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

FILE REFERENCE: 210121.462C11

CURRENT APPLICATION NUMBER: US/10/860,790

CURRENT FILING DATE: 2004-06-02

NUMBER OF SEQ ID NOS: 624

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 603

LENGTH: 20

TYPE: PRT

ORGANISM: Homo sapiens

US-10-860-790-603

Query Match 31.4%; Score 33; DB 5; Length 20;
Best Local Similarity 62.5%; Pred. No. 7.4e+02;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 13 VGESEVLS 20
3 IGEDGILS 10

RESULT 18
US-10-661-156-146

Sequence 146, Application US/10661156
Publication No. US20050100963A1

GENERAL INFORMATION:

APPLICANT: Sato, Aaron K.

APPLICANT: Sexton, Daniel J.

APPLICANT: Drensfeld, Daniel T.

APPLICANT: Ladner, Robert C.

APPLICANT: Arbogast, Christophe

APPLICANT: Bussat, Philippe

APPLICANT: Fan, Hong

APPLICANT: Khurana, Sudha

APPLICANT: Linder, Karen E.

APPLICANT: Marinelli, Edmund R.

APPLICANT: Nanjappa, Palaniappa

APPLICANT: Nunn, Adrian

APPLICANT: Pillai, Radhakrishna

APPLICANT: Pochon, Sibylle

APPLICANT: Ramalingam, Kondareddi

APPLICANT: Shrivastava, Ajay

APPLICANT: Song, Bo

APPLICANT: Swenson, Rolf E.

APPLICANT: Von Wronski, Mathew A.

TITLE OF INVENTION: KDR and VEGF/KDR Binding Peptides and

FILE REFERENCE: 0617.70012US00

CURRENT APPLICATION NUMBER: US/10/661,156

CURRENT FILING DATE: 2003-09-11

PRIOR APPLICATION NUMBER: US 10/382,082

PRIOR FILING DATE: 2003-03-03

PRIOR APPLICATION NUMBER: PCT/US03/06731

PRIOR FILING DATE: 2003-03-03

PRIOR APPLICATION NUMBER: US 60/440,411

PRIOR FILING DATE: 2003-01-15

PRIOR APPLICATION NUMBER: US 60/360,851

PRIOR FILING DATE: 2002-03-01

NUMBER OF SEQ ID NOS: 617

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 146

LENGTH: 20

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Library Isolate

US-10-661-156-146

Query Match 31.4%; Score 33; DB 5; Length 20;
Best Local Similarity 58.3%; Pred. No. 7.4e+02;

Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Db 8 PPGFVGESEVLS 19
2 PPGFVGESEVLS 13

RESULT 19
US-10-328-916-58

Sequence 58, Application US/10328916
Publication No. US20040002114A1

GENERAL INFORMATION:

APPLICANT: Gregoire, Francine M.

APPLICANT: Johnson, Jeffrey D.

APPLICANT: Blume, John E.

APPLICANT: Metabolix, Inc.

TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor

FILE REFERENCE: 016325-00721US

CURRENT APPLICATION NUMBER: US/10/328,916

CURRENT FILING DATE: 2003-01-06

PRIOR APPLICATION NUMBER: US 60/345,697

PRIOR FILING DATE: 2002-01-04

NUMBER OF SEQ ID NOS: 59

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 58

LENGTH: 15

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: C-terminal

US-10-328-916-58

Query Match 30.5%; Score 32; DB 4; Length 15;
Best Local Similarity 54.5%; Pred. No. 7.6e+02;

Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 6 MSPPGFVGESEVLS 16
4 MSPPGFVGESEVLS 14

RESULT 20
US-09-838-785-26

Sequence 26, Application US/09838785
Patent No. US20020009455A1

GENERAL INFORMATION:

APPLICANT: Lau, Ted

APPLICANT: Lin, Rick

APPLICANT: Parkes, Debbie

APPLICANT: Parry, Gordon

APPLICANT: Schneider, Douglas

APPLICANT: Steindreich, Renate

APPLICANT: Van Heult, Pam T

APPLICANT: Wu, John

TITLE OF INVENTION: DNA Encoding a No. US20020009455A1el PROST 03

FILE REFERENCE: 51831AUSM1

CURRENT APPLICATION NUMBER: US/09/838,785

CURRENT FILING DATE: 2001-04-20

PRIOR APPLICATION NUMBER: 60/200,065

PRIOR FILING DATE: 2000-04-27

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 26
LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
US-09-838-785-26

Query Match 30.5%; Score 32; DB 3; Length 16;
Best Local Similarity 55.6%; Pred. NO. 8.2e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DPAKMSPP 9
Db 3 EPAEGLSAP 11

RESULT 21
US-10-953-901-593
Sequence 593, Application US/10953901
Publication No. US20050181464A1
GENERAL INFORMATION:
APPLICANT: EDWARDS, ALED
APPLICANT: DHARAMSI, AKIL
APPLICANT: VEDADI, MASOUD
APPLICANT: ALAM, MUHAMMAD ZAHoor
APPLICANT: ARROWSMITH, CHERYL
APPLICANT: AMREY, DONALD E.
APPLICANT: BEATTIE, BRYAN
APPLICANT: BUZADZIOA, KRISTINA
APPLICANT: CLARKE, TERESA
APPLICANT: DOMAGALA, MEGAN
APPLICANT: HOUSTON, SIMON
APPLICANT: KANAGARAJAH, DHUSHY
APPLICANT: LI, QIN
APPLICANT: MANSOURY, KAMRAN
APPLICANT: McDONALD, MERRY-LYNN
APPLICANT: NETHERY, KATHLEEN
APPLICANT: NG, IVY
APPLICANT: OUYANG, HUI
APPLICANT: RICHARDS, DAMN
APPLICANT: VALLEE, FRANCOIS
APPLICANT: VIRAG, CRISTINA
TITLE OF INVENTION: NOVEL PURIFIED POLYPEPTIDES FROM BACTERIA
FILE REFERENCE: IPT-207.01
CURRENT APPLICATION NUMBER: US/10/953,901
CURRENT FILING DATE: 2004-09-29
PRIOR APPLICATION NUMBER: PCT/CA03/00465
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 60/370,060
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: 60/369,831
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: 60/369,819
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: 60/369,826
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: 60/370,852
PRIOR FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: 60/370,681
PRIOR FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: 60/371,014
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/371,180
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/371,008
PRIOR FILING DATE: 2002-04-09
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 901
SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 593
LENGTH: 16
TYPE: PRT
ORGANISM: Staphylococcus aureus

US-10-953-901-593

Query Match 30.5%; Score 32; DB 5; Length 16;
Best Local Similarity 70.0%; Pred. NO. 8.2e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 10 GFIVEGEVVL 19
Db 5 GDIVGEVGM 14

RESULT 22
US-10-661-156-170
Sequence 170, Application US/10661156
Publication No. US20050100963A1
GENERAL INFORMATION:
APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
APPLICANT: Fan, Hong
APPLICANT: Khurana, Sudha
APPLICANT: Linder, Karen E.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Nanjappan, Palaniappa
APPLICANT: Nunn, Adrian
APPLICANT: Pillai, Radhakrishna
APPLICANT: Pochon, Sibylle
APPLICANT: Ramalingam, Kondaredidhar
APPLICANT: Shrivastava, Ajay
APPLICANT: Song, Bo
APPLICANT: Swenson, Rolf E.
APPLICANT: von Wronski, Mathew A.
TITLE OF INVENTION: KDR and VEGF/KDR Binding Peptides and
FILE REFERENCE: D0617.70012US00
CURRENT APPLICATION NUMBER: US/10/661,156
CURRENT FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 617
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 170
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Library Isolate
US-10-661-156-170

Query Match 30.5%; Score 32; DB 5; Length 20;
Best Local Similarity 50.0%; Pred. NO. 1e+03;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 8 PGFIVEGEVVL 19
Db 2 PGFISYWEQNAL 13

RESULT 23
US-10-307-956-25
Sequence 25, Application US/10307956
Publication No. US20030119072A1
GENERAL INFORMATION:
APPLICANT: Hoekstra, Merl F.

```

; APPLICANT: Xie, Weilin
; APPLICANT: Murray, Brian
; APPLICANT: Mercurio, Frank
; TITLE OF INVENTION: METHODS FOR MODULATING SIGNAL
; FILE REFERENCE: 860098.433
; CURRENT APPLICATION NUMBER: US/10/307,956
; PRIOR FILING DATE: 2002-12-02
; PRIOR FILING DATE: 1999-08-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-307-956-25

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Query Match      29.5% Score 31; DB 4; Length 14;
Best Local Similarity 38.5%; Pred. No. 1e+03;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

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QY      5 GMSPPGFVSEEG 17
      |||:|:|
Db      2 GLTRPPGYLSEEG 14

```

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RESULT 24
US-10-211-088-356
; Sequence 356, Application US/10211088
; Publication No. US20030104479A1
; GENERAL INFORMATION:
; APPLICANT: Bright, Gary R.
; APPLICANT: Premkumar, D. David
; APPLICANT: Chen, Yih-Tai
; TITLE OF INVENTION: NO. US20030104479A1 Fusion Proteins And Assays For Molecular B
; FILE REFERENCE: 01-1022-US
; CURRENT APPLICATION NUMBER: US/10/211,088
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/309,395
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/341,589
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 356
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Post-translational modification site
US-10-211-088-356

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Query Match      29.5% Score 31; DB 4; Length 15;
Best Local Similarity 55.6%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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QY      2 PAKGMSPPG 10
      |||:|
Db      2 PGKGVKSPG 10

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RESULT 25
US-10-950-163-8
; Sequence 8, Application US/10950163
; Publication No. US2005015291A1
; GENERAL INFORMATION:
; APPLICANT: Hardy, Michele
; TITLE OF INVENTION: NOROVIRUS MONOCLONAL ANTIBODIES AND PEPTIDES
; FILE REFERENCE: 33576/US/2
; CURRENT APPLICATION NUMBER: US/10/950,163
; CURRENT FILING DATE: 2004-09-24
; PRIOR APPLICATION NUMBER: US 60/508,262

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; PRIOR FILING DATE: 2003-09-24
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Grimsby virus
US-10-950-163-8

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Query Match      29.5% Score 31; DB 5; Length 17;
Best Local Similarity 71.4%; Pred. No. 1.2e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY      2 PAKGMSPP 8
      |||:|
Db      7 PAEGISP 13

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Search completed: January 26, 2006, 08:38:40
Job time : 66 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 26, 2006, 08:05:12 : Search time 3.7911 Seconds
[without alignments]
57.099 Million cell updates/sec

Title: US-09-662-293-13

Perfect score: 105
Sequence: 1 DPAKGMSPGFIVGEGVL 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 37628

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database:

Published Applications AA New:
1: /cgn2_6/ptodata/1/pubpaa/us06_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/us07_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PTCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	31.4	20	6	US-10-939-890-146
2	32	30.5	20	6	US-10-939-890-170
3	31	29.5	20	6	US-10-623-155-463
4	31	29.5	20	6	US-10-623-155-441
5	29	27.6	20	6	US-10-623-155-413
6	29	27.6	20	6	US-10-623-155-524
7	29	27.6	20	7	US-11-094-142-16
8	28	26.7	12	6	US-10-889-197-25
9	28	26.7	15	6	US-10-939-890-203
10	28	26.7	16	7	US-11-054-515-1003
11	28	26.7	20	6	US-10-893-584-212
12	28	26.7	21	7	US-11-058-735-60
13	27	25.7	11	7	US-11-145-861-78
14	27	25.7	14	7	US-11-143-984A-164
15	27	25.7	15	6	US-10-516-676-1
16	27	25.7	15	6	US-10-532-426-2
17	27	25.7	16	7	US-11-054-515-2153
18	27	25.7	16	7	US-11-054-515-2780
19	27	25.7	16	7	US-11-054-515-2783
20	27	25.7	20	6	US-11-053-100-18
21	26.5	25.2	20	6	US-10-485-788A-598
22	26	24.8	8	7	US-11-147-994-10
23	26	24.8	9	7	US-11-178-269-27
24	26	24.8	9	7	US-11-043-788-482
25	26	24.8	9	7	US-11-147-994-8

26	24.8	9	7	US-11-147-994-9	Sequence 9, Appli
27	24.8	10	7	US-11-147-994-7	Sequence 7, Appli
28	24.8	15	6	US-10-939-890-193	Sequence 193, App
29	24.8	17	6	US-10-893-584-240	Sequence 240, App
30	24.8	18	6	US-10-842-206-26	Sequence 26, Appl
31	24.8	18	6	US-10-980-459-12	Sequence 12, Appl
32	24.8	19	6	US-10-503-575-131	Sequence 131, App
33	24.8	20	6	US-10-997-201A-31	Sequence 31, Appl
34	24.8	20	6	US-10-623-155-532	Sequence 532, App
35	24.8	20	6	US-10-623-155-542	Sequence 542, App
36	24.8	20	6	US-10-623-155-545	Sequence 545, App
37	24.8	21	6	US-10-893-584-205	Sequence 205, App
38	24.8	21	6	US-10-880-238-47	Sequence 47, Appl
39	23.8	8	6	US-10-989-226-81	Sequence 81, Appl
40	23.8	8	7	US-11-066-967-133	Sequence 133, App
41	23.8	9	7	US-11-053-100-9	Sequence 9, Appli
42	23.8	11	7	US-11-045-024-1467	Sequence 1467, Ap
43	23.8	11	7	US-11-045-024-6285	Sequence 6285, Ap
44	23.8	14	7	US-11-116-144-285	Sequence 285, App
45	23.8	16	7	US-11-060-646-5	Sequence 5, Appli
46	23.8	17	7	US-11-193-512-47	Sequence 47, Appl
47	23.8	19	6	US-10-893-584-233	Sequence 233, App
48	23.8	20	6	US-10-623-155-414	Sequence 414, App
49	23.8	20	6	US-10-623-155-525	Sequence 525, App
50	23.3	11	7	US-11-105-708-11	Sequence 11, Appl
51	22.9	6	6	US-10-986-501-338	Sequence 338, App
52	22.9	9	7	US-11-045-024-1247	Sequence 1247, Ap
53	22.9	9	7	US-11-045-024-8847	Sequence 8847, Ap
54	22.9	10	6	US-10-919-492-35	Sequence 35, Appl
55	22.9	10	7	US-11-045-024-5221	Sequence 5221, Ap
56	22.9	10	7	US-11-129-104-61	Sequence 61, Appl
57	22.9	10	7	US-11-129-104-62	Sequence 62, Appl
58	22.9	12	7	US-11-145-861-371	Sequence 371, App
59	22.9	13	7	US-11-145-861-6	Sequence 6, Appli
60	22.9	14	7	US-11-129-104-7	Sequence 7, Appli
61	22.9	15	6	US-10-866-120-4	Sequence 4, Appli
62	22.9	15	6	US-10-919-492-6	Sequence 6, Appli
63	22.9	15	6	US-10-919-492-13	Sequence 13, Appl
64	22.9	19	6	US-10-503-575-119	Sequence 119, App
65	22.9	20	7	US-11-022-562-145	Sequence 145, App
66	22.9	20	7	US-11-022-562-146	Sequence 146, App
67	22.9	21	7	US-11-058-735-72	Sequence 72, Appl
68	21.9	7	6	US-10-485-788A-79	Sequence 79, Appl
69	21.9	8	6	US-10-485-788A-80	Sequence 80, Appl
70	21.9	8	6	US-10-945-674A-52	Sequence 52, Appl
71	21.9	9	6	US-10-850-635-26	Sequence 26, Appl
72	21.9	9	6	US-10-945-674A-29	Sequence 29, Appl
73	21.9	9	6	US-10-945-674A-51	Sequence 51, Appl
74	21.9	9	7	US-11-010-748A-617	Sequence 617, App
75	21.9	9	7	US-11-010-748A-618	Sequence 618, App
76	21.9	9	7	US-11-010-748A-620	Sequence 620, App
77	21.9	9	7	US-11-010-748A-621	Sequence 621, App
78	21.9	9	7	US-11-010-748A-625	Sequence 625, App
79	21.9	9	7	US-11-010-748A-635	Sequence 635, App
80	21.9	9	7	US-11-010-748A-635	Sequence 635, App
81	21.9	9	7	US-11-055-557-28	Sequence 28, Appl
82	21.9	11	7	US-11-033-665-12	Sequence 12, Appl
83	21.9	12	6	US-10-893-584-102	Sequence 102, App
84	21.9	13	6	US-10-893-584-198	Sequence 198, App
85	21.9	14	6	US-10-746-959C-5	Sequence 5, Appli
86	21.9	14	6	US-10-945-674A-87	Sequence 87, Appl
87	21.9	15	6	US-10-939-890-200	Sequence 200, App
88	21.9	15	6	US-10-939-890-202	Sequence 202, App
89	21.9	15	6	US-10-893-584-247	Sequence 247, App
90	21.9	15	7	US-11-187-558-4	Sequence 4, Appli
91	21.9	16	6	US-10-919-492-3	Sequence 3, Appli
92	21.9	16	6	US-10-919-492-10	Sequence 10, Appl
93	21.9	16	7	US-11-108-189-12	Sequence 12, Appl
94	21.9	17	6	US-10-880-238-107	Sequence 107, App
95	21.9	17	6	US-10-880-238-109	Sequence 109, App
96	21.9	17	6	US-10-945-674A-18	Sequence 18, Appl
97	21.9	17	6	US-10-945-674A-91	Sequence 91, Appl
98	21.9	17	7	US-11-010-748A-405	Sequence 405, App

93 23 21.9 17 7 US-11-150-485-4
100 23 21.9 18 7 US-11-033-039-1324

Sequence 4, Appli
Sequence 1324, Ap

ALIGNMENTS

RESULT 1
US-10-939-890-146

; Sequence 146, Application US/10939890
; Publication No. US20050250700A1

GENERAL INFORMATION:

; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Ardogaat, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.

; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00

; CURRENT FILING DATE: 2004-09-13
; PRIOR FILING DATE: 2003-09-11

; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11

; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15

; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01

; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 146
; LENGTH: 20

; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Library Isolate

US-10-939-890-146

Query Match 31.4%; Score 33; DB 6; Length 20;
Best Local Similarity 58.3%; Pred. No. 19;

Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 8 PPGFVGEQV 19
||| | : |

Db 2 PPGFSYWEQV 13

RESULT 2
US-10-939-890-170

; Sequence 170, Application US/10939890
; Publication No. US20050250700A1

GENERAL INFORMATION:

; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.

; APPLICANT: Ardogaat, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.

; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00

; CURRENT FILING DATE: 2004-09-13
; PRIOR FILING DATE: 2003-09-11

; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11

; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15

; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01

; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 170
; LENGTH: 20

; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Library Isolate

US-10-939-890-170

Query Match 30.5%; Score 32; DB 6; Length 20;
Best Local Similarity 50.0%; Pred. No. 27;

Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 8 PPGFVGEQV 19
||| | : |

Db 2 PPGFSYWEQV 13

RESULT 3
US-10-623-155-463

; Sequence 463, Application US/10623155
; Publication No. US20050261166A1

GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong
; APPLICANT: Peckham, David W.

; APPLICANT: Recter, Marc W.
; APPLICANT: Fanger, Gary R.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C20

; CURRENT FILING DATE: US/10/623,155
; CURRENT FILING DATE: 2003-07-17

; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 463
; LENGTH: 20

; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-623-155-463

Query Match 29.5%; Score 31; DB 6; Length 20;
Best Local Similarity 62.5%; Pred. No. 39;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9
DB 9 PTSGMPP 16

RESULT 4

US-10-623-155-541
Sequence 541, Application US/10623155
Publication No. US20050261166A1
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Peckham, David W.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C20
CURRENT APPLICATION NUMBER: US/10/623.155
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 541
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-623-155-541

Query Match 29.5%; Score 31; DB 6; Length 20;
Best Local Similarity 62.5%; Pred. No. 39;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9
DB 9 PTSGMPP 16

RESULT 5

US-10-623-155-413
Sequence 413, Application US/10623155
Publication No. US20050261166A1
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Peckham, David W.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C20
CURRENT APPLICATION NUMBER: US/10/623.155
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 413
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-623-155-413

Query Match 27.6%; Score 29; DB 6; Length 20;
Best Local Similarity 62.5%; Pred. No. 79;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GFIVGEG 17
DB 9 GAIGKEG 16

US-10-623-155-524
Sequence 524, Application US/10623155
Publication No. US20050261166A1
GENERAL INFORMATION:

APPLICANT: Wang, Tonglong
APPLICANT: Peckham, David W.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C20
CURRENT APPLICATION NUMBER: US/10/623.155
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 524
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-623-155-524

Query Match 27.6%; Score 29; DB 6; Length 20;
Best Local Similarity 62.5%; Pred. No. 79;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GFIVGEG 17
DB 9 GAIGKEG 16

RESULT 7

US-11-094-142-16
Sequence 16, Application US/11094142
Publication No. US20050260770A1
GENERAL INFORMATION:
APPLICANT: Cohen, Irvin R.
APPLICANT: Quintana, Francisco Javier
APPLICANT: Doman, Eylan
APPLICANT: Elizur, Gad
APPLICANT: Hagedorn, Peter H.
TITLE OF INVENTION: ANTIGEN ARRAY AND DIAGNOSTIC USES THEREOF
FILE REFERENCE: 28462
CURRENT APPLICATION NUMBER: US/11/094.142
CURRENT FILING DATE: 2005-03-31
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.3
SEQ ID NO 16
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-11-094-142-16

Query Match 27.6%; Score 29; DB 7; Length 20;
Best Local Similarity 55.6%; Pred. No. 79;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 10 GFIVGEGV 18
DB 7 GAVFGEGV 15

RESULT 8

US-10-889-197-25
Sequence 25, Application US/10889197
Publication No. US20050271689A1
GENERAL INFORMATION:
APPLICANT: HUANG, CHUN-MING
APPLICANT: ZHANG, JIANFENG
APPLICANT: TANG, DE-CHU
TITLE OF INVENTION: NOVEL TARGETS AND COMPOSITIONS FOR USE IN
DECONTAMINATION, IMMUNOPROPHYLAXIS, AND POST-EXPOSURE
FILE REFERENCE: 858610-2006.1
CURRENT APPLICATION NUMBER: US/10/889.197
CURRENT FILING DATE: 2004-07-12

PRIOR APPLICATION NUMBER: 60/486,369
PRIOR FILING DATE: 2003-07-11
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 25
LENGTH: 12
TYPE: PRT
ORGANISM: Bacillus anthracis
US-10-889-197-25

Query Match 26.7%; Score 28; DB 6; Length 12;
Best Local Similarity 55.6%; Pred. No. 63;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 8 PGFVIGEE 16
Db 4 PAGFTFGEX 12

RESULT 9
US-10-939-890-203
Sequence 203, Application US/10939890
Publication No. US20050250700a1
GENERAL INFORMATION:
APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussac, Philippe
APPLICANT: Fan, Hong
APPLICANT: Khurana, Sucha
APPLICANT: Linder, Karen E.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Nanjappan, Palaniasappa
APPLICANT: Nunn, Adrian D.
APPLICANT: Pillai, Radhakrishna
APPLICANT: Pochon, Sibylle
APPLICANT: Ramalingam, Kondareddiar
APPLICANT: Shrivastava, Ajay
APPLICANT: Swenson, Rolf E.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617, 70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 203
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Library Isolate
US-10-939-890-203

Query Match 26.7%; Score 28; DB 6; Length 15;
Best Local Similarity 71.4%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 PAKGMSP 8
Db 4 PAKGMSP 8

Db 3 PCKGMPLP 9

RESULT 10
US-11-054-515-3003
Sequence 3003, Application US/11054515
Publication No. US2005025532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Buys
FILE REFERENCE: P5523P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 3003
LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-3003

Query Match 26.7%; Score 28; DB 7; Length 16;
Best Local Similarity 54.5%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 DPAKGMSPGF 11
Db 4 DPLTGYSLDGF 14

RESULT 11
US-10-893-584-212
Sequence 212, Application US/10893584
Publication No. US20050272048A1
GENERAL INFORMATION:
APPLICANT: Borgford, Thor
APPLICANT: Braun, Curtis
APPLICANT: Putac, Admir
APPLICANT: Scoll, Dominik
TITLE OF INVENTION: Right-Like Toxin Variants for Treatment of Cancer,
Viral or Parasitic Infections
FILE REFERENCE: 10447-025
CURRENT APPLICATION NUMBER: US/10/893,584
CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: US 09/551,151
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/403,752
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 10/089,058
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 274
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 212

LENGTH: 20
TYPE: PRT
ORGANISM: E. coli
US-10-893-584-212

Query Match 26.7%; Score 28; DB 6; Length 20;
Best Local Similarity 38.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 2 PAKGSPGPIVG 14
DB 2 PGRVVGPGRVVG 14

RESULT 12
US-11-058-735-60

Sequence 60, Application US/11058735
Publication No. US20050261475A1
GENERAL INFORMATION:

APPLICANT: TSENG, HUANG-CHUN

TITLE OF INVENTION: SOLID-PHASE CAPTURE-RELEASE-TAG METHODS FOR

FILE REFERENCE: HMV-094.01

CURRENT FILING DATE: 2005-02-14

PRIOR FILING DATE: 2004-02-13

NUMBER OF SEQ ID NOS: 80

SOFTWARE: PatentIn Ver. 3.3

LENGTH: 21

TYPE: PRT

ORGANISM: Mus musculus

US-11-058-735-60

OY 2 PAKGSPG 9

DB 10 PPKGLSVP 17

RESULT 13
US-11-145-861-78

Sequence 78, Application US/11145861
Publication No. US20060014138A1
GENERAL INFORMATION:

APPLICANT: Chinaiyan, Arul

FILE REFERENCE: UM-09899

CURRENT FILING DATE: 2005-06-06

NUMBER OF SEQ ID NOS: 464

SOFTWARE: PatentIn version 3.3

LENGTH: 11

TYPE: PRT

ORGANISM: Homo sapiens

US-11-145-861-78

OY 11 FIVEGEGVL 19

DB 3 FLEGEGQIL 11

RESULT 14
US-11-143-984A-164

Sequence 164, Application US/11143984A
Publication No. US20060014180A1
GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL HUMAN PHOSPHATASES

FILE REFERENCE: D0072 DIV1

CURRENT FILING DATE: 2005-06-02

PRIOR FILING DATE: 2000-12-20

PRIOR FILING DATE: 2001-03-30

PRIOR FILING DATE: 2001-05-01

PRIOR FILING DATE: 2001-06-05

NUMBER OF SEQ ID NOS: 208

SOFTWARE: PatentIn version 3.2

LENGTH: 14

TYPE: PRT

ORGANISM: Homo sapiens

US-11-143-984A-164

OY 5 GMSPPGF 11

DB 1 GVCPPNF 7

RESULT 15
US-10-516-676-1

Sequence 1, Application US/10516676
Publication No. US20050244393A1
GENERAL INFORMATION:

APPLICANT: Philippeart, Pierre

TITLE OF INVENTION: SEALANT OR TISSUE GENERATING PRODUCT

FILE REFERENCE: 232037

CURRENT FILING DATE: 2004-12-03

PRIOR FILING DATE: 2002-06-21

NUMBER OF SEQ ID NOS: 1

SOFTWARE: PatentIn version 3.2

LENGTH: 15

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Synthesized

US-10-516-676-1

OY 5 GMSPPGPIVGEGVL 19

DB 1 GTPGPGIAGOGGV 15

RESULT 16
US-10-532-426-2

Sequence 16, Application US/10532426A
Publication No. US20060014180A1
GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL HUMAN PHOSPHATASES

FILE REFERENCE: D0072 DIV1

; Sequence 2, Application US/10532426
; Publication No. US2006009516A1
; GENERAL INFORMATION:
; APPLICANT: Rosenberg, Lawrence
; TITLE OF INVENTION: USE OF IN GAP FOR REVERSING DIABETES
; FILE REFERENCE: 1912-0308PUS1
; CURRENT APPLICATION NUMBER: US/10/532,426
; PRIOR FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/420,677
; PRIOR FILING DATE: 2002-10-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: IN GAP peptide
US-10-532-426-2

Query Match 25.7%; Score 27; DB 6; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 1 DPAKMSPPG 10
|||
Db 4 DPGHGTLPNG 13

RESULT 17
US-11-054-515-2153
; Sequence 2153, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Buys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2153
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2153

Query Match 25.7%; Score 27; DB 7; Length 16;
Best Local Similarity 54.5%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 DPAKMSPPGF 11
|||

Db 4 DPLTGYSPDGF 14

RESULT 18
US-11-054-515-2780
; Sequence 2780, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Buys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2780
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2780

Query Match 25.7%; Score 27; DB 7; Length 16;
Best Local Similarity 54.5%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 DPAKMSPPGF 11
|||
Db 4 DPLTGYSPDGF 14

RESULT 19
US-11-054-515-2783
; Sequence 2783, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Buys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/2277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 2783
LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-2783

Query Match 25.7%; Score 27; DB 7; Length 16;
Best Local Similarity 54.5%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 DPAKMSPPGF 11
Db 4 DPLGYSFDGF 14

RESULT 20
US-11-053-100-18
Sequence 18, Application US/11053100
Publication No. US20050255554A1
GENERAL INFORMATION:
APPLICANT: CHIKOTI, Ashutosh
TITLE OF INVENTION: FUSION PEPTIDES ISOLATABLE BY PHASE TRANSITION
FILE REFERENCE: 4176-101 CIP
CURRENT APPLICATION NUMBER: US/11/053,100
CURRENT FILING DATE: 2005-02-08
PRIOR APPLICATION NUMBER: US 09/812,382
PRIOR FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: US 60/190,659
PRIOR FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn version 3.3
SEQ ID NO 18
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic Construct
FEATURE:
NAME/KEY: REPEAT
LOCATION: (1)-(20)
OTHER INFORMATION: ELP1 [K1V2FL-4]
US-11-053-100-18

Query Match 25.7%; Score 27; DB 7; Length 20;
Best Local Similarity 52.9%; Pred. No. 1.6e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 4; Gaps 2;

QY 2 PAKGMSPPGFVGEV 18
Db 2 PGKGV--PG--VGVPV 14

RESULT 21
US-10-485-788A-598
Sequence 598, Application US/10485788A
Publication No. US20050282743A1
GENERAL INFORMATION:
APPLICANT: Lu, Peter S.
APPLICANT: Rabinowitz, Joshua D.
APPLICANT: Schweitzer, Johannes
APPLICANT: Carrick, Deanna Marie
APPLICANT: Arbor Vita Corporation
TITLE OF INVENTION: Molecular Interactions in Cells
FILE REFERENCE: 20054-003320US

CURRENT APPLICATION NUMBER: US/10/485,788A
CURRENT FILING DATE: 2004-02-03
PRIOR APPLICATION NUMBER: US 60/309,841
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US 60/360,061
PRIOR FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: WO PCT/US02/24655
PRIOR FILING DATE: 2002-08-02
NUMBER OF SEQ ID NOS: 841
SOFTWARE: PatentIn version 3.1
SEQ ID NO 598
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-485-788A-598

Query Match 25.2%; Score 26.5; DB 6; Length 20;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 DPAKMSPP 9
Db 10 DPGF-MSP 17

RESULT 22
US-11-147-994-10
Sequence 10, Application US/11147994
Publication No. US20060013855A1
GENERAL INFORMATION:
APPLICANT: Medivac, LLC
APPLICANT: CARPENTER, Kenneth W.
APPLICANT: TURNELL, William G.
APPLICANT: DEFIFE, Kristin M.
APPLICANT: GRAKO, Kathryn A.
TITLE OF INVENTION: BIOACTIVE STENTS FOR TYPE II DIABETICS AND METHODS FOR USE
FILE REFERENCE: MEDIV2030-3
CURRENT APPLICATION NUMBER: US/11/147,994
CURRENT FILING DATE: 2005-06-07
PRIOR APPLICATION NUMBER: US 11/098,891
PRIOR FILING DATE: 2004-04-04
PRIOR APPLICATION NUMBER: US 60/559,937
PRIOR FILING DATE: 2004-04-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.3
SEQ ID NO 10
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Small proteinaceous motif
US-11-147-994-10

Query Match 24.8%; Score 26; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11
Db 2 PPGF 5

RESULT 23
US-11-178-269-27
Sequence 27, Application US/11178269
Publication No. US20050272661A1
GENERAL INFORMATION:
APPLICANT: Richelson, Elliott
APPLICANT: Cusack, Bernadette Marie
APPLICANT: Pang, Yuan-Ping
APPLICANT: McCormick, Daniel J.
APPLICANT: Faud, Abdul

; APPLICANT: Tyler, Beth Marie
; APPLICANT: Boules, Mona
; TITLE OF INVENTION: NEO-TRYPTOPHAN
; FILE REFERENCE: 07039/141001
; CURRENT APPLICATION NUMBER: US/11/178,269
; CURRENT FILING DATE: 2005-07-08
; PRIOR APPLICATION NUMBER: US/10/858,226
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US/10/265,099
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: US/09/755,638
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/289,693
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/098,119
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: US 60/092,195
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: US 60/081,356
; PRIOR FILING DATE: 1998-04-10
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-11-178-269-27

Query Match 24.8%; Score 26; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 8 PPGR 11
Db 2 PPGR 5

RESULT 24
US-11-043-788-482
; Sequence 482, Application US/11043788
; Publication No. US20060014166A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF ENDOMETRIOSIS
; FILE REFERENCE: 1847.1006
; CURRENT APPLICATION NUMBER: US/11/043,788
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 506
; SEQ ID NO 482
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-043-788-482

Query Match 24.8%; Score 26; DB 7; Length 9;
Best Local Similarity 80.0%; Pred. No. 5.8e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 MSPG 10
Db 4 LSPG 8

RESULT 25
US-11-147-994-8
; Sequence 8, Application US/11147994
; Publication No. US20060013855A1
; GENERAL INFORMATION:

; APPLICANT: Medivase, LLC
; APPLICANT: CARPENTER, Kenneth W.
; APPLICANT: TURNELL, William G.
; APPLICANT: DEFIFE, Kristin M.
; APPLICANT: GRAGO, Kathryn A.
; TITLE OF INVENTION: BIOACTIVE STENTS FOR TYPE II DIABETICS AND METHODS FOR USE
; FILE REFERENCE: MEDIV2030-3
; CURRENT APPLICATION NUMBER: US/11/147,994
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US 11/098,891
; PRIOR FILING DATE: 2004-04-04
; PRIOR APPLICATION NUMBER: US 60/559,937
; PRIOR FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Small proteinaceous motif
US-11-147-994-8

Query Match 24.8%; Score 26; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 8 PPGR 11
Db 3 PPGR 6

Search completed: January 26, 2006, 08:39:07
Job time : 3.7931 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:48:50 : Search time 10 Seconds

(without alignments)
192.434 Million cell updates/sec

Title: US-09-662-293-13

Perfect score: 105
Sequence: 1 DPAKMSPPGFIVGSEGLS 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 4071

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	32	30.5	15	2	F57789	galbladder stone
2	31	29.5	17	2	PH0082	neuroglian protein
3	28	26.7	10	2	S26506	collagen alpha 1(V
4	28	26.7	15	2	SS4712	zein Zp22/6 protei
5	28	26.7	20	2	B60801	acrosome stabilizi
6	28	26.7	21	2	PT0089	4-hydroxybenzoate
7	27	25.7	16	2	C49048	T-cell receptor be
8	27	25.7	16	2	PS0210	28K protein 4209 -
9	26	24.8	9	2	S65433	bradykinin - horn
10	26	24.8	9	2	A43065	hydroxyproline-3-b
11	26	24.8	9	2	B60246	ornitho-kinin - ch
12	26	24.8	9	2	A26744	bradykinin-like pe
13	26	24.8	9	2	A61057	Thr-6 bradykinin -
14	26	24.8	9	2	A60579	bradykinin-like pe
15	26	24.8	9	2	A61363	bradykinin - commo
16	26	24.8	9	2	A61358	bradykinin-like pe
17	26	24.8	11	2	S13279	ile-ser-bradykinin
18	26	24.8	11	2	B26744	megacoliakinin
19	26	24.8	11	2	A61365	phyllokinin - Rohd
20	26	24.8	12	2	A61360	vespakinin M - hor
21	26	24.8	12	2	A61359	vespakinin X - hor
22	26	24.8	13	2	A61361	bradykinin-like pe
23	26	24.8	14	2	A61362	bradykinin-like pe
24	26	24.8	15	2	A36279	chemotactacant pr
25	26	24.8	17	1	A61339	vespakinin I - e
26	26	24.8	20	2	S39380	pectinesterase (EC
27	26	24.8	21	2	S69502	NFI/CAAT-binding c
28	25	23.8	10	2	A36454	tyrosin-modulating
29	25	23.8	10	2	C60527	sperm-activating p

30	25	23.8	12	2	T46794	hypothetical prote
31	25	23.8	20	2	A33878	myosin light chain
32	25	23.8	20	2	A61576	insulin-like growt
33	25	23.8	20	2	A46644	temperature-labile
34	24	22.9	10	2	B60588	sperm-activating p
35	24	22.9	10	2	B60788	sperm-activating p
36	24	22.9	15	2	I65478	c-Ki-raz - hamster
37	24	22.9	15	2	PT0097	glutathione peroxi
38	24	22.9	17	2	S77834	DNA-directed RNA p
39	24	22.9	17	2	S57518	T cell receptor be
40	24	22.9	19	2	C37072	proteoglycan 65K c
41	24	22.9	19	2	S11611	ribosomal protein
42	24	22.9	20	2	P00688	photosystem I 14.0
43	24	22.9	20	2	P00687	photosystem I 14.1
44	23	21.9	9	2	S35538	ribosomal protein
45	23	21.9	10	2	C60588	sperm-activating p
46	23	21.9	10	2	B60527	sperm-activating p
47	23	21.9	10	2	I60588	sperm-activating p
48	23	21.9	12	2	C36201	1-aminocyclopropan
49	23	21.9	13	2	A59387	VCAM-1 5'UTR bindi
50	23	21.9	18	2	S13974	chlorophyll a/b-bi
51	23	21.9	19	2	S29766	cytochrome c (EDH)
52	23	21.9	19	2	B28457	proteoglycan II, b
53	23	21.9	20	2	B39108	lectin, galactose/
54	23	21.9	20	2	A31516	50K allergen - per
55	23	21.9	20	2	S38288	photosystem I chai
56	23	21.9	20	2	S06150	nephritogenoside -
57	23	21.9	21	2	A60696	malate dehydrogena
58	22	21.4	15	2	PA0040	protein QA300033 -
59	22	21.0	9	2	PA0033	sperm-activating p
60	22	21.0	10	2	D60527	28K protein 4412 -
61	22	21.0	12	2	PS0213	histone H2B - huma
62	22	21.0	12	2	S65409	GTP-binding protei
63	22	21.0	14	2	A35377	20K protein 5503 -
64	22	21.0	14	2	PS0255	translation elonga
65	22	21.0	15	2	PA0110	alpha-conotoxin Ep
66	22	21.0	16	2	A59042	hypothetical prote
67	22	21.0	18	2	A36133	human leukocyte an
68	22	21.0	18	2	I59649	histone H2B (clone
69	22	21.0	20	2	S19240	histone H2B - huma
70	22	21.0	20	2	B33290	nitrophorin 3 - Rh
71	22	21.0	20	2	C56385	proteasome chain 7
72	22	21.0	21	2	S09088	T-cell receptor al
73	21	20.0	8	2	A35768	pev-cachykinin - p
74	21	20.0	9	2	PD0027	sperm-activating p
75	21	20.0	10	2	F60527	lysvi-bradykinin -
76	21	20.0	10	2	S39030	transgelin - sheep
77	21	20.0	11	2	A40693	cytochrome P450 UT
78	21	20.0	12	2	S39762	43.2K bile stone p
79	21	20.0	12	2	E58502	malate dehydrogena
80	21	20.0	14	2	B60683	hypothetical 1.5K
81	21	20.0	15	2	B39109	insulin-like growt
82	21	20.0	15	2	S05700	complement factor
83	21	20.0	16	2	PL0110	glutathione transf
84	21	20.0	16	2	S55307	pyruvate dehydrog
85	21	20.0	16	2	A31963	hypothetical prote
86	21	20.0	17	2	S01104	thyroid hormone re
87	21	20.0	17	2	I55612	myosin heavy chain
88	21	20.0	17	2	I51203	group III allergen
89	21	20.0	18	2	A39997	hypothetical prote
90	21	20.0	18	2	A35678	fibrinopeptide A -
91	21	20.0	19	2	B29501	phosphocartier pro
92	21	20.0	19	2	A48400	vitronectin - shee
93	21	20.0	19	2	S22233	vitronectin - bovine
94	21	20.0	19	2	S02808	vitronectin - goat
95	21	20.0	20	2	S22232	immunodeficiency v
96	21	20.0	20	2	B48400	chymotrypsin (EC 3
97	21	20.0	20	2	S65399	neurofilament heav
98	21	20.0	20	2	A61414	transitional endop
99	21	20.0	20	2	I53671	
100	21	20.0	21	2	S38273	

hypothetical prote
myosin light chain
insulin-like growt
temperature-labile
sperm-activating p
sperm-activating p
c-Ki-raz - hamster
glutathione peroxi
DNA-directed RNA p
T cell receptor be
proteoglycan 65K c
ribosomal protein
photosystem I 14.0
photosystem I 14.1
ribosomal protein
sperm-activating p
sperm-activating p
sperm-activating p
1-aminocyclopropan
VCAM-1 5'UTR bindi
chlorophyll a/b-bi
cytochrome c (EDH)
proteoglycan II, b
lipoprotein Acid p
lectin, galactose/
50K allergen - per
photosystem I chai
nephritogenoside -
malate dehydrogena
protein QA300033 -
sperm-activating p
28K protein 4412 -
histone H2B - huma
GTP-binding protei
20K protein 5503 -
translation elonga
alpha-conotoxin Ep
hypothetical prote
human leukocyte an
histone H2B (clone
histone H2B - huma
nitrophorin 3 - Rh
proteasome chain 7
T-cell receptor al
pev-cachykinin - p
sperm-activating p
lysvi-bradykinin -
transgelin - sheep
cytochrome P450 UT
43.2K bile stone p
malate dehydrogena
hypothetical 1.5K
insulin-like growt
complement factor
glutathione transf
pyruvate dehydrog
hypothetical prote
thyroid hormone re
myosin heavy chain
group III allergen
hypothetical prote
fibrinopeptide A -
phosphocartier pro
vitronectin - shee
vitronectin - bovine
vitronectin - goat
immunodeficiency v
chymotrypsin (EC 3
neurofilament heav
transitional endop

ALIGNMENTS

RESULT 1

F57789 galbladder stone matrix protein 2, 41K - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
 C/Accession: F57789
 R:Binette, J.P.; Binette, M.B.
 submitted to the Protein Sequence Database, February 1996
 A/Description: The proteins of galbladder stones.
 A/Reference number: A57789
 A/Accession: F57789
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-15 <BIN>
 A/Cross-references: UNIPROT:Q7M4P9; UNIPARC:UPI000017C122
 A/Note: 9-Phe was also found

Query Match 30.5%; Score 32; DB 2; Length 15;
 Best Local Similarity 60.0%; Pred. No. 79;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 8 PGFVGEEG 17
 |||||
 Db 5 PDGFEGSSG 14

RESULT 2

PH0082 neuroglial protein, short form - fruit fly (Drosophila sp.) (fragment)
 C/Species: Drosophila sp.
 C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
 C/Accession: PH0082
 R:Hottsch, M.; Bieber, A.J.; Patel, N.H.; Goodman, C.S.
 Neuron 4, 697-709, 1990
 A/Title: Differential splicing generates a nervous system-specific form of Drosophila ne
 A/Reference number: PH0082; MUID:90262720; PMID:1693086
 A/Accession: PH0082
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-17 <HOR>
 A/Cross-references: UNIPARC:UPI000017BEEF

Query Match 29.5%; Score 31; DB 2; Length 17;
 Best Local Similarity 40.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 5 GMSPPGFVGEGLV 19
 ||:|:|:|
 Db 1 GNMEDGFRIGOTRL 15

RESULT 3

S26506 collagen alpha 1(VI) chain - bovine (fragment)
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C/Accession: S26506
 R:Jander, R.; Rautenberg, J.; Gianville, R.W.
 Eur. J. Biochem. 133, 39-46, 1983
 A/Title: Further characterization of the three polypeptide chains of bovine and human st
 A/Reference number: S26506; MUID:83209648; PMID:6852033
 A/Accession: S26506
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-10 <JAN>
 A/Cross-references: UNIPROT:Q7M2N0; UNIPARC:UPI000017C4E3
 C/Keywords: hydroxyproline
 F/9/Modified site: hydroxyproline (Pro) #status experimental
 Query Match 26.7%; Score 28; DB 2; Length 10;

Best Local Similarity 66.7%; Pred. No. 2.1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

OY 2 PAKGMSPPG 10
 ||:|:|
 Db 4 PARQ-PPG 10

RESULT 4

S54712 zein Zp22/6 protein - maize
 C/Species: Zea mays (maize)
 C/Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
 C/Accession: S54712
 R:Chaudhuri, S.; Messing, J.
 Mol. Gen. Genet. 246, 707-715, 1995
 A/Title: RFLP mapping of the maize dzr1 locus, which regulates methionine-rich 10 kDa ze
 A/Reference number: S54712; MUID:95206245; PMID:7898438
 A/Accession: S54712
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-15 <CHA>
 A/Cross-references: UNIPROT:Q7M1F8; UNIPARC:UPI000017B16A

Query Match 26.7%; Score 28; DB 2; Length 15;
 Best Local Similarity 36.4%; Pred. No. 3.4e+02;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 2 PAKGMSPPGF 12
 ||:|:|
 Db 4 PQOSLAPPAIL 14

RESULT 5

B60801 acrosome stabilizing factor small chain - rabbit (fragment)
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C/Accession: B60801
 R:Wilson, W.L.; Oliphant, G.
 Biol. Reprod. 37, 159-169, 1987
 A/Title: Isolation and biochemical characterization of the subunits of the rabbit sperm
 A/Reference number: A60801; MUID:88000873; PMID:3651543
 A/Accession: B60801
 A/Molecule type: protein
 A/Residues: 1-20 <WIL>
 A/Cross-references: UNIPARC:UPI000017C5B4
 C/Comment: spermatozoa must undergo capacitation and the acrosome reaction to become cap
 C/Keywords: glycoprotein; semen

Query Match 26.7%; Score 28; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 4.7e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 DPAKMSPPG 10
 |||||
 Db 1 DTKKAAPP 10

RESULT 6

PT0089 4-hydroxybenzoate 3-monoxygenase (EC 1.14.13.2) - Comamonas testosteroni (fragment)
 A/Alternate names: p-hydroxybenzoate 3-hydroxylase
 C/Species: Comamonas testosteroni
 C/Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
 C/Accession: PT0089
 R:Taugita, A.
 submitted to JIPID, May 1996
 A/Description: Purification and characterization of p-hydroxybenzoate 3-hydroxylase from
 A/Reference number: PT0089
 A/Accession: PT0089
 A/Molecule type: protein
 A/Residues: 1-21 <CHR>

A:Cross-references: UNIPROT:Q7M1D8; UNIPARC:UPI0000175264
 C:Superfamily: 4-hydroxybenzoate 3-monooxygenase
 C:Keywords: PAD; homodimer; oxidoreductase

Query Match 26.7%; Score 28; DB 2; Length 21;
 Best Local Similarity 36.4%; Pred. No. 5e+02;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 5 GMSPPGFVGE 15
 DB 9 GAGPSGLLGG 19

RESULT 7

C49048
 T-cell receptor beta chain V region (CDR3 junction, clone Vbeta20.1) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
 C:Accession: C49048

R:Sioud, M.; Kjeldsen-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O.
 Eur. J. Immunol. 22, 2413-2418, 1992

A:Title: Limited heterogeneity of T cell receptor variable region gene usage in juvenile
 A:Reference number: A49048; MUID:92387250; PMID:1187614

A:Accession: C49048

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-16 <STO>

A:Cross-references: UNIPARC:UPI000017C3A9

A:Experimental source: patient EV, IL-2R+ synovial T-cells

A>Note: sequence extracted from NCBI backbone (NCBIP:113265)

C:Keywords: T-cell receptor

Query Match 25.7%; Score 27; DB 2; Length 16;
 Best Local Similarity 57.1%; Pred. No. 5.2e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 8 PPGFVVG 14
 DB 10 PPGVTFG 16

RESULT 8

PS0210
 28K protein 4209 - rice (strain Nihonbare) (fragment)

C:Species: Oryza sativa (rice)

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004

C:Accession: PS0210

R:Taniguchi, A.; Miyatake, N.
 submitted to JIPID, April 1993

A:Reference number: PS0208

A:Accession: PS0210

A:Molecule type: protein

A:Residues: 1-16 <TSA>

A:Cross-references: UNIPROT:Q7M281; UNIPARC:UPI000017B0F9

A:Experimental source: germ. bran, strain Nihonbare

C:Comment: molecular weight 28k, pI 7.3.

Query Match 25.7%; Score 27; DB 2; Length 16;
 Best Local Similarity 42.9%; Pred. No. 5.2e+02;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 9 PPGFVGE 15
 DB 1 PGLVIGD 7

RESULT 9

S65433
 bradykinin - horn fly (fragment)

C:Species: Haematobia irritans (horn fly)

C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997

C:Accession: S65433

R:Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen, H.

Eur. J. Biochem. 237, 414-423, 1996
 A:Title: Cloning and characterisation of angiotensin-converting enzyme from the dipter
 A:Reference number: S65431; MUID:56215437; PMID:8647080

A:Accession: S65433

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-9 <WIS>

A:Cross-references: UNIPARC:UPI000002CF4A

A>Note: the source is designated as Haematobia irritans exigua

Query Match 24.8%; Score 26; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PPGF 11
 DB 2 PPGF 5

RESULT 10

A43065
 hydroxyproline-3-bradykinin - frog (Helleophryne purcelli)

C:Species: Helleophryne purcelli

C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004

C:Accession: A43065

R:Nakajima, T.; Yasuhara, T.; Erspamer, G.F.; Visser, J.
 Experientia 35, 1133, 1979

A:Title: Occurrence of Hyp(3)-bradykinin in methanol extracts of the skin of the South

A:Reference number: A43065; MUID:80024576; PMID:488255

A:Accession: A43065

A:Molecule type: protein

A:Residues: 1-9 <NAK>

A:Cross-references: UNIPROT:Q7LZ17; UNIPARC:UPI000002CF4A

A:Keywords: bradykinin; hydroxyproline; skin

F:3/Modified site: hydroxyproline (Pro) #status experimental

Query Match 24.8%; Score 26; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PPGF 11
 DB 2 PPGF 5

RESULT 11

B60246
 ornitho-kinin - chicken

C:Species: Gallus gallus (chicken)

C>Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 16-Aug-2004

C:Accession: B60246

R:Kimura, M.; Sueyoshi, T.; Morita, T.; Tanaka, K.; Iwanaga, S.
 Adv. Exp. Med. Biol. 247A, 359-367, 1989

A:Title: Ornitho-kininogen and ornitho-kinin: isolation, characterization and chemical

A:Reference number: A60246; MUID:90102072; PMID:2603803

A:Accession: B60246

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-9 <KIM>

A:Cross-references: UNIPROT:Q7LZ50; UNIPARC:UPI000017A4F8

Query Match 24.8%; Score 26; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PPGF 11
 DB 2 PPGF 5

RESULT 12

A26744
 bradykinin-like peptide - garden dagger wasp

N:Alternate names: Thr-6-bradykinin
C:Species: Megascalia flavifrons (garden dagger wasp)
C:Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 05-Oct-2004
C:Accession: A26744
R:Yasuhara, T.; Mantel, P.; Nakajima, T.; Piek, T.
R:Yasuhara, T.; Mantel, P.; Nakajima, T.; Piek, T.
A:Title: Two kinins isolated from an extract of the venom reservoirs of the solitary wasp
A:Reference number: A94322; MUID:87293024; PMID:3617088
A:Accession: A26744
A:Molecule type: protein
A:Residues: 1-9 <YAS>
A:Cross-references: UNIPARC:UPI000012DF29

Query Match 24.8%; Score 26; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PGPF 11
Db 2 PGPF 5

RESULT 13
A61057
Thr-6 bradykinin - scollid wasp (Colpa interrupta)
C:Species: Colpa interrupta
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 05-Oct-2004
C:Accession: A61057
R:Piek, T.; Hue, B.; Mantel, P.; Nakajima, T.; Pelhate, M.; Yasuhara, T.
Comp. Biochem. Physiol. C 96, 157-162, 1990
A:Title: Theconine(6)-bradykinin in the venom of the wasp Colpa interrupta (F.) presynap
A:Reference number: A61057; MUID:91130217; PMID:1980872
A:Accession: A61057
A:Molecule type: protein
A:Residues: 1-9 <PIE>
A:Cross-references: UNIPARC:UPI000012DF29
C:Keywords: bradykinin; presynaptic neurotoxin; venom

Query Match 24.8%; Score 26; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PGPF 11
Db 2 PGPF 5

RESULT 14
A60579
bradykinin-like peptide - slider turtle
C:Species: Pseudemys scripta (slider)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 05-Oct-2004
C:Accession: A60579
R:Conlon, J.M.; Hicke, J.W.; Smith, D.D.
Endocrinology 126, 985-991, 1990
A:Title: Isolation and biological activity of a novel kinin ((Thr(6))bradykinin) from th
A:Reference number: A60579; MUID:90126625; PMID:2298179
A:Accession: A60579
A:Molecule type: protein
A:Residues: 1-9 <CON>
A:Cross-references: UNIPARC:UPI000012DF29
C:Comment: This peptide increases aortic blood flow but, unlike bradykinin in mammalian
C:Keywords: plasma

Query Match 24.8%; Score 26; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PGPF 11
Db 2 PGPF 5

RESULT 15
A61363
bradykinin - common frog
C:Species: Rana temporaria (common frog)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Oct-2004
C:Accession: A61363
R:Anastasi, A.; Erspamer, V.; Bertaccini, G.
Comp. Biochem. Physiol. A 14, 43-52, 1965
A:Title: Occurrence of bradykinin in the skin of Rana temporaria.
A:Reference number: A61363
A:Accession: A61363
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <ANA>
A:Cross-references: UNIPROT:Q7LZJ8; UNIPARC:UPI00002CF4A
C:Keywords: skin

Query Match 24.8%; Score 26; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PGPF 11
Db 2 PGPF 5

RESULT 16
A61358
bradykinin-like peptide I - Japanese pond frog
C:Species: Rana nigromaculata (Japanese pond frog)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Oct-2004
C:Accession: A61358
R:Nakajima, T.
Chem. Pharm. Bull. 16, 769-770, 1968
A:Title: Occurrence of a new active peptide on smooth muscle and bradykinin in the skin
A:Reference number: A61358; MUID:68412013; PMID:5677658
A:Accession: A61358
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <NAK>
A:Cross-references: UNIPROT:Q7LZ54; UNIPARC:UPI000017A4F0
C:Keywords: skin

Query Match 24.8%; Score 26; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PGPF 11
Db 2 PGPF 5

RESULT 17
S13279
Ile-Ser-bradykinin - human (fragment)
N:Alternate names: T-kinin
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S13279
R:Wunderer, G.; Walter, I.; Eschenbacher, B.; Lang, M.; Kellermann, J.; Kindermann, G.
Biol. Chem. Hoppe-Seyler 371, 977-981, 1990
A:Title: Ile-Ser-bradykinin is an aberrant permeability factor in various human malignan
A:Reference number: S13279; MUID:91166748; PMID:2076202
A:Accession: S13279
A:Molecule type: protein
A:Residues: 1-11 <WUN>
A:Cross-references: UNIPROT:Q7M4P1; UNIPARC:UPI0000148EBE
C:Keywords: bradykinin

Query Match 24.8%; Score 26; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGPF 11
 ||||
 Db 4 PGPF 7

RESULT 18

B26744
 megascollaktinin - garden dagger wasp
 N:Alternate names: 6-Thr-bradykinin-Lys-Ala
 C:Species: Megascollia flavifrons (garden dagger wasp)
 C:Date: 08-Mar-1999 #sequence_revision 08-Mar-1999 #text_change 05-Oct-2004
 C:Accession: B26744; A28609
 R:Yasuhara, T.; Mantel, P.; Nakajima, T.; Piek, T.
 A:Title: Two kinins isolated from an extract of the venom reservoirs of the solitary wasp
 A:Reference number: A94322; MUID:87293024; PMID:3617088
 A:Accession: B26744
 A:Molecule type: protein
 A:Residues: 1-11 <YAS>
 A:Cross-references: UNIPROT:P12797; UNIPARC:UPI0000126AD6
 R:Nakajima, T.; Piek, T.; Yasuhara, T.; Mantel, P.
 A:Title: Two kinins isolated from the venom of Megascollia flavifrons.
 A:Reference number: A28609
 A:Accession: A28609
 A:Molecule type: protein
 A:Residues: 1-11 <NAK>
 A:Cross-references: UNIPARC:UPI0000126AD6
 C:Keywords: bradykinin; presynaptic neurotoxin; venom

Query Match 24.8%; Score 26; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGPF 11
 ||||
 Db 2 PGPF 5

RESULT 19

A61365
 Phyllokinin - Rohde's leaf frog
 N:Alternate names: bradykinin-1-isoleucyl-tyrosine-O-sulfate
 C:Species: Phyllomedusa rohdei (Rohde's leaf frog)
 C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Oct-2004
 C:Accession: A61365
 R:Anastasi, A.; Bertaccini, G.; Erepaner, V.
 B: J. Pharmacol. 27, 479-485, 1966
 A:Title: Pharmacological data on phyllokinin (bradykinin-1-isoleucyl-tyrosine-O-sulphate)
 A:Reference number: A61365; MUID:67179312; PMID:5970899
 A:Accession: A61365
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-11 <ANA>
 A:Cross-references: UNIPROT:Q7LZ52; UNIPARC:UPI000017A4F2
 C:Keywords: sulfoprotein
 F:11/Binding site: sulfate (Tyr) (covalent) #status experimental

Query Match 24.8%; Score 26; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGPF 11
 ||||
 Db 2 PGPF 5

RESULT 20

A61360
 Vespakinin M - hornet (Vespa mandarinia)
 C:Species: Vespa mandarinia
 C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Oct-2004
 C:Accession: A61360

R:Kishimura, H.; Yasuhara, T.; Yoshida, H.; Nakajima, T.
 Chem. Pharm. Bull. 24, 2896-2897, 1976
 A:Title: Vespakinin-M, a novel bradykinin analogue containing hydroxyproline, in the ve
 A:Reference number: A61360; MUID:77114342; PMID:1017116
 A:Accession: A61360
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-12 <KIS>
 A:Cross-references: UNIPROT:Q7M3T3; UNIPARC:UPI000017A4F3
 C:Keywords: hydroxyproline; venom
 F:4/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 24.8%; Score 26; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGPF 11
 ||||
 Db 3 PGPF 6

RESULT 21

A61359
 vespakinin X - hornet (Vespa xanthoptera)
 C:Species: Vespa xanthoptera
 C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Oct-2004
 C:Accession: A61359
 R:Yasuhara, T.; Yoshida, H.; Nakajima, T.
 Chem. Pharm. Bull. 25, 936-941, 1977
 A:Title: Chemical investigation of the hornet (Vespa xanthoptera Cameron) venom. The st
 A:Reference number: A61359; MUID:87187852; PMID:264186
 A:Accession: A61359
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-12 <YAS>
 A:Cross-references: UNIPROT:Q7M3T2; UNIPARC:UPI000017A4F4
 C:Keywords: venom

Query Match 24.8%; Score 26; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGPF 11
 ||||
 Db 3 PGPF 6

RESULT 22

A61361
 bradykinin-like peptide - Bombina orientalis
 C:Species: Bombina orientalis
 C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Oct-2004
 C:Accession: A61361
 R:Yasuhara, T.; Hira, M.; Nakajima, T.; Yanahara, N.; Yanahara, C.; Hashimoto, T.; Sa
 Chem. Pharm. Bull. 21, 1388-1391, 1973
 A:Title: Active peptides on smooth muscle in the skin of Bombina orientalis Boulenger a
 A:Reference number: A61361; MUID:73256822; PMID:4732297
 A:Accession: A61361
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-13 <YAS>
 A:Cross-references: UNIPROT:P83060; UNIPARC:UPI000017A4F5
 C:Keywords: skin

Query Match 24.8%; Score 26; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGPF 11
 ||||
 Db 2 PGPF 5

RESULT 23

A61362
bradykinin-like peptide III - Japanese pond frog
C:Species: Rana nigromaculata (Japanese pond frog)
C>Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Oct-2004
C:Accession: A61362
R:Nakajima, T.
Chem. Pharm. Bull. 16, 2088-2089, 1968
A:Title: On the third active peptide on smooth muscle in the skin of Rana nigromaculata
A:Reference number: A61362; MUID:65117202; PMID:5751736
A:Accession: A61362
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <NAK>
A:Cross-references: UNIPROT:Q7LZ53; UNIPARC:UPI000017A4F1
C:Keywords: skin

Query Match 24.8%; Score 26; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11
|||
Db 2 PPGF 5

RESULT 24

A36279
chemoattractant protein - earthworm (Lumbricus terrestris) (fragment)
C:Species: Lumbricus terrestris (common earthworm)
C>Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 09-Jul-2004
C:Accession: A36279
R:Jiang, X.C.; Inouchi, J.; Wang, D.; Halpern, M.
J. Biol. Chem. 265, 8736-8744, 1990
A:Title: Purification and characterization of a chemoattractant from electric shock-induced snakes.
A:Reference number: A36279; MUID:90256800; PMID:2160465
A:Accession: A36279
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <JIA>
A:Cross-references: UNIPROT:O44335; UNIPARC:UPI000017BD77

Query Match 24.8%; Score 26; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11
|||
Db 5 PPGF 8

RESULT 25

A61339
vespulinin 1 - eastern yellowjacket
N:Contains: vespulinin 2
C:Species: Vespa maculifrons (eastern yellowjacket)
C>Date: 17-Jul-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C:Accession: A61339
R:Yoshida, H.; Geller, R.G.; Pisano, J.J.
Biochemistry 15, 61-64, 1976
A:Title: Vespulinin: new carbohydrate-containing bradykinin derivatives.
A:Reference number: A61339; MUID:76114777; PMID:1247511
A:Accession: A61339
A:Molecule type: protein
A:Residues: 1-17 <YOS>
A:Cross-references: UNIPROT:P57672; UNIPARC:UPI0000138459
C:Superfamily: vespulinin
C:Keywords: antihypertensive; bradykinin; glycoprotein; venom
F:1-17/Product: vespulinin 1 #status experimental <MAT1>
F:3-17/Product: vespulinin 2 #status experimental <MAT2>
F:9-17/Region: bradykinin-like
F:3,4/Binding site: carbohydrate (Thr) (covalent) #status experimental

Query Match 24.8%; Score 26; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11
|||
Db 10 PPGF 13

Search completed: January 26, 2006, 08:05:06
Job time : 11 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 07:47:56 : Search time 59,4828 Seconds
(without alignments)
237.221 Million cell updates/sec

Title: US-09-662-293-13

Perfect score: 105

Sequence: 1 DPAKGMSPPGFVCEGVLS 20

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 15779

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : Uniprot 05.80.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	30.5	15	2	Q7M4P9_HUMAN
2	30	28.6	17	2	Q6N6G9_VITTVI
3	30	28.6	18	2	Q8NFB4_HUMAN
4	28	26.7	10	2	Q7M2N0_BOVIN
5	28	26.7	15	2	Q7M1F8_MAIZE
6	28	26.7	16	2	Q7SM54_DELA
7	28	26.7	20	2	Q71HRS_LACDU
8	28	26.7	20	2	Q79CFO_RHILE
9	28	26.7	21	2	Q7M1D8_COMTE
10	27	25.7	16	2	Q7M2B1_ORYSA
11	27	25.7	16	2	Q9T2Q4_BRANA
12	27	25.7	19	2	Q9N195_BOVIN
13	27	25.7	21	2	Q9S554_MOUSE
14	26	24.8	9	1	BRK1_RANNI
15	26	24.8	9	1	KNL3_BOVIA
16	26	24.8	9	1	KNL3_CYPDO
17	26	24.8	9	2	P84497_TRASC
18	26	24.8	9	2	P84497_TRACHEMYX
19	26	24.8	9	2	Q7L250_CHICK
20	26	24.8	9	2	Q7L278_RANTE
21	26	24.8	9	2	Q7L277_SNEOB
22	26	24.8	11	1	BRKP_PHYRO
23	26	24.8	11	1	BRKP_MEGFL
24	26	24.8	11	2	Q7S811_HUMAN
25	26	24.8	11	2	Q7M4P1_HUMAN
26	26	24.8	12	1	VESP_VESMA
27	26	24.8	12	1	VESP_VESXA
28	26	24.8	13	1	BRK_FARID
29	26	24.8	13	1	SCX2_TITDI
30	26	24.8	14	1	BRK3_RANNI
31	26	24.8	15	2	Q9R5T1_9FLAO
			17	1	TL09_SPIOL

32	26	24.8	17	1	VESP_VESMC	P57672 vespuia mac
33	26	24.8	18	2	Q16053_HUMAN	Q16053 homo sapien
34	25.5	24.3	18	2	Q763U4_USEUD	Q763U4 naravelia l
35	25.5	24.3	18	2	Q763U5_CLEVI	Q763U5 clematis vi
36	25.5	24.3	20	2	Q763W5_USEUD	Q763W5 clematis ja
37	25.5	24.3	21	2	Q763T7_USEUD	Q763T7 knowltonia
38	25.5	24.3	21	2	Q763T9_USEUD	Q763T9 pulsatilla
39	25.5	24.3	21	2	Q763U0_USEUD	Q763U0 anemone fla
40	25.5	24.3	21	2	Q763U1_USEUD	Q763U1 clematis vi
41	25.5	24.3	21	2	Q763U2_USEUD	Q763U2 clematis ge
42	25.5	24.3	21	2	Q763U3_USEUD	Q763U3 clematis ei
43	25.5	24.3	21	2	Q763U6_USEUD	Q763U6 clematis no
44	25.5	24.3	21	2	Q763U7_USEUD	Q763U7 clematis se
45	25.5	24.3	21	2	Q763U8_USEUD	Q763U8 clematis fr
46	25.5	24.3	21	2	Q763U9_USEUD	Q763U9 clematis ba
47	25.5	24.3	21	2	Q763V0_USEUD	Q763V0 clematis de
48	25.5	24.3	21	2	Q763V3_USEUD	Q763V3 clematis an
49	25.5	24.3	21	2	Q763V4_USEUD	Q763V4 clematis po
50	25.5	24.3	21	2	Q763V5_USEUD	Q763V5 clematis te
51	25.5	24.3	21	2	Q763V6_USEUD	Q763V6 clematis or
52	25.5	24.3	21	2	Q763V7_USEUD	Q763V7 clematis ta
53	25.5	24.3	21	2	Q763V8_USEUD	Q763V8 clematis cr
54	25.5	24.3	21	2	Q763V9_USEUD	Q763V9 clematis af
55	25.5	24.3	21	2	Q763W0_USEUD	Q763W0 clematis ta
56	25.5	24.3	21	2	Q763W1_USEUD	Q763W1 clematis pi
57	25.5	24.3	21	2	Q763W2_USEUD	Q763W2 clematis al
58	25.5	24.3	21	2	Q763W3_USEUD	Q763W3 clematis un
59	25.5	24.3	21	2	Q763W4_USEUD	Q763W4 clematis st
60	25.5	24.3	21	2	Q763W7_USEUD	Q763W7 clematis la
61	25.5	24.3	21	2	Q763W8_USEUD	Q763W8 clematis pa
62	25.5	24.3	21	2	Q763X0_USEUD	Q763X0 clematis oc
63	25.5	24.3	21	2	Q763X1_USEUD	Q763X1 clematis wi
64	25.5	24.3	21	2	Q763X2_USEUD	Q763X2 clematis ap
65	25.5	24.3	21	2	Q763X3_USEUD	Q763X3 clematis fu
66	25.5	24.3	21	2	Q763V1_CLELI	Q763V1 clematis li
67	25.5	24.3	21	2	Q763W9_CLELA	Q763W9 clematis le
68	25.5	24.3	21	2	Q763V2_CLELA	Q763V2 clematis la
69	25.5	24.3	21	2	Q763W6_CLEFL	Q763W6 clematis fl
70	25	23.8	10	1	TMOF_AEDAE	P19425 aedes aegypt
71	25	23.8	10	2	Q7M3T6_TRIGR	Q7M3T6 tritipneutes
72	25	23.8	12	2	Q4W620_9CALI	Q4W620 norovirus n
73	25	23.8	12	2	Q84268_9PAPI	Q84268 human papil
74	25	23.8	13	1	FARB_ASCSU	P33173 ascaris suu
75	25	23.8	13	2	Q16007_HUMAN	Q16007 homo sapien
76	25	23.8	18	2	Q9Z190_MOUSE	Q9Z190 mus musculu
77	25	23.8	19	1	TRPJ_LEOMA	P81735 leucophaea
78	25	23.8	20	1	PYRX_PSEFL	P65586 pseudomonas
79	25	23.8	20	2	Q9OV83_GMURI	Q9OV83 rattus sp.
80	25	23.8	20	2	Q7L2H3_MELCA	Q7L2H3 meleagris g
81	25	23.8	21	2	Q5HCH6_HUMAN	Q5HCH6 homo sapien
82	25	23.8	21	2	Q9UC26_HUMAN	Q9UC26 homo sapien
83	24	22.9	10	2	Q7M4B6_STRNU	Q7M4B6 strongyloce
84	24	22.9	11	2	Q7M4D4_PSEDP	Q7M4D4 pseudocentr
85	24	22.9	11	2	P82436_TOBAC	P82436 nicotiana t
86	24	22.9	15	2	Q80XQ4_MEASU	Q80XQ4 mesocricetu
87	24	22.9	17	2	Q9HE01_PARER	Q9HE01 paracoccidi
88	24	22.9	17	2	Q9HE02_AJEBE	Q9HE02 ajelomyces
89	24	22.9	17	2	Q9HEQ3_AJEBE	Q9HEQ3 ajelomyces
90	24	22.9	17	2	Q49077_MYCCA	Q49077 mycoplasma
91	24	22.9	19	2	Q7MS46_HALSA	Q7MS46 halobacteri
92	24	22.9	19	2	Q7RS06_GCTIC	Q7RS06 porcine cir
93	24	22.9	19	2	Q9YIT3_GCTIC	Q9YIT3 bovine circ
94	24	22.9	20	2	Q9T2I8_NICSY	Q9T2I8 nicotiana s
95	24	22.9	20	2	Q9T2I9_NICSY	Q9T2I9 nicotiana s
96	24	22.9	21	2	Q9MBH5_9CAUD	Q9MBH5 streptococc
97	23.5	22.4	12	2	Q5ISY4_9CALI	Q5ISY4 norovirus t
98	23.5	22.4	12	2	Q5ISY5_9CALI	Q5ISY5 norovirus t
99	23.5	22.4	16	2	Q506K8_9CALI	Q506K8 norovirus h
100	23.5	22.4	18	2	Q88290_9CALI	Q88290 small round

ALIGNMENTS

```

RESULT 1
Q7MAP9_HUMAN PRELIMINARY; PRT; 15 AA.
ID Q7MAP9_HUMAN PRELIMINARY; PRT; 15 AA.
AC Q7MAP9;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Galbladder stone matrix protein 2, 41k (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1];
RP PROTEIN SEQUENCE.
RA Binette J.P., Binette M.B.;
RL Submitted (FBS-1996) to the PIR data bank.
DR PIR; F57789; F57789.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 15 AA; 1539 MW; DD8774ED4B7A4786 CRC64;

Query Match 30.5%; Score 32; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 8.3e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 PPGFIVEEG 17
Db 5 PDGFIEGSSG 14

RESULT 2
Q66N69_VITVI PRELIMINARY; PRT; 17 AA.
ID Q66N69_VITVI PRELIMINARY; PRT; 17 AA.
AC Q66N69;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE 20S proteasome beta subunit (Fragment).
OS Vitis vinifera (Grape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Vitaceae; Vitis.
OX NCBI_TaxID=29760;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RA TISSUE-Leaf;
RA Carvalho M.B., Caeiro A.S., Price C.B., Teixeira A.R., Ferreira R.B.;
RL Submitted (JUL-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY684130; AAU04834.1.; mRNA.
DR GO; GO:0005829; C:cytosol; IEA.
KW Proteasome.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 17 AA; 1808 MW; C19F776A03AE8D9F CRC64;

Query Match 28.6%; Score 30; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 PAKGMSPPGIVE 15
Db 3 PAKGTTTAFIFKE 16

RESULT 3
Q8NFB4_HUMAN PRELIMINARY; PRT; 18 AA.
ID Q8NFB4_HUMAN PRELIMINARY; PRT; 18 AA.
AC Q8NFB4;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

```

```

DE Mutant enamelrin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22294456; PubMed=12407086;
RA Kida M., Ariga T., Shirakawa T., Oguchi H., Sakiyama Y.;
RT "Autosomal-dominant hypoplastic form of amelogenesis imperfecta caused
RT by an enamelrin gene mutation at the exon-intron boundary.";
RL J. Dent. Res. 81:738-742(2002).
DR EMBL; AF530444; AAM97323.1.; Genomic_DNA.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 18 AA; 1893 MW; 492D282E3B8BE512 CRC64;

Query Match 28.6%; Score 30; DB 2; Length 18;
Best Local Similarity 43.8%; Pred. No. 2.1e+03;
Matches 7; Conservative 2; Mismatches 3; Indels 4; Gaps 1;

QY 6 MSPPGF---IVGEEG 17
Db 2 LPPPGYGRPPISNBE 17

RESULT 4
Q7M2N0_BOVIN PRELIMINARY; PRT; 10 AA.
ID Q7M2N0_BOVIN PRELIMINARY; PRT; 10 AA.
AC Q7M2N0;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Collagen alpha 1(VI) chain (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1];
RP PROTEIN SEQUENCE.
RA Jander R., Rautenberg J., Glanville R.W.;
RX PubMed=6852033;
RT "Further characterization of the three polypeptide chains of bovine
RT and human short-chain collagen (intima collagen).";
RL Eur. J. Biochem. 133:39-46(1983).
DR PIR; S26506; S26506.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 10 AA; 965 MW; CAA96668640DC776 CRC64;

Query Match 26.7%; Score 28; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.3e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 2 PAKGMSPPG 10
Db 4 PARG--PPG 10

RESULT 5
Q7M1F8_MAIZE PRELIMINARY; PRT; 15 AA.
ID Q7M1F8_MAIZE PRELIMINARY; PRT; 15 AA.
AC Q7M1F8;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Zein Zp22/6 protein.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoidae; Andropogoneae; Zea.

```


OK NCBI_TaxID=4577;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=95206245; PubMed=7898438; DOI=10.1007/BF00290716;
 RA Chaudhuri S., Messing J.,
 RT "RFLP mapping of the maize dzrl locus, which regulates methionine-rich
 RL 10 kDa zein accumulation.";
 DR Mol. Gen. Genet. 246:707-715(1995).
 SO PIR: S54712; S54712.
 SEQUENCE 15 AA; 1605 MW; 5DFB414D8D001609 CRC64;

Query Match 26.7%; Score 28; DB 2; Length 15;
 Best Local Similarity 36.4%; Pred. No. 3.5e+03;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 PAKMSPPGPF 12
 DB 4 PGOOLAPPAII 14

RESULT 6
 Q7SM54_9DELA
 ID Q7SM54_9DELA PRELIMINARY; PRT; 16 AA.
 AC Q7SM54;
 DT 01-OCT-2003 (TReMBLrel. 25, Created)
 DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
 DE Tax protein (Fragment).
 OS Human T-lymphotropic virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Deltaretrovirus.
 NC NCBI_TaxID=11908;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Gonzalez Perez M.P., Garcia Salz A.,
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF529962; AAB87693.1; -; Genomic DNA.
 FT NON TER 1
 SO SEQUENCE 16 AA; 1782 MW; 9CDDDFE4146E2F CRC64;

Query Match 26.7%; Score 28; DB 2; Length 16;
 Best Local Similarity 66.7%; Pred. No. 3.7e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 GMSPPG 10
 DB 2 GLEPPG 7

RESULT 7
 Q71HR5_LACDL
 ID Q71HR5_LACDL PRELIMINARY; PRT; 20 AA.
 AC Q71HR5;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE Histidyl-tRNA synthetase (EC 6.1.1.21) (Fragment).
 OS Lactobacillus delbrueckii (subsp. lactis).
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 NC NCBI_TaxID=29397;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Langenheim J.F., Ulrich R.L.,
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF96531; AAQ07223.1; -; Genomic DNA.
 DR GO; GO:0004821; F:histidine-tRNA ligase activity; IEA.
 KW GO; GO:0016874; F:ligase activity; IEA.
 DR Aminoacyl-tRNA synthetase; Ligase.
 FT NON TER 1
 SO SEQUENCE 20 AA; 2123 MW; 43ABC93211F8210C CRC64;

Query Match 26.7%; Score 28; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 4.7e+03;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 10 GFIVGEGVL 19
 DB 11 GFGIGERLM 20

RESULT 8
 Q79CF0_RHILE
 ID Q79CF0_RHILE PRELIMINARY; PRT; 20 AA.
 AC Q79CF0;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE 4-hydroxybenzoate hydroxylase (EC 1.14.13.2) (Fragment).
 GN Name=poba.
 OS Rhizobium leguminosarum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
 NC NCBI_TaxID=384;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA STRAIN=B155;
 RC Wong C.M., Dilworth M.J., Glenn A.R.,
 RT "4-Hydroxybenzoate hydroxylase (poba) is positively regulated by pobR
 RT in Rhizobium leguminosarum bv. viciae.";
 RL FEWS Microbiol. Lett. 0:0-0(1995).
 DR EMBL; U40388; AAA83007.1; -; Genomic DNA.
 DR HSSP: P20586; 1K01.
 DR GO; GO:0018659; F:4-hydroxybenzoate 3-monooxygenase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR InterPro; IPR002938; MoxY_FAD_binding.
 DR Pfam; PF01494; FAD_binding_3; 1.
 KM Oxidoreductase.
 FT NON TER 20
 SO SEQUENCE 20 AA; 2011 MW; 378D1B9CB7605522 CRC64;

Query Match 26.7%; Score 28; DB 2; Length 20;
 Best Local Similarity 36.4%; Pred. No. 4.7e+03;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 GMSPPG 15
 DB 9 GSGSPGILGQ 19

RESULT 9
 Q7MID8_COMTE
 ID Q7MID8_COMTE PRELIMINARY; PRT; 21 AA.
 AC Q7MID8;
 DT 01-MAR-2004 (TReMBLrel. 26, Created)
 DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE 4-hydroxybenzoate 3-monooxygenase (EC 1.14.13.2) (Fragment).
 OS Comamonas testosteroni (Pseudomonas testosteroni).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Comamonadaceae; Comamonas.
 NC NCBI_TaxID=285;
 RN [1]
 RP PROTEIN SEQUENCE.
 RA Taugita A.,
 RL Submitted (MAY-1996) to the PIR data bank.
 DR PIR; PTO089; PTO089.
 DR HSSP: P20586; 11UT.
 DR GO; GO:0018659; F:4-hydroxybenzoate 3-monooxygenase activity; IEA.
 DR InterPro; IPR002938; MoxY_FAD_binding.
 DR Pfam; PF01494; FAD_binding_3; 1.
 FT NON TER 21
 SO SEQUENCE 21 AA; 2109 MW; 52178D0D46B76055 CRC64;

Query Match 26.7%; Score 28; DB 2; Length 21;

Best Local Similarity 36.4%; Pred. No. 5e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 GMSPPGFIGVE 15
DB 9 GAGSGLLGQ 19

RESULT 10

Q7M281_ORYSA PRELIMINARY; PRT; 16 AA.
ID Q7M281_ORYSA
AC Q7M281;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE 28k protein 4209 (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriocaridaceae; Oryzaeae; Oryza.
NCBI_TaxID=4530;

PROTEIN SEQUENCE:
RP Tsugita A., Miyake N.;
RA Submitted (APR-1993) to the PIR data bank.
DR PIR; PS0210; PS0210.
DR Gramene; Q7M281; -.
FT NON_TER 1 1
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1579 MW; DAC3ABBA6B47CAC CRC64;

Query Match 25.7%; Score 27; DB 2; Length 16;
Best Local Similarity 42.9%; Pred. No. 5.3e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 9 PGFIGVE 15
DB 1 PGLVIGD 7

RESULT 11

Q9T204_BRANA PRELIMINARY; PRT; 16 AA.
ID Q9T204_BRANA
AC Q9T204;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Chaperonin-60 Ls3 fragment (Fragment).
OS Brassica napus (Rape).
OC Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucotids 11; Brassicales; Brassicaceae; Brassica.
NCBI_TaxID=3708;
[1]

PROTEIN SEQUENCE:
RX MEDLINE=96302168; PubMed=7913238; DOI=10.1104/pp.105.1.233;
RA Cloney L.P., Bekkaoui D.R., Feist G.V., Lane W.S., Hemmingsen S.M.;
RT "Brassica napus plastid and mitochondrial chaperonin-60 proteins
contain multiple distinct polypeptides.";
RL Plant Physiol. 105:233-241(1994).
FT NON_TER 1 1
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1901 MW; CFAE799B7C938063 CRC64;

Query Match 25.7%; Score 27; DB 2; Length 16;
Best Local Similarity 42.9%; Pred. No. 5.3e+03;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 3 AKGMSPPGFIGVE 16
DB 3 ARGYSPPYFIDDK 16

RESULT 12
Q9N195_BOVIN PRELIMINARY; PRT; 19 AA.
ID Q9N195_BOVIN
AC Q9N195;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE Parvalbumin (Fragment).
OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
[1]

NUCLEOTIDE SEQUENCE:
RX MEDLINE=21599054; PubMed=11736808;
RA Ariza F., Harrison B., Drinkwater R.D.;
RT "The assignment by linkage mapping of four genes from human chromosome 22 to bovine chromosome 5 and 17.";
RL Anim. Genet. 32:371-374(2001).
DR EMBL; AF217654; AAF26420.1; -; Genomic_DNA.
FT NON_TER 1 1
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2151 MW; D5EA9D89BC3EE951 CRC64;

Query Match 25.7%; Score 27; DB 2; Length 19;
Best Local Similarity 71.4%; Pred. No. 6.4e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 KGMSPPG 10
DB 5 KGFSPPG 11

RESULT 13

Q95554_MOUSE PRELIMINARY; PRT; 21 AA.
ID Q95554_MOUSE
AC Q95554;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Major histocompatibility complex antigen H-2Kd29 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]

NUCLEOTIDE SEQUENCE:
RC TISSUE=Liver;
RX MEDLINE=21891563; PubMed=11894963;
RA Weiss E., Golden L., Zakut R., Mellor A., Fahrner K., Kvist R.,
RA Flavell R.A.;
RT "The DNA sequence of the H-2Kb gene: Evidence for gene conversion as a
mechanism for the generation of polymorphism in histocompatibility
antigens.";
RL EMBL J. 2:453-462(1983).
[2]

NUCLEOTIDE SEQUENCE:
RC TISSUE=Liver;
RX MEDLINE=92013151; PubMed=1717590;
RA Horton R.M., Loveland B.E., Parwani A., Pease L.R., Lindahl K.F.;
RT "Characterization of the spontaneous mutant H-2Kd29 indicates that
gene conversion in H-2 occurs at a higher frequency than detected by
skin grafting.";
RL J. Immunol. 147:3180-3184(1991).
DR EMBL; M34542; AAA39607.1; -; mRNA.
FT NON_TER 1 1
FT NON_TER 21 21
SQ SEQUENCE 21 AA; 2366 MW; 103EC45620595224 CRC64;

Query Match 25.7%; Score 27; DB 2; Length 21;

Thu Jan 26 10:50:48 2006

Best Local Similarity 40.0%; Pred. No. 7.1e+03;
Matches 8; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

Qy 1 DPAKMSPPRIVEEGULS 20
Db 5 DPARLQP-----ERGLS 18

RESULT 14

BRK1_RANNI STANDARD; PRT; 9 AA.
AC Q7L254;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Bradykinin-like peptide 1.
OS Rana nigromaculata (Japanese pond frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana;
OC Pelophylax.
OX NCBI_TaxID=8409;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=68412013; PubMed=5677638;
RA Nakajima T.;
RT "Occurrence of a new active peptide on smooth muscle and bradykinin in the skin of Rana nigromaculata hallowell.",
RL Chem. Pharm. Bull. 16:769-770(1968).
CC -1- FUNCTION: Induces smooth muscle contraction.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the bradykinin family.

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DR PIR; A61358; A61358.
KW Bradykinin; Direct protein sequencing; Vasoactive; Vasodilator.
SQ SEQUENCE 9 AA; 1017 MW; 3687D771A9C86777 CRC64;

Query Match 24.8%; Score 26; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PPGF 11
Db 2 PPGF 5

RESULT 15

KNL3_BOMVA STANDARD; PRT; 9 AA.
AC P83058;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE [Thr6]bradykinin.
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archaeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=8348;
RN [1]
RP PROTEIN SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RX MEDLINE=22217713; PubMed=12230583;
RA Chen T., Orr D.F., Bjournson A.J., McClean S., O'Rourke M., Hirst D.G., Rao P., Shaw C.;
RT "Novel bradykinins and their precursor cDNAs from European yellow-bellied toad (Bombina variegata) skin.",
RL Eur. J. Biochem. 269:4693-4700(2002).

CC -1- FUNCTION: Produces in vitro relaxation of rat arterial smooth muscle and constriction of intestinal smooth muscle.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Expressed by the skin glands.

CC -1- SIMILARITY: Belongs to the bradykinin family.

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KW Amphibian defense peptide; Bradykinin; Direct protein sequencing; Vasoactive; Vasodilator.
SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;

Query Match 24.8%; Score 26; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PPGF 11
Db 2 PPGF 5

RESULT 16

KNL3_CYPDO STANDARD; PRT; 9 AA.
AC P83659;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE [Thr6]bradykinin.
OS Cyphononyx dorsalis (Spider wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Pompilidae; Cyphononyx.
OX NCBI_TaxID=246266;
RN [1]
RP PROTEIN SEQUENCE, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS SPECTROMETRY.
RX MEDLINE=21203862; PubMed=11306139; DOI=10.1016/S0041-0101(00)00262-2;
RA Kono K., Hisada M., Naoki H., Itagaki Y., Yasuhara T., Tulliano M.A., Tulliano L., Palma M.S., Yamane T., Nakajima T.;
RT "Isolation and sequence determination of peptides in the venom of the spider wasp (Cyphononyx dorsalis) guided by matrix-assisted laser desorption/ionization time of flight (MALDI-TOF) mass spectrometry.",
RT Toxicon 39:1257-1260(2001).

CC -1- FUNCTION: Produces in vitro relaxation of rat arterial smooth muscle and constriction of intestinal smooth muscle (By similarity).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.

CC -1- MASS SPECTROMETRY: MW=1074.58; METHOD=MALDI; RANGE=1-9; NOTE=Ref.1.

CC -1- SIMILARITY: Belongs to the bradykinin family.

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DR GO: GO:0005615; C:extracellular space; IDA.

DR GO: GO:0045776; P:negative regulation of blood pressure; ISS.

DR GO: GO:0045987; P:positive regulation of smooth muscle contra. . .; ISS.

KW Bradykinin; Direct protein sequencing; Vasoactive; Vasodilator.
SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;

Query Match 24.8%; Score 26; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PGPF 11
 ||||
 DB 2 PGPF 5

RESULT 17

ID P84497 TRASC PRELIMINARY; PRT; 9 AA.
 AC P84497;
 DT 10-MAY-2005 (TREMBLrel. 30, Created)
 DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
 DE [Thr6]bradykinin.
 OS Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Testudines; Cryptodira; Testudinoidae; Emydidae; Trachemys.
 OX NCBI_TaxID=34903;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX PubMed=2298179;
 RA Conlon J.M., Hicks J.W., Smith D.D.;
 RT "Isolation and biological activity of a novel kinin
 [Thr(6)]bradykinin) from the turtle, Pseudemys scripta.";
 RL Endocrinology 126:985-991(1990).
 KW Direct protein sequencing.
 SO SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;

Query Match 24.8%; Score 26; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PGPF 11
 ||||
 DB 2 PGPF 5

RESULT 18

ID Q7LZ50 CHICK PRELIMINARY; PRT; 9 AA.
 AC Q7LZ50;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Ornitho-kinin.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=90102072; PubMed=2603803;
 RA Kimura M., Sueyoshi T., Morita T., Tanaka K., Iwanaga S.;
 RT "Ornitho-kininogen and ornitho-kinin: isolation, characterization and
 chemical structure.";
 RL Adv. Exp. Med. Biol. 247A:359-367(1989).
 DR PIR; B60246; B60246.
 SO SEQUENCE 9 AA; 1040 MW; 339D3771A9C86777 CRC64;

Query Match 24.8%; Score 26; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PGPF 11
 ||||
 DB 2 PGPF 5

RESULT 19
 Q7LZJ8 RANTE
 ID Q7LZJ8 RANTE PRELIMINARY; PRT; 9 AA.
 AC Q7LZJ8;

DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Bradykinin.
 OS Rana temporaria (European common frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana;
 OC Rana.
 OX NCBI_TaxID=8407;
 RN [1]
 RP PROTEIN SEQUENCE.
 RA Anastasi A., Erspamer V., Bertaccini G.;
 RT "Occurrence of bradykinin in the skin of Rana temporaria.";
 RL Comp. Biochem. Physiol. 14:43-52(1965).
 DR PIR; A61363; A61363.
 SO SEQUENCE 9 AA; 1060 MW; 339D75B9C86777 CRC64;

Query Match 24.8%; Score 26; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 20

ID Q7LZ17 9NEOB PRELIMINARY; PRT; 9 AA.
 AC Q7LZ17;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Hydroxyproline-3-bradykinin.
 OS Heleophryne purcellii (Cape ghost frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Heleophrynidae;
 OC Heleophryne.
 OX NCBI_TaxID=31911;
 RN [1]
 RP PROTEIN SEQUENCE.
 RA Nakajima T., Yasuhara T., Erspamer G.F., Visser J.;
 RT "Occurrence of Hyp(3)-bradykinin in methanol extracts of the skin of
 the South African leptodactylid frog Heleophryne purcellii.";
 RL Experientia 35:1133-1133(1979).
 RN [2]
 RP PROTEIN SEQUENCE.
 RX PubMed=488255;
 RA Nakajima T., Yasuhara T., Erspamer G.F., Visser J.;
 RT "Occurrence of Hyp3-bradykinin in methanol extracts of the skin of the
 South African leptodactylid frog Heleophryne purcellii.";
 RL Experientia 35:1133-0(1979).
 DR PIR; A43065; A43065.
 SO SEQUENCE 9 AA; 1060 MW; 339D75B9C86777 CRC64;

Query Match 24.8%; Score 26; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PGPF 11
 ||||
 DB 2 PGPF 5

RESULT 21

BRKP_PHYRO
 ID BRKP_PHYRO STANDARD; PRT; 11 AA.
 AC Q7LZ52;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Phyllokinin (Bradykinyl-isoleucyl-tyrosine O-sulfate).
 OS Phylomedusa rohdei (Rohde's leaf frog).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 CC Phyllomedusinae; Phyllomedusa.
 CC NCBI_TaxID=8394;
 CC
 CC [1]
 CC PROTEIN SEQUENCE AND SULFATION OF TYR-11.
 CC MEDLINE=67179312; PubMed=5970899;
 CC RA Anastasi A., Bertaccini G., Erspamer V.;
 CC RT "Pharmacological data on phyllokinin (bradykinin-1-isoleucyl-L-tyrosine O-
 CC sulphate) and bradykinin-1-isoleucyl-L-tyrosine";
 CC RL Br. J. Pharmacol. 27:479-485(1966).
 CC
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC
 CC -1- SIMILARITY: Belongs to the bradykinin family.
 CC
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 CC removed.
 CC
 CC DR PIR: A61365.
 CC KM Bradykinin; Direct protein sequencing; Sulfation; Vasoactive;
 CC KW Vasodilator.
 CC FT MOD_RES 11 Sulfotyrosine.
 CC SQ SEQUENCE 11 AA; 1337 MW; 25051393D75B9C8 CRC64;
 CC
 CC Query Match 24.8%; Score 26; DB 1; Length 11;
 CC Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 8 PGPF 11
 CC [1]
 CC [1]
 CC [1]
 CC Db 2 PGPF 5

RESULT 22
 BRK_MEGFL STANDARD; PRT; 11 AA.
 AC P12797;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Megascollakinin ([Thr6]bradykinin-Lys-Ala) [Contains: Bradykinin-like
 DE peptide ([Thr6]bradykinin)].
 OS Megascollia flavifrons (Garden dagger wasp) (Solitary wasp).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pelegrypoda;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Scolidae; Megascollia.
 CC NCBI_TaxID=7437;
 CC RN [1]
 CC RP PROTEIN SEQUENCE.
 CC RC TISSUE=Venom;
 CC RA MEDLINE=87293024; PubMed=3617088; DOI=10.1016/0041-0101(87)90288-1;
 CC Yashuara T., Mantel P., Nakajima T., Plek T.;
 CC RT "Two kinds isolated from an extract of the venom reservoirs of the
 CC solitary wasp Megascollia flavifrons";
 CC RL Toxicon 25:527-535(1987).
 CC
 CC [2]
 CC PROTEIN SEQUENCE.
 CC RC TISSUE=Venom;
 CC RA Nakajima T., Plek T., Yashuara T., Mantel P.;
 CC RT "Two kinds isolated from the venom of Megascollia flavifrons";
 CC RL Toxicon 26:34-34(1988).
 CC
 CC -1- FUNCTION: Both proteins have bradykinin-like, although lower
 CC activities (e.g. smooth muscle contraction).
 CC -1- SUBCELLULAR LOCATION: Secreted; venom reservoirs.
 CC
 CC -1- SIMILARITY: Belongs to the bradykinin family.
 CC
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 CC removed.

CC
 CC PIR: A26744; A26744.
 CC DR PIR: B26744; B26744.
 CC DR GO: GO:0005615; C:extracellular space; IDA.
 CC DR GO: GO:0045776; P:negative regulation of blood pressure; ISS.
 CC DR GO: GO:0045987; P:positive regulation of smooth muscle contra. TAS.
 CC KW Bradykinin; Direct protein sequencing; Vasoactive; Vasodilator.
 CC FT PEPTIDE 11
 CC SEQUENCE 11 AA; 1274 MW; 33867393D771A9C8 CRC64;
 CC
 CC Query Match 24.8%; Score 26; DB 1; Length 11;
 CC Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 8 PGPF 11
 CC [1]
 CC [1]
 CC [1]
 CC Db 2 PGPF 5

RESULT 23
 075811_HUMAN PRELIMINARY; PRT; 11 AA.
 ID 075811;
 AC 075811;
 DT 01-NOV-1998 (TRENBLUREL. 08, Created)
 DT 01-NOV-1998 (TRENBLUREL. 08, Last sequence update)
 DT 01-NOV-1998 (TRENBLUREL. 08, Last annotation update)
 DE ETD-3 R2 (Fragment).
 OS Homo sapiens (Human).
 CC Name=c-erbB-3;
 CC NCBI_TaxID=9606;
 CC RN [1]
 CC RP NUCLEOTIDE SEQUENCE.
 CC RC TISSUE=Ovarian carcinoma;
 CC RX MEDLINE=98345147; PubMed=9681822; DOI=10.1038/sj.onc.1201866;
 CC RA Lee H., Mainle N.J.;
 CC RT "Isolation and characterization of four alternate c-erbB3 transcripts
 CC expressed in ovarian carcinoma-derived cell lines and normal human
 CC tissues";
 CC RL Oncogene 16:3243-3252(1998).
 CC FT EMBL, U88358; AAC39858.1; -. mRNA.
 CC NON_TIR 1
 CC SQ SEQUENCE 11 AA; 1017 MW; 21B236366EB72878 CRC64;
 CC
 CC Query Match 24.8%; Score 26; DB 2; Length 11;
 CC Best Local Similarity 40.0%; Pred. No. 5.1e+03;
 CC Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 CC
 CC QY 1 DPAKMSPPG 10
 CC [1]
 CC [1]
 CC [1]
 CC Db 1 EPCGGCPCPG 10

RESULT 24
 07M4P1_HUMAN PRELIMINARY; PRT; 11 AA.
 ID 07M4P1;
 AC 07M4P1;
 DT 01-MAR-2004 (TRENBLUREL. 26, Created)
 DT 01-MAR-2004 (TRENBLUREL. 26, Last sequence update)
 DT 01-MAR-2004 (TRENBLUREL. 26, Last annotation update)
 DE Ile-Ser-Bradykinin (Fragment).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 CC Homo.
 CC NCBI_TaxID=9606;
 CC RN [1]
 CC RP PROTEIN SEQUENCE.
 CC RX MEDLINE=9116748; PubMed=2076202;
 CC Wunderer G., Walter I., Eschenbacher B., Lang M., Kellermann J.,

RA Kindermann G.;
 RT "Ile-ser-bradykinin is an aberrant permeability factor in various
 RL human malignant effusions.";
 DR Biol. Chem. Hoppe-Seyler 371:977-981(1990).
 PIR; S13279; S13279.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1260 MW; 33D55258B9C86777 CRC64;

Query Match 24.8%; Score 26; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PPGF 11
 ||||
 Db 4 PPGF 7

RESULT 25

VESP_VESMA STANDARD; PRT; 12 AA.
 ID_VESP_VESMA Q7M3T3;
 AC 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Vespakinin M.
 OS Vespina mandarina (Hornet).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespidae;
 OC Vespidae; Vespinae; Vespa.
 OX NCBI_TaxID=7446;
 RN [1]
 RP PROTEIN SEQUENCE, AND HYDROXYLATION.
 RC TISSUE=Venom;
 RX MEDLINE=77114342; PubMed=1017116;
 RA Kishimura H., Yasuhara T., Yoshida H., Nakajima T.;
 RT "Vespakinin-M, a novel bradykinin analogue containing hydroxyproline,
 in the venom of Vespa mandarina Smith.";
 RL Chem. Pharm. Bull. 24:2896-2897(1976).
 CC -! FUNCTION: Bradykinins are a potent but short-lived agent of
 arteriolar dilation and increased capillary permeability (By
 similarity).
 CC -! SUBCELLULAR LOCATION: Secreted; venom reservoirs.
 CC -! SIMILARITY: Belongs to the bradykinin family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC PIR; A61360; A61360.
 KW Bradykinin; Direct protein sequencing; Hydroxylation; Vasoactive;
 KW Vasodilator.
 FT MOD_RES 4 4 4-hydroxyproline.
 SQ SEQUENCE 12 AA; 1346 MW; 34F513C44C75B9C8 CRC64;

Query Match 24.8%; Score 26; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 5.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PPGF 11
 ||||
 Db 3 PPGF 6

Search completed: January 26, 2006, 08:04:04
 Job time : 61.4828 secs